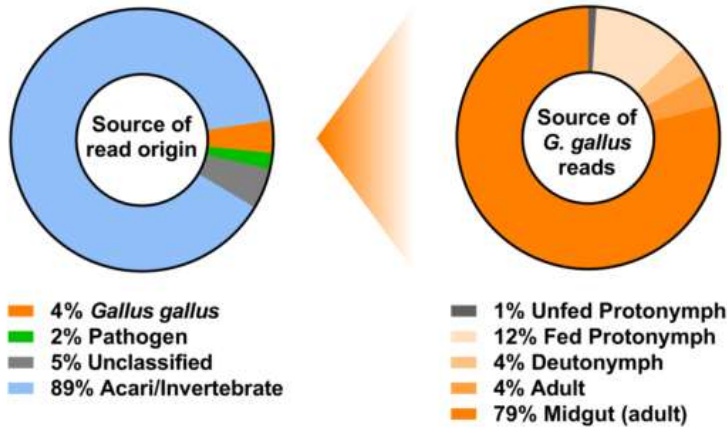


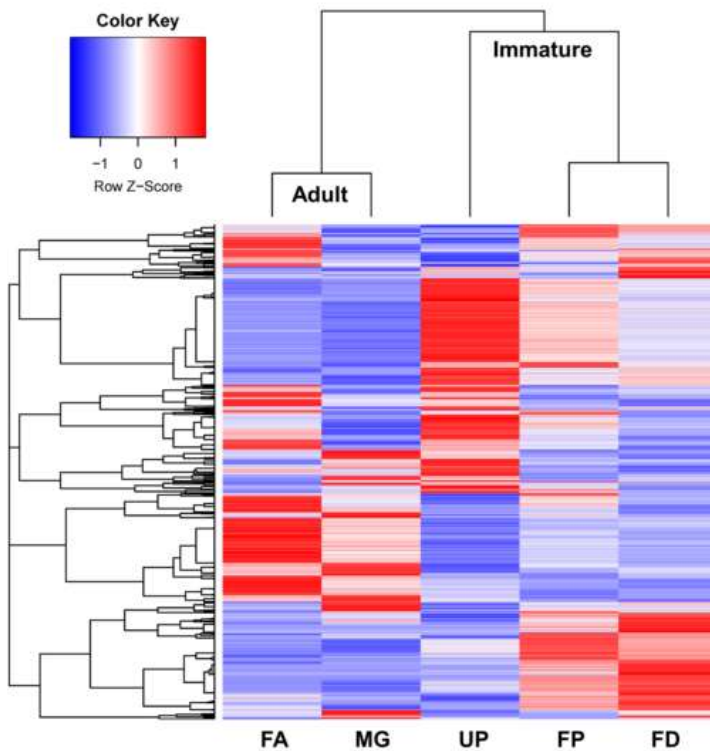
Supplementary information (Figures and Tables)

Supplementary Fig. S1:

a

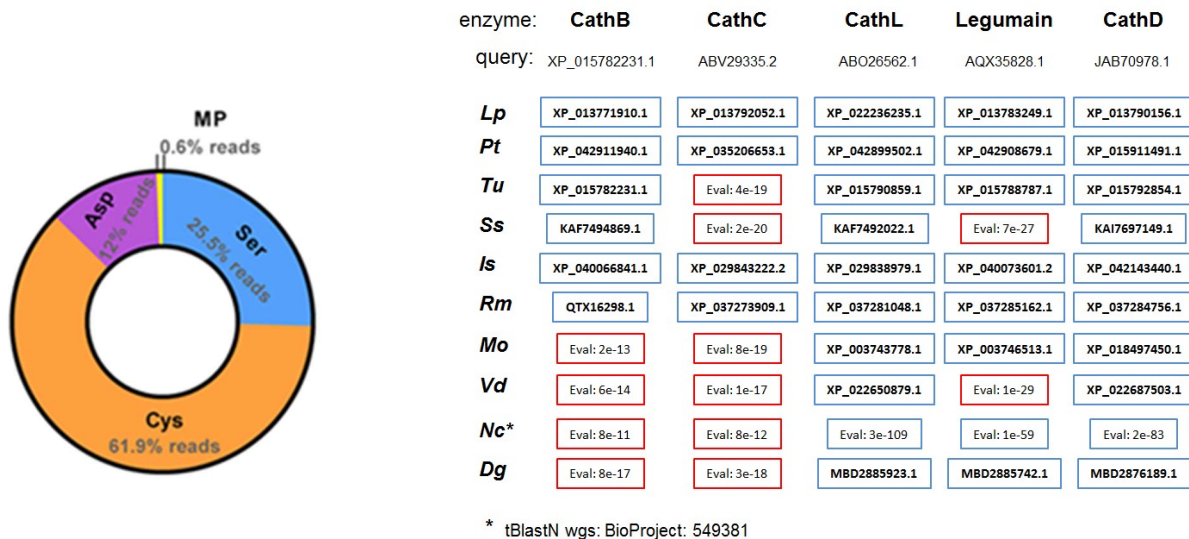


b



Supplementary Figure S1. a Attributed origin of the reads, from all libraries, according to the matched organism (left pie chart). The library origin of the chicken (*Gallus gallus*)-derived contigs is shown in the right pie chart. **b** Heat map for 12,484 selected transcripts showing diversity of transcripts expressions among studied libraries. UP - unfed protonymph, FP - fed protonymph, FD - fed deutonymph, FA - fed adult, MG - midgut.

Supplementary Fig. S2:

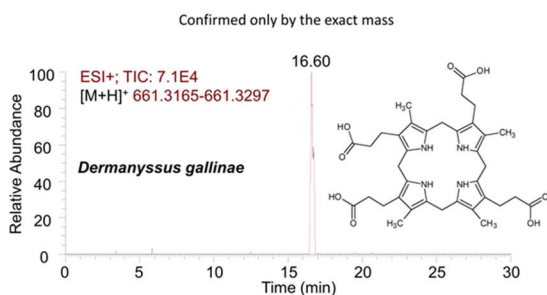


Supplementary Figure S2. Left: A pie chart of the partition of individual protease families identified in the *D. gallinae* transcriptome; Asp, Cys, Ser, MP - Aspartyl, Cysteine, Serine proteases, and Metalloproteases. Right: BlastP results of known cysteine and aspartic proteases against selected Chelicerates with a specific focus on Acari species. Accession IDs of homologues identified, as well as query sequences used, presented in Figure 3a are shown here. *Lp*, *Limulus polyphemus*; *Pt*, *Parasteatoda tepidariorum* (a representative of Araneae); *Tu*, *Tetranychus urticae*; *Ss*, *Sarcoptes scabiei*; *Is*, *Ixodes scapularis*; *Rm*, *Rhipicephalus microplus*; *Mo*, *Metaseiulus occidentalis*; *Vd*, *Varroa destructor*; *Nc*, *Neoseiulus cucumeris*; *Dg*, *Dermanyssus gallinae*.

Supplementary Fig. S3:

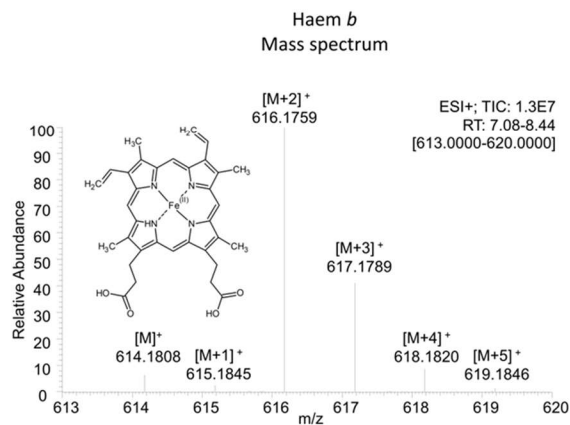
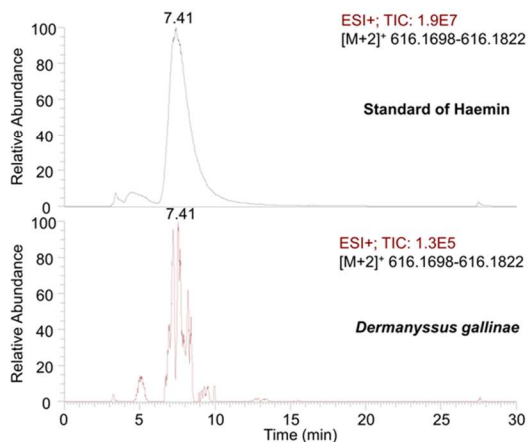
a

Coproporphyrinogen III



b

Haem *b*



Supplementary Figure S3. a The reconstructed chromatogram for Coproporphyrinogen III [M+H]⁺ 661.3165-661.3297 for *Dermanyssus gallinae* samples, confirmed only by the exact mass. **b** The reconstructed chromatogram for Haem *b* [M+2]⁺ 616.1698-616.1822, first for standard (Haemin) and second for *Dermanyssus gallinae* sample and mass spectrum of Haemin for explanation of diagnostic mass [M+2]⁺.

Supplementary Fig. S4:

Dg Ferritin 1 - intracellular

gctcoggttagccttg
 ttaacgactgaactcagcattatcatcgtgataccaccgaagagacggcctgaagctgcc
 caggaagattaaactgccttcaactgagtagtgcaacagcctgtogttggtgaccaaggt
 tctcaagttccttctgtctagcgttgctgtgttctgagccgcttaccgcgaccocaa
 atgtcagccgctgcgctcccccgcagaacttccacgctgattgogaggatgcaatcaac
 M S T A S R P R Q N F H A D C E D A I N
 aagcaaatcaacatggagctcagcgcctcctacgtctacatgctgatggccttctaactc
 K Q I N M E L Y A S Y V Y M S M G F Y F
 gatcgtgatgacgtgggttcaagaacgtgaagaagttttcttaagcttctgaggag
 D R D D V A F K N V K K F F L K A S E E
 gagagggaaacacgcatgaagctcagctcaccagaatagcggcggagcgaattgtg
 E R E H A M K L M S Y Q N M R G G R I V
 ctgcagcctgtggctaaagcgggaacgagatgagtgggattcttaccagcagcttttgag
 L Q P V A K P E R D E W D S I Q Q A F E
 tcggccatcgaacttgagaaaaaggtcaacgagagctgctggaatccacaagatcgcc
 S A I E L E K K V N E S L L N I H K I A
 agtgatcagcggagccagcttctgcgactcctcagacacactaccttgaggaacag
 S D H A D A Q F C D F L E T H Y L E E Q
 gtgaaatcagcgaagcagctgctgatacaccagaacattacgcgctcggcagtgcc
 V K S I K Q L S D H I T N I I R V G S G
 ctgcggaggttcaatcacaagagctcggcagcagctaa
 L G E F I F N K E L G D D -

Dg Ferritin 2 - secretory

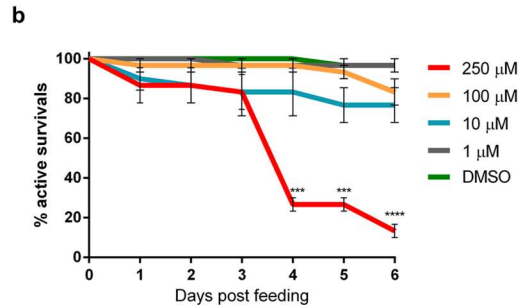
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 M K R L V C I L V P L L F A A V L A R Q
 gattcctctgtgtggttcacagggcttagcggggctggcaaaaaggcgaaccagctgat
 D S S V W F T G L S G A G K K A N Q A D
 gctgtgagactcaaacgcgctcctagggctgtagataatgccaccoccatcgggcaatcg
 A V R L K R A P R A V D N A T P S G N T
 aacaaatcagctgctcagggacagctgtctgggggcttgcgagccacagctaaacctcgag
 N K Y V L E D S C L G G L R A Q L N L E
 atgcagcctcgtcctcctaccaacagatggccgcacactttgactccaaccaggttgcc
 M H A S L L Y Q Q M A A H F D S N Q V A
 cacaagggctcgtcgaagtcttcgagaagagttcggagcagggagcgtgagcaacggaag
 H K G F A K F F E K S S D E E R E H A K
 aaaatcacaactacattaacgcagctggcggcaccatcggccatctcaacatacggatg
 K I T N Y I N A R G G T I G H L N I R M
 ccgagtcocaaactcagggatagcggcaaaaagggccctcgaagcgccttagtctcogag
 P S S N S W D T A K E A L Q A A L V L E
 catcagctcaacaacgagttgcaacttctccacagaacggcgcagggagctgctgat
 H H V N N E L H L L H R T A D E D C R D
 cccagttgcaggactcttagagagcaactcctcagcagcaggtggaatccatcogct
 P Q L Q D F L E S N F L S E Q V E S I A
 cagatgagcgtttgataacgaacctcaacaagttcgggtgagtgatctcggagaatac
 Q I E R L I T N L N K F G D V H L G E Y
 tttgtcaacaaggaccatctctag
 F V N K D H L -

Supplementary Figure S4. Intracellular and secretory ferritins from *D. gallinae* – cDNA and deduced amino-acid sequences. Putative Iron-Responsive-Element in *D. gallinae* 5' UTR of Ferritin 1 transcript: Green, the “head” part of the stem-loop structure; violet, complementary bases forming the stem; Signal peptide of secretory ferritin 2 is highlighted in yellow.

Supplementary Fig. S5:

a

libraries	Unfed Prototymph	Fed Prototymph	Fed Deutonymph	Fed Adult	Midgut (adult)	overview	Protein Link	Protein ID
Complex								
<i>mTOR</i>	19.5	17.1	14.6	14.8	9.7		Dg-569977_FR6_51-2668	MBD2884038.1
<i>Raptor</i>	29.2	18.1	12.4	14.7	8.3		Dg-679943_FR5_1-1337	MBD2889451.1
<i>Rictor</i>	15.8	16.6	13.3	9.6	8.7		I-SigP-380157_FR2_397-1973	MBD2888345.1
Interactors								
<i>raga</i>	48.5	45.6	38.4	74.1	91.1		Dg-407637_FR2_180-488	MBD2884893.1
<i>ragc</i>	60.2	58.7	70.6	94.8	123.5		I-SigP-551279_FR5_1238-1718	MBD2875944.1
Substrates								
<i>S6K</i>	74.3	77.4	81.9	78.3	80.1		Dg-361189_FR3_761-1234	MBD2877919.1
<i>4E-BP</i>	950.0	261.7	150.7	283.9	169.6		Dg-409360_FR3_337-498	MBD2883246.1
<i>AKT</i>	92.6	68.2	61.7	66.3	44.6		Dg-369246_FR2_19-555	MBD2884288.1
IIS								
<i>InR</i>	30.2	24.3	22.0	17.9	9.2		Dg-656129_FR5_567-2204	MBD2883038.1
<i>Ilp4</i>	38.4	24.3	25.9	7.9	2.6		I-SigP-1069941	MBD2883068.1
<i>Ilp7</i>	108.4	50.3	24.3	4.5	1.1		I-SigP-787143	MBD2882243.1
<i>Insulinase</i>	92.0	110.5	86.3	127.4	137.4		I-SigP-393788	MBD2890617.1



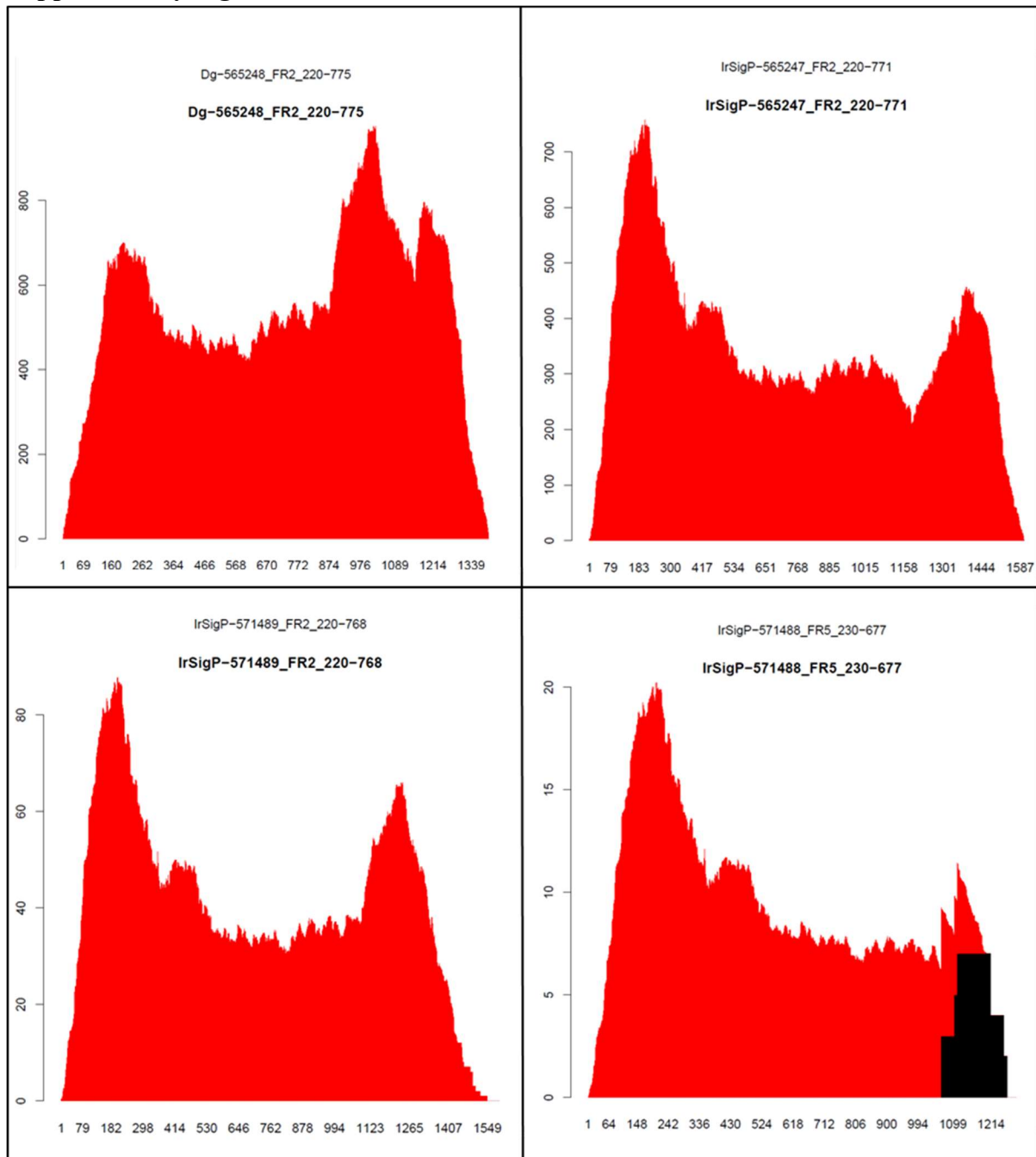
Supplementary Figure S5. Overview of transcripts encoding proteins implicated in nutrient status signaling pathways. IIS, insulin/IGF signaling; InR, insulin receptor; Ilp, insulin-like peptide. **a** Mapping of nutrient sensing and storage, and TOR-mediated signaling pathway in *D. gallinae* developmental stages, using *Caenorhabditis elegans* homologues, FPKMs and accession numbers are shown. **b** Survival plot of mites exposed to Torin2 inhibitor, through an *ex vivo* membrane feeding system. Each value is derived from 10 engorged mites in the feeding chamber; Mean and SEM from three independent chambers are shown from two independent experiments. Statistical t-test indicate *** p = 0.0001 and **** p < 0.0001.

Supplementary Fig. S6:

Signal peptide										
MBD2887064	MSVNIQNAL	SAMYILLGTI	LLGSATVLA	ALSPNHHKQ	QMQEFAQVSS	PSLYQQPLPL	PQAIRGKPKS			70
MBD2876840	MSVNIQNAL	SAMYILLGTI	LLGSATVLA	ALSPNHHKQ	QMQEFAQVSS	PSLYQQPLPL	PQAIRGKPKS			
MBD2886266	MSVNIQNAL	SAMYILLGTI	LLGSATVLA	ALSPNHHKQ	QMQEFAQVSS	PSLYQQPLPL	PQAIRGKPKS			
MBD2879406	MSVNIQNAL	SAMYILLGTI	LLGSATVLA	ALSPNHHKQ	QMQEFAQVSS	PSLYQQPLPL	PQAIRGKPKS			
NP_507090.	MATWIVGKLI	IASLLLGIA	QQARTKSQDI	FEDDNDNGTT	TLESARLTS	P-----	-----			
NP_491470.	-----	-----	-----	-----	-----	-----	-----			
MBD2887064	--MTSDKEGK	ANFRAIEKRI	LDSIIGVGRY	DSRIRPMGIN	N-TDGPALVR	VNIYIRSIGK	IDDVIMEYTV			140
MBD2876840	PYMTSDKEGK	ANFRAIEKRI	LDSIIGVGRY	DSRIRPMGIN	N-TDGPALVR	VNIYIRSIGK	IDDVIMEYTV			
MBD2886266	PYMTSDKEGK	ANFRAIEKRI	LDSIIGVGRY	DSRIRPMGIN	N-TDGPALVR	VNIYIRSIGK	IDDVIMEYTV			
MBD2879406	PYMTSDKEGK	ANFRAIEKRI	LDSIIGVGRY	DSRIRPMGIN	N-TDGPALVR	VNIYIRSIGK	IDDVIMEYTV			
NP_507090.	--IHIPIEQP	Q---TSDSKI	LAHLFTSG-Y	DFRVRPPTDN	G---GPVVVS	VNMLLRTISK	IDDVIMMEYSA			
NP_491470.	--VVTVNGEYS	M---QSEQEI	LNALLKN--Y	DMRVRPPPAN	SSTEGAVNVR	VNIMIRMLSK	IDDVIMMEYSI			
MBD2887064	QLTFRQQWRD	ERLQYDDLG-	--GQIRYLTL	TDQKKLWQPD	LFFSNEKEGH	LHQIIVPNVL	LRIYPNGDVL			210
MBD2876840	QLTFRQQWRD	ERLQYDDLG-	--GQIRYLTL	TDQKKLWQPD	LFFSNEKEGH	LHQIIVPNVL	LRIYPNGDVL			
MBD2886266	QLTFRQQWRD	ERLQYDDLG-	--GQIRYLTL	TDQKKLWQPD	LFFSNEKEGH	LHQIIVPNVL	LRIYPNGDVL			
MBD2879406	QLTFRQQWRD	ERLQYDDLG-	--GQIRYLTL	TDQKKLWQPD	LFFSNEKEGH	LHQIIVPNVL	LRIYPNGDVL			
NP_507090.	QLTLRESWID	KRLSYGVKGD	GQPD--FVIL	TVGHQIWMPD	TFFPNEKQAY	KHTIDKPNVL	IRIHNDGTVL			
NP_491470.	QLTFREQWID	PRLAYENLGF	YNPPAFLTVP	HVKKSLWIPD	TFFPTEKAAH	RHLIDMENMF	LRIYDPGKIL			
Cys loop										
MBD2887064	FSIRISLVLS	CPMNLKFYPL	DKQICISILMA	SYGYTTEDLV	FLWKEGDPVQ	VTKNLH--LP	RFTLER-FNT			280
MBD2876840	FSIRISLVLS	CPMNLKFYPL	DKQICISILMA	SYGYTTEDLV	FLWKEGDPVQ	VTKNLH--LP	RFTLER-FNT			
MBD2886266	FSIRISLVLS	CPMNLKFYPL	DKQICISILMA	SYGYTTEDLV	FLWKEGDPVQ	VTKNLH--LP	RFTLER-FNT			
MBD2879406	FSIRISLVLS	CPMNLKFYPL	DKQICISILMA	SYGYTTEDLV	FLWKEGDPVQ	VTKNLH--LP	RFTLER-FNT			
NP_507090.	YSVRIISLVLS	CPMYLQYYPM	DVQCCSIDLA	SYAYTTKDIE	YLWKEHSPLQ	LKVGLSSSLP	SFQLTN-TST			
NP_491470.	YSSRISLTSS	CPMRLLQLYPL	DVQSCNFDLV	SYAHTMNDIM	YEWDPSTPVQ	LKPGVGSLLP	NFILKNYTN			
out TM1 in TM2										
MBD2887064	DYCTSRLNTG	EYSCLKVDLV	FKREFSYyli	QIYIPCCMLV	VVSWSEWLD	PTSI PARVS L	GVTTLTMTAT			350
MBD2876840	DYCTSRLNTG	EYSCLKVDLV	FKREFSYyli	QIYIPCCMLV	VVSWSEWLD	PTSI PARVS L	GVTTLTMTAT			
MBD2886266	DYCTSRLNTG	EYSCLKVDLV	FKREFSYyli	QIYIPCCMLV	VVSWSEWLD	PTSI PARVS L	GVTTLTMTAT			
MBD2879406	DYCTSRLNTG	EYSCLKVDLV	FKREFSYyli	QIYIPCCMLV	VVSWSEWLD	PTSI PARVS L	GVTTLTMTAT			
NP_507090.	TYCTSRLNTG	IYSLRRTTIQ	LKREFSYyli	QIYIPCCMLV	IVSWSEWLD	RTAI PARVT L	GVTTLTMTA			
NP_491470.	ADCTSRLNTG	SYGCLRMQLL	FKRQFSYyLV	QLYAPTTMIV	IVSWSEWLD	LHSTACRVAL	GVTTLTMTT			
TM3										
MBD2887064	QISGINASLP	PVSYTKAIDV	WTGVCILTFVF	GALLEEALVN	YASRSQRRQ	NIHKQSVPA	SQQRQKLLP			420
MBD2876840	QISGINASLP	PVSYTKAIDV	WTGVCILTFVF	GALLEEALVN	YASRSQRRQ	NIHKQ---	A SQQRQKLLP			
MBD2886266	QISGINASLP	PVSYTKAIDV	WTGVCILTFVF	GALLEEALVN	YASRSQRRQ	NIHKQSVPA	SQQRQKLLP			
MBD2879406	QISGINASLP	PVSYTKAIDV	WTGVCILTFVF	GALLEEALVN	YASRSQRRQ	NIHKQ---	-----			
NP_507090.	QAGINSQLP	PVSYTKAIDV	WLGACQTFVF	GALLEEALVN	HIANKQGVSR	KARTE---	-----			
NP_491470.	MQSAINAKLP	PVSYVKWVDV	WLGACQTFVF	GALLEEAFVS	YQDSVRQNDR	SREKA---	-----			
MBD2887064	ASIAAAGLEN	NQSAIDHCDE	AFAMPFQGS	AERGGMARNA	LPNDADILVP	RQRHTAPPQ	EIROQCEVHMK			490
MBD2876840	ASIAAAGLEN	NQSAIDHCDE	AFAMPFQGS	AERGGMARNA	LPNDADILVP	RQRHTAPPQ	EIROQCEVHMK			
MBD2886266	ASIAAAGLEN	NQSAIDHCDE	AFAMPFQGS	AERGGMARNA	LPNDADILVP	RQRHTAPPQ	EIROQCEVST			
MBD2879406	-----	-----	-----	-----	-----	-----	-----VCIT			
NP_507090.	-----	-----	-----	-----	-----	-REKAEIPLL	QNLHNDVPTK	VFNQEEKVRT		
NP_491470.	-----	-----	-----	-----	-----	-ARKAQR--R	REKLEMVDAE	VYQPCTCHT		
in TM4 out										
MBD2887064	GPSSTSSNLC	RSWLSRFPT	S---KRIDV	ISRIFFPIMF	ALFNLVYWT	YLFREDAD--	-----			555
MBD2876840	GPSSTSSNLC	RSWLSRFPT	S---KRIDV	ISRIFFPIMF	ALFNLVYWT	YLFREDAD--	-----			
MBD2886266	SPRQHTALFC	CLIIYNYFTG	N---SDLIV	NSVLKVNIIF	RMS---WQL	AIIGT---	-----			
MBD2879406	CSYTNLSLVV	LVFLYIILQS	Y---STINL	N-----	-----	-----	-----			
NP_507090.	VPLNRRQMS	FINLLETKTE	WINDISKRVDL	ISRALEFPVLF	FVFNILYWS-	-----RFGQ	QNVLF			
NP_491470.	FEA-RETFRD	KVRRYFTKPD	Y--LPKIDF	YARFVVPALF	LAFNVIVYVS	CLIMSANAST	PESLV			

Supplementary Figure S6. Amino acid alignment of identified sequences of *D. gallinae* glutamate-gated chloride channels (in bold). Alpha and beta subunits of *C. elegans* homologues (NP_507090 and NP_491470, respectively) served as templates for identifications of secondary structures. Residues involved in interactions with ivermectin are highlighted in green.

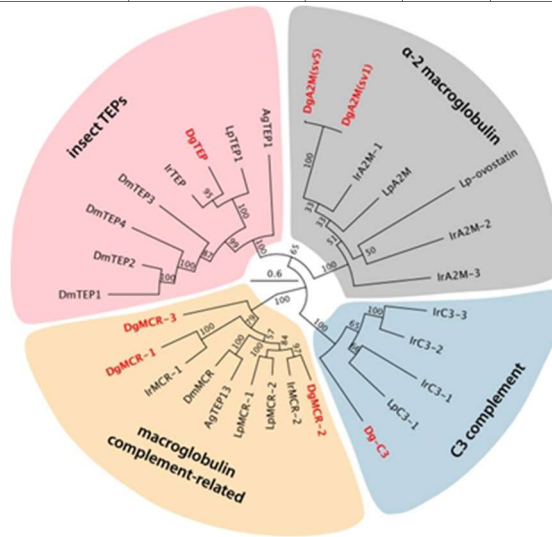
Supplementary Fig. S7:



Supplementary Figure S7. Visualisation of read coverage of glutamate-gated chloride channels encoding transcripts, assessed through RNA-Seq by Expectation-Maximization (RSEM) software package. Red indicates aligned read assignment over multiple transcripts, while black indicates uniquely assigned reads.

Supplementary Fig. S8:

Type	Thiol	Protein-ID ^a	RNAseq-ID	Unfed Protonymph FPKM	Fed Protonymph FPKM	Deutonymph FPKM	Adult FPKM	Midgut (adult) FPKM
DgA2M(sv1)	Yes	MBD2876438.1	Dg-350935_FR6_221-1770	193,66	78,56	60,35	59,62	76,14
DgA2M(sv2)	Yes	MBD2883834.1	IrSigP-350924_FR6_98-1629	23,34	120,29	149,36	47,93	20,13
DgA2M(sv3)	Yes	MBD2876440.1	IrSigP-350933_FR6_221-1778	15,71	11,66	12,86	0,33	0,86
DgA2M(sv4)	Yes	MBD2879613.1	IrSigP-1160473_FR1_175-1366	8,87	20,43	20,51	6,63	7,4
DgA2M(sv5)	Yes	MBD2878485.1	Dg-350932_FR3_95-1489	0,1	11,37	8,72	9,18	9,41
DgC3	Yes	MBD2883842.1	IrSigP-433789_FR5_615-2320	39,31	21,25	23,05	27,66	28,98
DgTEP	Yes	MBD2879163.1	IrSigP-580656_FR2_299-1580	33,55	77,78	83,56	26,9	8,46
DgMCR-1	No	MBD2885045.1	Dg-370713_FR6_393-2047	12,62	12,64	15,08	1,62	0,17
DgMCR-2	Yes	MBD2885046.1	IrSigP-392592_FR1_123-1721	16,12	36,15	28,07	0,98	0,06
DgMCR-3	No	MBD2882826.1	Dg-594457_FR6_1037-2807	7,2	4,1	5,21	0,26	0,02



Alternative splicing within the ‘bait regions’ of *D. gallinae* α_2 -macroglobulins:

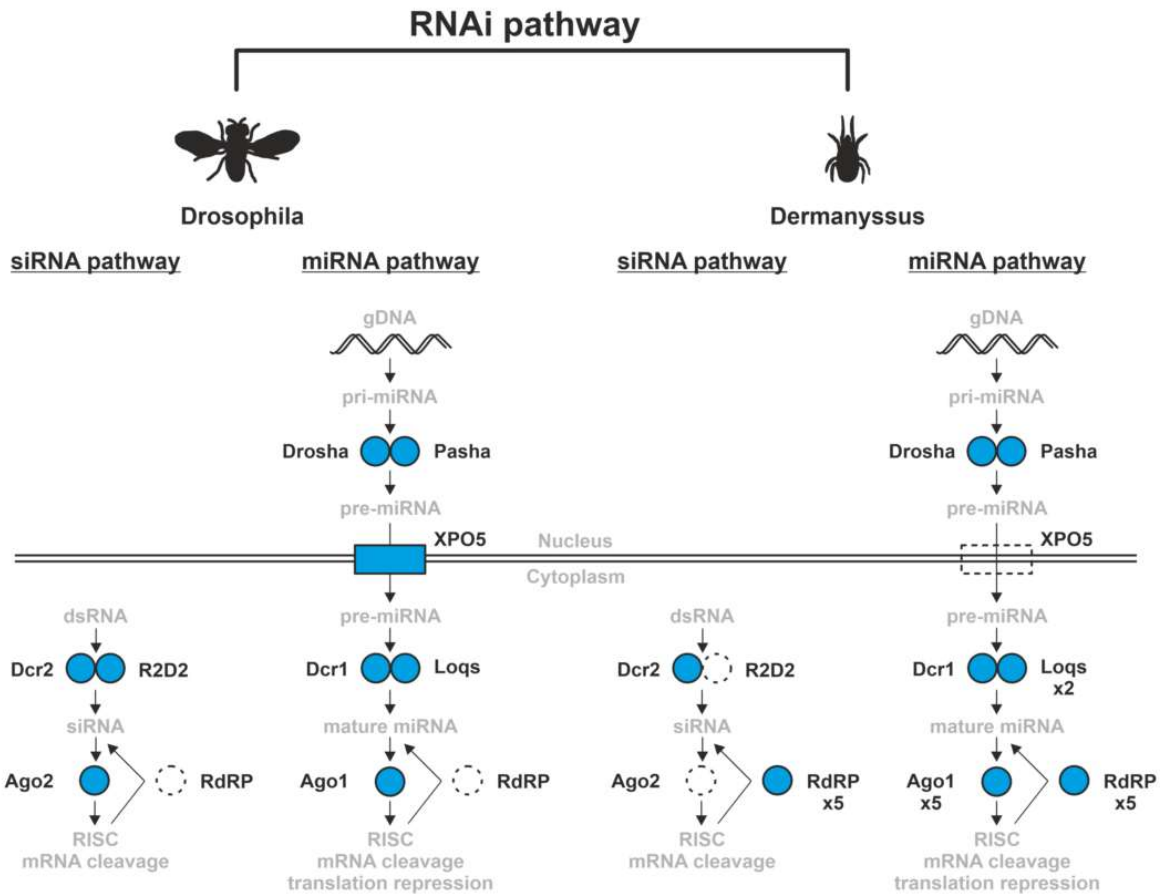
```

DgA2M (sv5) 1 PCRSTRDGSHTSVPEI GVTLEELA-----GEM-----ATGTYAAPSASRIGNDFGGATATASQSVVEVRDYFPELW
DgA2M (sv4) 1 PCRSTRDGSHTSVPEIAPAEEAMVEFDS-----EAAADGDDTAAADRDLVRPQTTTFSTTAAPSASRIGNDFGGATATASQSVVEVRDYFPELW
DgA2M (sv3) 1 PCRSTRDGSHTSVPEI VSKINGFVPTPLAVSGHLAGSLAAHRPAAAARPPPIPR---PPPAAPSASRIGNDFGGATATASQSVVEVRDYFPELW
DgA2M (sv1) 1 PCRSTRDGSHTSVPEI RVSLSLQVAFST-----SS---GERRFAPSASRIGNDFGGATATASQSVVEVRDYFPELW
DgA2M (sv2) 1 PCRSTRDGSHTSVPEI P-----APSASRIGNDFGGATATASQSVVEVRDYFPELW

```

Supplementary Figure S8. Identified transcripts encoding *D. gallinae* members of thiol-ester containing protein (TEP) family and phylogenetic tree with selected well-annotated TEPs from other invertebrates. The tree was reconstructed using the maximum likelihood method based on the alignment of full amino acid sequences (~1500 residues). Ag – malaria mosquito *Anopheles gambiae*; Dg (in red) – red poultry mite *Dermanyssus gallinae*; Dm – the fruit fly *Drosophila melanogaster*; Ir – the hard tick *Ixodes ricinus*; Lp – the horseshoe crab *Limulus polyphemus*. Numbers at the branches represent bootstrap support values calculated from 1,000 replicates. **GenBank Accession Nos. to the TEP sequences of other invertebrates shown in the phylogenetic tree:** AgTEP1 (AVK92986.1); AgTEP13 (XP_317044.4); DmTEP1 (CAB87807.1); DmTEP2 (CAB87808.1); DmTEP3 (CAB87809.1); DmTEP4 (CAB87810.1); DmMCR (AAF52601.1); IrA2M-1 (QOJ54010.1); IrA2M-2 (QOJ54011.1); IrA2M-3 (QOJ54012.1); IrC3-1 (QOJ54014.1); IrC3-2 (QOJ54015.1); IrC3-3 (QOJ54016.1); IrMCR-1 (QOJ54017.1); IrMCR-2 (QOJ54018.1); IrTEP (QOJ54013.1); LpA2M (BAA19844.1); LpC3-1 (XP_013775397.1); LpMCR-1 (XP_022254489.1); LpMCR-2 (XP_013776899.1); Lp-ovostatin (XP_022249030.1); LpTEP1 (XP_013786421.1). Expression values (FPKM) are shown in the Table below, ^a [blue Accession Nos.](#) are used in the phylogenetic tree.

Supplementary Fig. S9:



Supplementary Figure S9. Identified transcripts encoding components of RNAi pathway in the *D. gallinae* transcriptomes. Protein sequences of *Drosophila* or *Tribolium* (Tube) RNAi pathway were used to search in our *D. gallinae* translated protein database by using program Bioedit (Local BLAST, E value 0.1, Matrix BLOSUM62). Conservation of the domains was checked by CD-search (NCBI). Only hits with similar domain structures and an E-value $< 10e^{-3}$ were considered as putative homologues. Accession numbers are available as **Supplementary Table S9**.

Supplementary Table S1: Information on read counts and quality scores achieved by Illumina sequencing.

Sample	Raw Reads	Effective Rate (%)	GC content (%)	Error Rate (%)	Q20 (%)	Q30 (%)
unfed protonymphs	57338502	97.58	49.19	0.03	97.89	94.09
fed protonymphs	58861591	97.54	49.69	0.03	97.79	93.90
deutonymphs	58727555	97.99	49.87	0.03	97.85	94.00
adults	54699347	97.73	50.75	0.02	98.14	94.77
midguts from adults	61346035	98.09	49.51	0.03	97.90	94.33

Supplementary Table S2: Summary of reads origin.

	Sum of reads	% total reads	Contigs	% total contigs
REFSEQ-INVERTEBRATE	126,948,051	41.52	19,590	23.02
ACARI	153,704,406	50.27	11,739	13.79
GALLUS	3,301,469	1.08	11,258	13.23
TICK-PATHOGENS	6,432,162	2.10	4,251	4.99
UK	15,389,923	5.03	38,279	44.97
Total	305,776,011	100	85,117	100

Supplementary Table S3: Accession IDs to differentially expressed transcripts in blood-fed protonymphs over transcriptomes of unfed protonymphs, shown in Figure 2c. Oligoes used in RT-qPCR in Figure 2c' are shown in the last column.

DET No	Annotation	Transcript ID (hyper-linked Excel file)	Protein ID (NCBI)	RT-qPCR primers
2	Carboxypeptidase	IrSigP-456705_FR5_11-515	MBD2876455	F: GAGAATCGCCAGCAGAACCT R: CGTATGGTACTGGGTCAGGC
3	717131_FR2_65-201	Dg-717131_FR2_65-201	MBD2886605	F: AAACCTTTGGCAGCGTACTC R: CGCTCCCTCGGTAGAAATCT
4	465142_FR6_1943-2222	IrSigP-465142_FR6_1943-2222	MBD2879726	F: GACGAGAAGGGTTTGTCCCTC R: TGTCGAGGTAGATGTGCTGG
5	Stubble	IrSigP-702379_FR6_1752-2725	MBD2890242	F: TGATCGGCATCATCTCGTGG R: CCTCGTGATGCGGGTGTA
6	Cathepsin L5	Dg-417098_FR1_205-573	MBD2876666	F: GTGTTTCGATCCGTGGTTCTG R: AGTTCTTCACGAGCCAGGAG
7	Cuticle protein 7	IrSigP-633645_FR4_104-234	MBD2890009	F: CGATTACCGGCCGAGTCTAC R: GGCGCTATGTACGAGGTGAC
8	464593_FR5_41-172	IrSigP-464593_FR5_41-172	MBD2874827	F: TGTTTGCTCACATGGTACGC R: GATCTTTCCGGCAGCTTAGC
9	Chitinase-like	Dg-426972_FR5_591-1070	MBD2887237	F: ACAGAAAAGACCTGGTGGCC R: CACCAGGTTTTCTCCGTCGA
10	Neyo-like	Dg-429223_FR6_180-923	MBD2886979	F: TGGCGTTGACAATTCGAGA R: GTACAGAGGCCCATGATGG
11	Astacin-like metalloprotease	Dg-768351_FR2_357-560	MBD2887970	F: ACGGTGGTTCACGAGTTTGG R: GCTTGATGAATTGGTCGCGG
12	703171_FR2_257-506	IrSigP-703171_FR2_257-506	MBD2883573	F: GAAGCCGCTGTGAAGCTAGA R: GCACTGCGCATAGATCTGGA
13	Mucin	Dg-385271_FR5_1-555	MBD2881848	F: AGTACCAGGCTCCTCAACCT R: TATAGGCAGGTTGACGGGGA
14	Peritrophin 1	IrSigP-436463_FR6_542-720	MBD2890592	F: GTGCTTTCAGTCGCCGTATG R: CAAGTTGCTTCACCTGACGC
15	Peritrophin 2	IrSigP-436466_FR2_223-511	MBD2889708	F: GGCACCTACTTTGTTTCGCA R: CACGTGATAGAATGGGCAGC
	Legumain isoenzyme 4	IrSigP-379957_FR2_1085-1545	MBD2885568	F: CCATAGCGGTGTGTGCCTC R: GTTTGGCCACCATCTTCAGC

Supplementary Table S4: Accession IDs to differentially expressed transcripts in midguts over whole bodies of adult mites, shown in Figure 2d. Oligoes used in RT-qPCR in Figure 2d' are shown in the last column.

DET No	Annotation	Transcript ID (hyper-linked Excel file)	Protein ID (NCBI)	RT-qPCR primers
1	Trypsin-like serine protease	IrSigP-562590_FR6_227-579	MBD2888300	F: CGGACGGACTTCTTTGACGA R: GAACGCTACTTCCGCTCGTA
2	Caspase-1-like isoform X2	Dg-598524_FR2_222-566	MBD2885764	F: AGGTATTCTGGCCACTGACC R: TAGCCGGCCACAGTTGAATA
3	Amino acid transporter	Dg-370073_FR3_533-1060	MBD2877231	F: ACACCAATGCCAGCACTCAT R: TTAGTTGGCCAATGTCCGCA
4	Apolipoporphorins-like	Dg-404344_FR1_98-2680	MBD2886271	F: TCTCGACATCGTTGATCGGC R: CGAGTCGCTCCGTGATGATT
5	P2X purinoceptor 4	Dg-950939_FR2_274-714	MBD2886414	F: GAAGTGGAGTACAGACGGGC R: CCAGCCTCGGATTTCCGATA
6	S-adenosylmethionine synthetase	Dg-620064_FR5_192-681	MBD2883952	F: GTAGTGGTGAGAGCGGTCAT R: ATTGGGCCTCCTTCGATGAA
7	Ferritin 2	IrSigP-384458_FR2_148-399	MBD2883635	F: TCCTCGAGCATCACGTCAAC R: GGATCACGACAGTCCTCGTC
8	Sulfotransferase family cytosolic 2B	Dg-807076_FR4_126-470	MBD2875543	F: AACGGATCAACGAGTGGAGG R: GTCGTACTTCACCGAGCAGT
9	Ferrochelatase	Dg-649831_FR2_303-703	MBD2876119	F: GAGCTGGCCAAAGAGCTGAA R: AGACCCCGAATGAAGTGCTC
10	Acid sphingomyelinase	IrSigP-602409_FR5_87-754	MBD2884868	F: ATCGGGGTTAACTTCGTTCGC R: CGTCGATACTGTAGACGCGG
11	Cathepsin D1	IrSigP-519820_FR3_359-840	MBD2876745	F: TTCAGTACGGCTCAGGATCC R: ACTCCTTTGTGATCTCGCCA
12	Solute carrier family 35 member F6-like	IrSigP-662643_FR6_1690-2093	MBD2876932	F: ATATCGGGTTCGTGCCCTTC R: CTTCGCGTGTCTCCTCTTC
13	GABA receptor	Dg-565248_FR2_220-775	MBD2887064	F: CCCAACGATGCCGACATTCT R: TGAACCTCACATTGCCGGAT
14	Cathepsin L3	IrSigP-413246_FR4_193-533	MBD2885740	F: GTCAAGGATCAGCAGCAGTG R: TCGACAAGGTTCTGTTCGGA
15	Hemolymph lipoprotein	Dg-350407_FR6_167-1642	MBD2878204	F: GTTGCAGATGCTTGCTCGTG R: TTTCGCCAGTTGTCAGCTCA

Supplementary Table S5: Accession IDs to transcripts encoding cysteine and aspartic proteases shown in Figure 3b.

Protease	isoenzyme type	Transcript ID (hyper-linked Excel file)	Protein ID (NCBI)
Serine Proteases	1. Chymotrypsin	Dg-651195 , IrSigP-651191, Dg-651193, Dg-404258, IrSigP-651189	MBD2881020
	2. Anionic trypsin	Dg-404994	MBD2877379
	3. Chymotrypsin-like elastase	IrSigP-607270	MBD2881713
	4. Chymotrypsin-like elastase	IrSigP-76325 , IrSigP-355347	MBD2878320
	5. Stubble-like serine protease, trypsin	IrSigP-387896	MBD2880678
	6. Stubble-like serine protease, trypsin	Dg-615055	MBD2879484
	7. Chymotrypsin	IrSigP-417374 , Dg-417373	MBD2877373
	8. Chymotrypsin	IrSigP-622345	MBD2875824
	9. Chymotrypsin	IrSigP-997083	MBD2875973
	10. Chymotrypsin	Dg-602081 , Dg-602079	MBD2879331
	11. Prolyl oligopeptidase	Dg-1021459 , IrSigP-1081927	MBD2887264
	12. Serine protease K12H4.7	IrSigP-351248 , IrSigP-351247	MBD2884270
Cysteine Proteases	1. Cathepsin L1	Dg-632847 , IrSigP-632845	MBD2879342
	2. Cathepsin L2	IrSigP-354374 , IrSigP-354370	MBD2878524
	3. Cathepsin L3	IrSigP-413246 , IrSigP-10997, IrSigP-413245,	MBD2885740
	4. Cathepsin L4	IrSigP-349742 , IrSigP-349741	MBD2885566
	5. Cathepsin L5	Dg-417098 , Dg-417097,	MBD2876666
	6. Cathepsin L6	IrSigP-1037340	MBD2884871
	7. Legumain 1	IrSigP-439085 , Dg-439086	MBD2885742
	8. Legumain 2	Dg-445098	MBD2886063
	9. Legumain 3	IrSigP-535196	MBD2885743
	10. Legumain 4	IrSigP-379957	MBD2885568
Aspartyl Proteases	1. Cathepsin D1	Dg-519818 , IrSigP-476369, IrSigP-519820, IrSigP-519817	MBD2876748
	2. Cathepsin D2	Dg-370446 , IrSigP-808266	MBD2879957
	3. Cathepsin D3	IrSigP-16089 , Dg-1042377, Dg-1042375	MBD2876189

Supplementary Table S6: Overview of transcripts encoding proteins involved in haem and iron biology.

Reference genome				
<i>Aedes aegypti</i>				
Strain: Liverpool AGWG				
Assembly: AaegL5				
BioProject Query: 597301				
tBlastN				
Query protein + ID's	transcript ID	protein ID	% coverage	E value
ALAS: XP_001658653.1	Dg-608857_FR3_129-736	MBD2882839.1	91	0.0
PBGS: XP_001661237.1	Dg-568812_FR5_621-1005	MBD2885691.1	98	2e-133
HMBS: XP_001654431.1	Dg-541660_FR4_65-424	MBD2879167.1	54	5e-82
UROS: XP_001660743.2	Dg-987039_FR1_193-481	MBD2880820.1	94	1e-33
UROD: XP_001657958.2	Dg-478956_FR4_182-541	MBD2884748.1	83	6e-126
CPOX: XP_001663577.1	Dg-945296_FR1_180-609	MBD2883466.1	87	2e-151
PPOX: XP_021693143.1	IrSigP-605064_FR5_94-622	MBD2885503.1	99	1e-93
FECH: XP_001650846.1	Dg-649831_FR2_303-703 / Dg-381015_FR5_530-916	MBD2876119.1	94	2e-149
HO:				
XP_001658955.1 (aedes)	NI (not identified)			0.0001
GETP01214966.1 (varroa)	NI			0.0001
Fer1 (Ir-108507)	Dg-367272_FR4_390-576	MBD2884432.1	99	1,00E-80
Fer2 (Ir-108441)	IrSigP-384454_FR3_720-940/IrSigP-384458_FR2_148-399/IrSigP-384452_FR6_307-551/IrSigP-384456_FR6_68-245/Dg-384450_FR2_2079-2251	MBD2876852.1	82	6,00E-62
IRP (c-Aconitase, Ir-109153)	Dg-351924_FR3_573-1476	MBD2876478.1	100	0
Insect transferrins				
Tf1 (XP_001647719)	NI		37	1,00E-14
Tf2 (XP_021699709)	IrSigP-523377_FR5_87-930	MBD2877432.1	93	0,00E+00
Tf3 (EAT34844)	NI		45	2,00E-18
Tf4 (XP_001661801)	NI		51	5,00E-15

Supplementary Table S7: Accession IDs to transcripts encoding adult-specific transcripts shown in Figure 5b. Oligoes used in RT-qPCR in Figure 5b' are shown in the last column.

DET No	Annotation	Transcript ID (hyper-linked Excel file)	Protein ID (NCBI)	RT-qPCR primers
1	Vitellogenin 1	IrSigP-350331_FR2_207-2055	MBD2876257	F: GTCTCAAGCAACGCGAACTG R: AACGGAGATGCGTACTTCCC
2	Vitellogenin 2	Dg-9795_FR3_189-2089	MBD2876256	F: CCCGTCAACGAGGAACTTCA R: GAGTCCACATGCTGTTGGGA
3	Vitellogenin receptor	Dg-353835_FR3_42-1900	MBD2877430	F: GTGGTGGAGGTGGTAGCTTC R: CCTCCTTTGGTGTCTCGCA
4	Vitellogenin-like	IrSigP-349783_FR3_1-1870	MBD2876000	F: TGCCTATCAAACGGGTCACT R: CCGTTGAACATGACCACGAG
5	Arginine kinase	Dg-844682_FR1_111-471	MBD2886196	F: ACACGCGTGATGGACATCTT R: CCGGTCAATGGGTGGTAGAC
6	Tubulin alpha-8 chain	Dg-579987_FR2_129-594	MBD2876362	F: CCCTACAATTCGGTGCTGAC R: CGGCAGATGTTGTAGATGGC
7	Paramyosin-like isoform X2	Dg-573818_FR1_53-613	MBD2885035	F: ACTCAAGCTGAACGAGACCG R: TTTTCACCCGTTCTGCAGT
8	Elongation of very long chain fatty acids	IrSigP-1087573_FR5_204-473	MBD2890092	F: GACTTTCCCTCGACTCAGGC R: GCAGAAATTTGCGCTGAGGTC
9	Epoxide hydrolase 1	Dg-415549_FR2_82-620	MBD2877337	F: CTTATGGTTCATGGCTGGCC R: ACGTCAAAAGCAAGACCGTC
10	Histone-lysine N-methyltransferase	Dg-404921_FR2_1-529	MBD2889185	F: AAGGCTGTGATCGTTCTGGA R: TCTTTGGCCGAGTACCCTTT
11	Serine protease 27-like	Dg-423801_FR3_697-1274	MBD2884827	F: CCTGAAGCTCCATCCGA R: ACTTTACGCGCCGATCTAGT

Supplementary Table S8: The list of taxa used for the phylogenetic analysis of arthropod vitellogenins.

Taxonomy		Vg1	Vg1-like	Vg2	
PARASITIFORM MITES					
Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Mesostigmata; Monogynaspida; Gamasina; Dermanyssoidea					
Varroidae	<i>Varroa jacobsoni</i>	XP_022710380	XP_022700578	XP_022701897	
	<i>Varroa destructor</i>	AFN88463	XP_022657753	AFN88464	
	<i>Stratiolaelaps scimitus</i>	JABWDB010000015 (00009700-RA)	JABWDB010000015 (00009665-RA)	JABWDB010000015 (00009740-RA)	
Laelapidae	<i>Tropilaelaps mercedesae</i>	OQR72561	OQR79705 + OQR72029	OQR67440	
Macronyssidae	<i>Ornithonyssus sylviarum</i>	GIXZ01020088	GIXZ01000835	GIXZ01000591	
Dermanyssidae	<i>Dermanyssus gallinae</i>	MBD2876257 (IrSigP- 350331_FR2_207-2055)	MBD2876000.1 (IrSigP- 349783_FR3_1-1870)	MBD2876256 (Dg- 9795_FR3_189-2089)	
Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Mesostigmata; Monogynaspida; Gamasina; Phytoseioidea					
Phytoseidae	<i>Amblyseius swirskii</i>	GHIT01048819 + GHIT01041025	absent	GHIT01045440	
	<i>Amblyseius eharai</i>	QKO00543	absent	QBZ96191	
	<i>Neoseiulus cucumeris</i>	AGQ56698	absent	AGQ56699	
	<i>Neoseiulus barkeri</i>	ASB34115	absent	ASB34116	
	<i>Galendromus occidentalis</i>	XP_003746410	absent	XP_018494463	
	<i>Euseius nicholsi</i>	QKO00545	absent	QCX36526	
TICKS					
Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea					
Ixodidae	<i>Rhipicephalus microplus</i>	XP_037287934	absent	XP_037287793	
	<i>Rhipicephalus sanguineus</i>	XP_037527682	absent	XP_037528003	
	<i>Rhipicephalus haemaphysaloides</i>	QEL09190	absent	GIIA01010490	
	<i>Hyalomma asiaticum</i>	KAH6940719	absent	KAH6940634	
	<i>Dermacentor silvarum</i>	XP_037555503	absent	XP_037555480	
	<i>Dermacentor variabilis</i>	AAW78557	absent	ABW82681	
	<i>Amblyomma hebraeum</i>	AGQ57039	absent	AGQ57040	
	<i>Haemaphysalis longicornis</i>	GHLT01005427	absent	GHLT01004136 + GHLT01003656	
	<i>Ixodes scapularis</i>	MOY43367	absent	MOY34203	
	<i>Ixodes ricinus</i>	GIDG01029412	absent	GIDG01034908.1	
	<i>Ixodes holocyclus</i>	GIBQ01001668	absent	GIBQ01041644	
	Argasidae	<i>Ornithodoros moubata</i>	JAW06414		BAH02666
	ACARIFORM MITES				
Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata					
Eleutherengona; Raphignathae; Tetranychoidae; Tetranychidae	<i>Tetranychus urticae</i>	XP_015793828; XP_015793699			
	<i>Tetranychus truncatus</i>	AYV88983			
	<i>Tetranychus evansi</i>	AYV89292			

Panonychus citri AHN48900
Anystina; Parasitengona;
Trombidioidea; Trombididae
Dinotrombium tinctorium RWS06019; RWS07112

Anystina; Parasitengona;
Trombiculoidea; Trombiculidae
Leptotrombidium deliense RWS27858

Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Sarcoptiformes; Astigmata

Dermatophagoides pteronyssinus XP_027195573
Psoroptidia; Analgoidea;
Pyroglyphidae;
Dermatophagoidea
Dermatophagoides farinae KAH7640524

Psoroptidia; Sarcoptoidea;
Sarcoptidae; Sarcoptinae
Sarcoptes scabiei KAF7496282

SPIDERS

Arthropoda; Chelicerata; Arachnida; Araneae

Trichonephila clavata GFQ69744, GFQ69748

Parasteatoda tepidariorum XP_015930209; XP_015921257

Pardosa pseudoannulata AXN69712; AXN69713

SCORPIONS

Arthropoda; Chelicerata; Arachnida; Scorpiones

Centruroides sculpturatus XP_023225368

HORSESHOE CRAB

Arthropoda; Chelicerata; Merostomata; Xiphosura

Limulus polyphemus XP_022258932; XP_022244466

CRUSTACEANS

Arthropoda; Mandibulata; Pancrustacea; Crustacea; Multicrustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda

Penaeus vannamei AAP76571

Metapenaeus ensis AAM48287, AAN40701, AAT01139

Macrobrachium rosenbergii BAB69831

Pandalus hypsinotus BAD11098

Cherax quadricarinatus AAG17936

INSECTS

Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta

Solenopsis invicta AAP47155; AAY22960; AAY22961

Cimex lectularius CLEC001325-RA; CLEC001323-RA

Aedes albopictus XP_019542945; XP_019542959

Bombyx mori NP_001037309

Pediculus humanus corporis XM_002431351; XM_002431353

Tribolium castaneum XP_970210; XP_971398

Papilio xuthus KPJ04900

Supplementary Table S9: Accession IDs to transcripts encoding Toll, IMD, and RNAi pathway components.

Toll pathway	<i>Drosophila / Tribolium</i>	<i>According to Palmer and Jiggins, MBE, 2015</i>	<i>D. gallinae</i>	e-value	<i>Bioedit, local blast 0.1</i>	Identities	Protein ID	Final number of genes	Unique sequences
Tagret	NP_572727.1	Dg-540147_FR1_164-359	6,00E-40	76/163 (46%)	MBD2887001.1	3	2		
PGRP-SA		Dg-540146_FR1_117-298	6,00E-40	76/163 (46%)	MBD2886483.1				
		IrSigP-364299_FR6_987-1226	8,00E-27	57/193 (29%)	MBD2876088.1				
GNBP1	NP_524142.2	missing				0	0		
GNBP3	NP_523986.2	missing				0	0		
spz	NP_524526.1	Dg-700091_FR4_344-668	9,00E-11	34/108 (31%)	MBD2885047.1	11	9		
		Dg-453081_FR2_746-1664	2,00E-05	33/116 (28%)	MBD2881466.1				
		Dg-1044839_FR6_83-641	2,00E-05	33/116 (28%)	MBD2881465.1				
		Dg-518881_FR1_385-2031	2,00E-05	37/152 (24%)	MBD2886331.1				
		Dg-382595_FR1_94-374	3,00E-05	30/111 (27%)	MBD2875246.1				
		Dg-382596_FR1_549-829	3,00E-05	30/111 (27%)	MBD2875239.1				
		IrSigP-382594_FR1_134-419	3,00E-05	30/111 (27%)	MBD2875245.1				
		IrSigP-512652_FR1_183-755	8,00E-05	35/146 (23%)	MBD2886337.1				
		IrSigP-1079353_FR4_183-755	8,00E-05	35/146 (23%)	MBD2886336.1				
		IrSigP-778055_FR6_423-704	8,00E-05	31/105 (29%)	MBD2890046.1				
		Dg-782185_FR4_112-753	8,00E-05	31/105 (29%)	MBD2882432.1				
Toll-1	NP_524518.1	Dg-576571_FR1_304-1394	9,00E-92	267/914 (29%)	MBD2880219.1	12	8		
		Dg-567274_FR5_43-1875	2,00E-91	278/968 (28%)	MBD2879243.1				
		Dg-578655_FR2_164-1257	4,00E-91	266/909 (29%)	MBD2880160.1				
		IrSigP-382316_FR3_61-1433	1,00E-77	257/985 (26%)	MBD2882696.1				
		Dg-446710_FR5_49-1280	3,00E-73	247/971 (25%)	MBD2885043.1				
		IrSigP-446711_FR2_241-1533	4,00E-73	246/971 (25%)	MBD2883423.1				
		Dg-709305_FR5_596-2090	3,00E-71	222/852 (26%)	MBD2877998.1				
		Dg-32901_FR5_352-1601	7,00E-71	257/1002 (25%)	MBD2885673.1				
		Dg-446923_FR2_336-1582	2,00E-68	241/981 (24%)	MBD2875902.1				
		Dg-1068943_FR6_265-1548	1,00E-65	248/992 (25%)	MBD2885481.1				
		IrSigP-1142933_FR4_826-2108	7,00E-58	232/912 (25%)	MBD2885044.1				

		Dg-964834_FR3_197-1494	2,00E-57	243/1033 (23%)	MBD2883165.1		
Myd88	NP_610479.1	Dg-366848_FR6_409-694	7,00E-10	64/274 (23%)	MBD2883109.1	1	1
tube	XP_008198084 (<i>T. castaneum</i>)	Dg-1030207_FR3_288-932	1,00E-30	87/277 (31%)	MBD2875407.1	1	1
pele	NP_476971.1	Dg-520307_FR2_978-1673	1,00E-57	137/329 (41%)	MBD2887978.1	2	1
		Dg-520315_FR1_520-1491	3,00E-36	83/194 (42%)	MBD2889692.1		
dorsal	NP_724052.1	Dg-476498_FR5_529-1233	5,00E-72	175/459 (38%)	MBD2879760.1	3	1
		Dg-476504_FR3_183-907	5,00E-72	175/459 (38%)	MBD2875479.1		
		Dg-476503_FR2_303-1034	5,00E-72	175/459 (38%)	MBD2878093.1		
Dif	NP_523589.2	missing				0	0
cactus	NP_723960.1	Dg-359173_FR2_263-734	1,00E-20	92/338 (27%)	MBD2878651.1	1	1
Imd pathway							
PGRP-LB	NP_650079.1	Dg-540147_FR1_164-359	2,00E-36	76/162 (46%)		0	0
		Dg-540146_FR1_117-298	2,00E-36	76/162 (46%)			
		IrSigP-364299_FR6_987-1226	4,00E-24	58/170 (34%)			
		Dg-540150_FR4_273-459	1,00E-21	54/124 (43%)			
PGRP-SC	NP_610410.1	Dg-540147_FR1_164-359	7,00E-34	65/160 (40%)		0	0
		Dg-540146_FR1_117-298	7,00E-34	65/160 (40%)			
		IrSigP-364299_FR6_987-1226	2,00E-25	48/160 (30%)			
		Dg-540150_FR4_273-459	3,00E-23	49/128 (38%)			
PGRP-LC	NP_729468.2	Dg-540147_FR1_164-359	1,00E-33	68/162 (41%)		0	0
		Dg-540146_FR1_117-298	1,00E-33	68/162 (41%)			
		IrSigP-364299_FR6_987-1226	3,00E-26	54/156 (34%)			
		Dg-540150_FR4_273-459	3,00E-22	51/125 (40%)			
PGRP-LE	NP_573078.1	Dg-540147_FR1_164-359	2,00E-33	71/161 (44%)		0	0
		Dg-540146_FR1_117-298	2,00E-33	71/161 (44%)			
		Dg-540150_FR4_273-459	2,00E-21	52/125 (41%)			
		IrSigP-364299_FR6_987-1226	3,00E-20	41/117 (35%)			
imd	NP_573394.1	missing				0	0
tak1	NP_524080.1	Dg-625516_FR6_1422-2006	5,00E-67	150/374 (40%)	MBD2883593.1	2	1
		Dg-540567_FR1_999-1370	6,00E-35	88/231 (38%)	MBD2880322.1		

IKKgamma	NP_523856.2	missing				0	0
IKKbeta	NP_524751.3	Dg-442267_FR6_1351-2127	1,00E-35	119/375 (31%)	MBD2885575.1	3	2
		Dg-444853_FR2_344-1010	1,00E-35	119/375 (31%)	MBD2887170.1		
		Dg-823437_FR6_191-936	8,00E-27	91/283 (32%)	MBD2885364.1		
Fadd	NP_651006.1	missing				0	0
Dredd	NP_477251.3	Dg-598513_FR3_41-413	9,00E-17	86/308 (27%)	MBD2878667.1	7	4
		Dg-598516_FR3_41-422	9,00E-17	86/308 (27%)	MBD2885764.1		
		Dg-598535_FR2_222-590	4,00E-16	71/223 (31%)	MBD2885765.1		
		Dg-598533_FR3_41-446	4,00E-16	71/223 (31%)	MBD2885765.1		
		Dg-971248_FR1_366-698	8,00E-10	71/261 (27%)	MBD2875414.1		
		Dg-559693_FR4_576-1463	2,00E-05	33/137 (24%)	MBD2880927.1		
		Dg-559695_FR1_592-1466	2,00E-05	33/137 (24%)	MBD2880926.1		
Relish	NP_477094.1	missing				0	0
Caspar	NP_611080.1	missing				0	0
RNAi pathway							
Dicer-1	NP_524453	IrSigP-590221_FR1_364-2293	e-157	293/533 (54%)	MBD2887739.1	2	1
		Dg-590223_FR1_2376-2596	3,00E-64	128/197 (64%)	MBD2890853.1		
Dicer-2	NP_523778	Dg-575620_FR6_62-1581	6,00E-55	256/1059 (24%)	MBD2876567.1	1	1
Drosha	NP_477436	IrSigP-360170_FR2_1-1800	0	607/1247 (48%)	"MBD2878995.1	1	1
Pasha	NP_651879					0	0
R2D2	NP_609152					0	0
XPO5						0	0
Argonaute-1	NP_725341	Dg-708394_FR3_85-1031	0	715/904 (79%)	MBD2877359.1	6	5
		Dg-708392_FR1_92-1020	0	707/906 (78%)	MBD2877356.1		
		Dg-632068_FR1_374-1365	e-143	343/942 (36%)	MBD2878837.1		
		Dg-632065_FR4_131-1166	e-142	342/945 (36%)	MBD2878839.1		
		Dg-571008_FR5_218-1092	e-140	314/854 (36%)	MBD2877547.1		
		Dg-400391_FR1_369-1469	e-108	308/974 (31%)	MBD2875929.1		
Argonaute-2	NP_648775					0	0
Loquacious	NP_723813	Dg-1131049_FR2_355-836	9,00E-55	146/395 (36%)	MBD2882785.1	2	2
		Dg-364025_FR4_2135-2633	3,00E-05	36/136 (26%)	MBD2881328.1		