Supporting Information

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SI Materials and Methods

In the spring of 2011, we collected queens that emerged from hibernation in northern Switzerland (B. L. Aesch and T. G. Neunforn). These queens established colonies in the laboratory. At the end of their colony cycle, these colonies produced gynes (daughter queens) and males, which we then mated; subsequently, we hibernated the gynes. On removal from hibernation, these gynes established colonies that were then used for the experiment. We intentionally used second-generation bees to avoid the known effect of maternal immunological history (1, 2). All colonies were confirmed to be free of common bumblebee parasites by repeated microscopic checks. When colonies had reached a sufficient size (~20–30 workers), we removed callow workers (i.e., workers that had emerged within the last 24 h) daily and provided them with ad libitum sugar water and pollen. Once these workers were 7 d old, they were exposed to a dose of 10,000 *Crithidia bombi* cells in 10 μL of 50% sugar water. Treatments comprised infecting the honeybees with one of three genotypes of *C. bombi* (internal codes 08.068, 08.075, and 08.161; henceforth, shortened to nos. 68, 75, and 161) or with a sham inoculum without the parasite. After exposure, we housed them in pairs for 18 h with ad libitum sugar water, but not with pollen, during this time. Eighteen hours after exposure, we anesthetized half of the bees on ice and removed their guts. We then snap-froze the guts in liquid nitrogen and stored them at −80 °C until RNA extraction. We chose this time point based on previous work showing differential expression of immune genes (3, 4). The remaining bees were given ad libitum sugar water and pollen, and they were maintained for an additional 7 d. After 7 d, we collected feces from these bees, assessed infection visually, and quantified infection load in the feces with quantitative real-time PCR (5). At this time point, the number of transmitting parasite cells in the feces correlates with infection intensities in the gut (6). Infection intensity data were analyzed with ANOVA after Yeo–Johnson transformation to improve normality and homoscedasticity of variance [CAR package (7)]. Because the sample size was unbalanced, we used type III sums of squares. We also analyzed the results of the visual checks, which were scored as presence/absence of *C. bombi* in the feces using a binomial generalized linear model with both host and parasite genotypes as crossed independent factors. We analyzed all our data with R (8).

We homogenized the guts from the bees that were killed after 18 h using 0.5-g zirconium beads at between 0 °C and 10 °C using an Omni Bead Ruptor 24 Homogenizer (OMNI International). We then extracted RNA using the RNeasy Plus Mini Kit (Qiagen) following the manufacturer's protocols. All RNA was assessed for quality using a 2100 Bioanalyzer (Agilent Technologies) with the RNA 6000 Nano Kit (Agilent Technologies). The RNA from three individuals per treatment per colony was pooled and then sequenced with an Illumina HiSeq 2000 sequencing system. After quality control steps to trim adapters and remove poor-quality reads, we mapped these reads to the official gene set of the *Bombus terrestris* genome project using SOAP [version 2.21 (9)]. We analyzed the resulting read counts using edgeR (10). We excluded genes where less than one read per million mapped in fewer than half of our groups, as suggested by the edgeR manual. We analyzed these data in two ways. On one hand, we considered the normalized read count of each gene as a dependent variable of the respective *C. bombi* genotype and analyzed this differential transcript abundance using the glmFit function relative to the uninfected controls. Hence, the expression response is considered here as a "fingerprint" of a particular parasite genotype's infection. We also compared how each host genotype responded to each parasite genotype to explore whether host genotypes responded to the parasite genotypes differently. The results from this second analysis should be interpreted with caution, however, because each comparison is the expression of a single infected group relative to a single control group but can be viewed as a heuristic assessment of the overall patterns of infection with different parasite genotypes.

We assigned gene ontology (GO) terms by homology using Blast2GO (11). We then analyzed the over- or underrepresentation of GO categories among significantly differentially expressed transcripts using the hypergeometric test in FUNC (12), requiring at least five genes per category. We report the GO categories that are over- or underrepresented relative to a random sample of 1,000 genes within our total mapped set (Tables S1–S3). We used a cutoff of $P < 0.05$ and report the GO categories that were significant before refinement and the results after refinement by excluding categories that are significant by virtue of the importance of the daughter categories (12).

To confirm the differential expression of genes identified in the RNA-sequencing experiment, we designed quantitative real-time PCR primers of a selection of these genes using QuantPrime (3, 13) (Table S4). We then assessed the expression of 29 target genes relative to three housekeeping genes (ef1a, AK, and PLA2) in five individual bees per colony per treatment using Fluidigm 96.96 Dynamic Array IFCs on the BioMark System (Fluidigm) with EvaGreen DNA Binding Dye (Biotium) according to the Advanced Development Protocol 14 (PN 100-1208 B) developed by Fluidigm. We measured each reaction across three technical replicates and used the average cycle threshold (Ct) value of these for further analysis. We dropped three samples due to bubbles in the chip, but only one bee was dropped from any host genotype (G_H) by parasite genotype (G_P) combination.

We analyzed the expression of these genes using the difference in the Ct (dCt) of the genes of interest relative to the geometric mean of the three housekeeping genes (14). This composite average of the housekeeping genes was invariant across treatments ($F_{3,60} = 0.46$, $P = 0.71$) and colonies ($F_{3,60} = 0.62$, $P = 0.61$), and there was no interaction between these factors ($F_{9,60} = 0.82$, $P = 0.60$), suggesting that this housekeeping value is robust. We then transformed the dCt values to improve normality and homoscedasticity of variance using Yeo–Johnson power transformations. We analyzed the resulting transformed values with two separate multivariate ANOVAs with the transformed dCt value as the dependent variable. In the first analysis, we assessed the overall bumblebee response to parasite exposure by treating expression values as dependent on bumblebee genotype and exposure in a crossed model. We then explored how host and parasite genotypes interact by analyzing the expression values as explained by bumblebee genotype and *C. bombi* genotype as crossed independent factors. We also explored patterns of co-expression by producing a heat map of the correlation matrix of expression of the transformed dCt expression values of all genes.

1. Sadd BM, Schmid-Hempel P (2007) Facultative but persistent trans-generational immunity via the mother's eggs in bumblebees. *Curr Biol* 17(24):R1046–R1047.

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4. Riddell CE, Sumner S, Adams S, Mallon EB (2011) Pathways to immunity: Temporal dynamics of the bumblebee (*Bombus terrestris*) immune response against a trypanosomal gut parasite. *Insect Mol Biol* 20(4):529–540.
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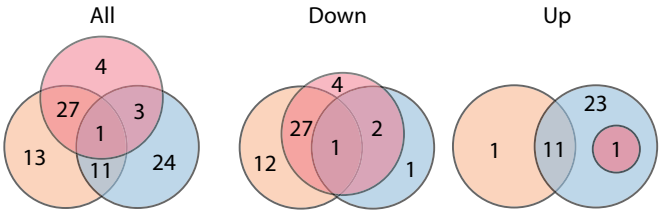

Fig. S1. Venn diagrams of the number of differentially expressed genes upon exposure to three genotypes of *C. bombi* relative to unexposed workers [nos. 68 (orange), 75 (blue), and 161 (red)] across all host colonies at a false discovery rate of 0.01.

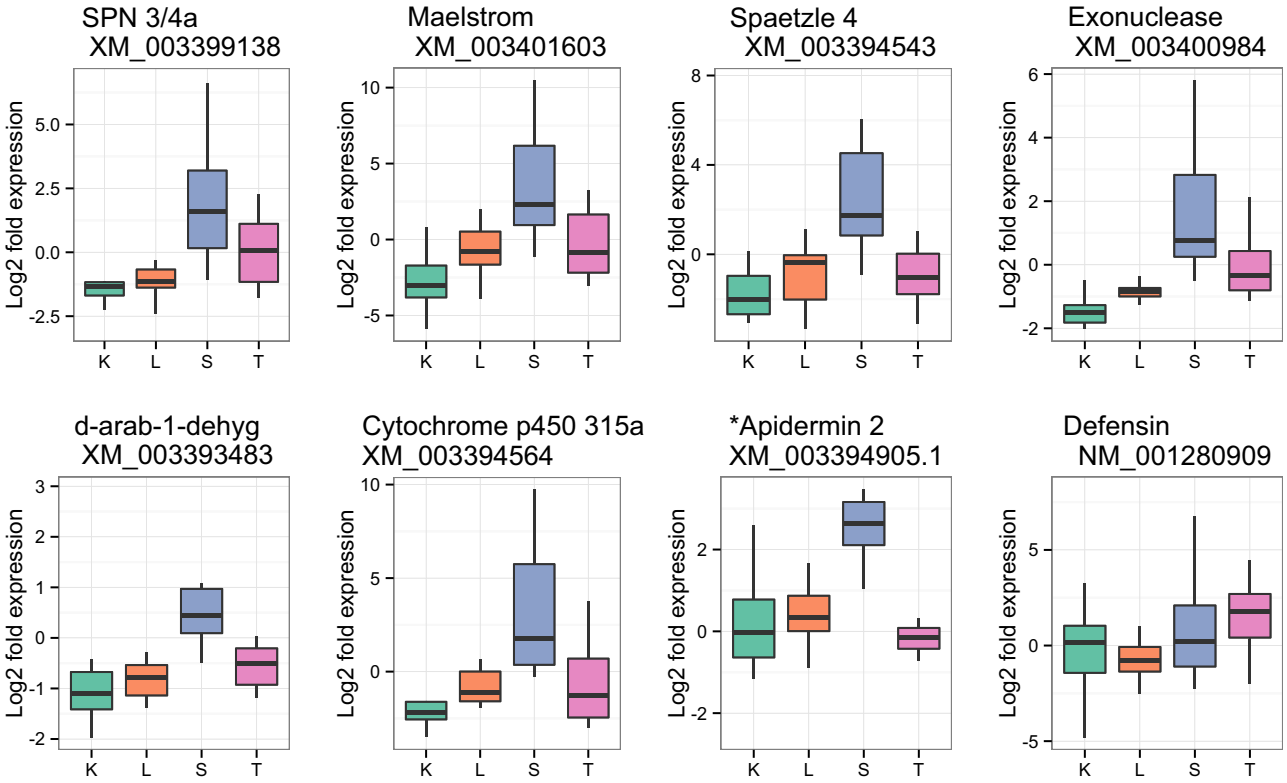

Fig. S2. Logfold change in expression of genes upon parasite exposure across all parasite genotypes based on quantitative PCR (qPCR), where there is a significant effect of host genotype (*x* axis and differently colored) and parasite exposure (exposed vs. unexposed) [$G_H \times$ Exposure: $F_{3,64} = 3.17$*, $F_{3,64} = 3.48$*, $F_{3,64} = 3.35$*, $F_{3,64} = 5.44$**, $F_{3,64} = 6.64$***, $F_{3,64} = 2.77$* (read from left to right and top to bottom); *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, $^{\dagger}P < 0.01$] and where the interaction approached significance (apidermin 2: $F_{3,64} = 2.34^{\dagger}$). Expression of defensin varied significantly based on bee genotype only ($F_{3,64} = 3.12$*). Values above zero can be interpreted as an up-regulation of the gene relative to unexposed individuals from the same colony. Inversely, values below zero are down-regulated upon parasite exposure. d-arab-1-dehyg, D-arabinose-1-dehydrogenase; SPN 3/4a, serpin 3/4a.

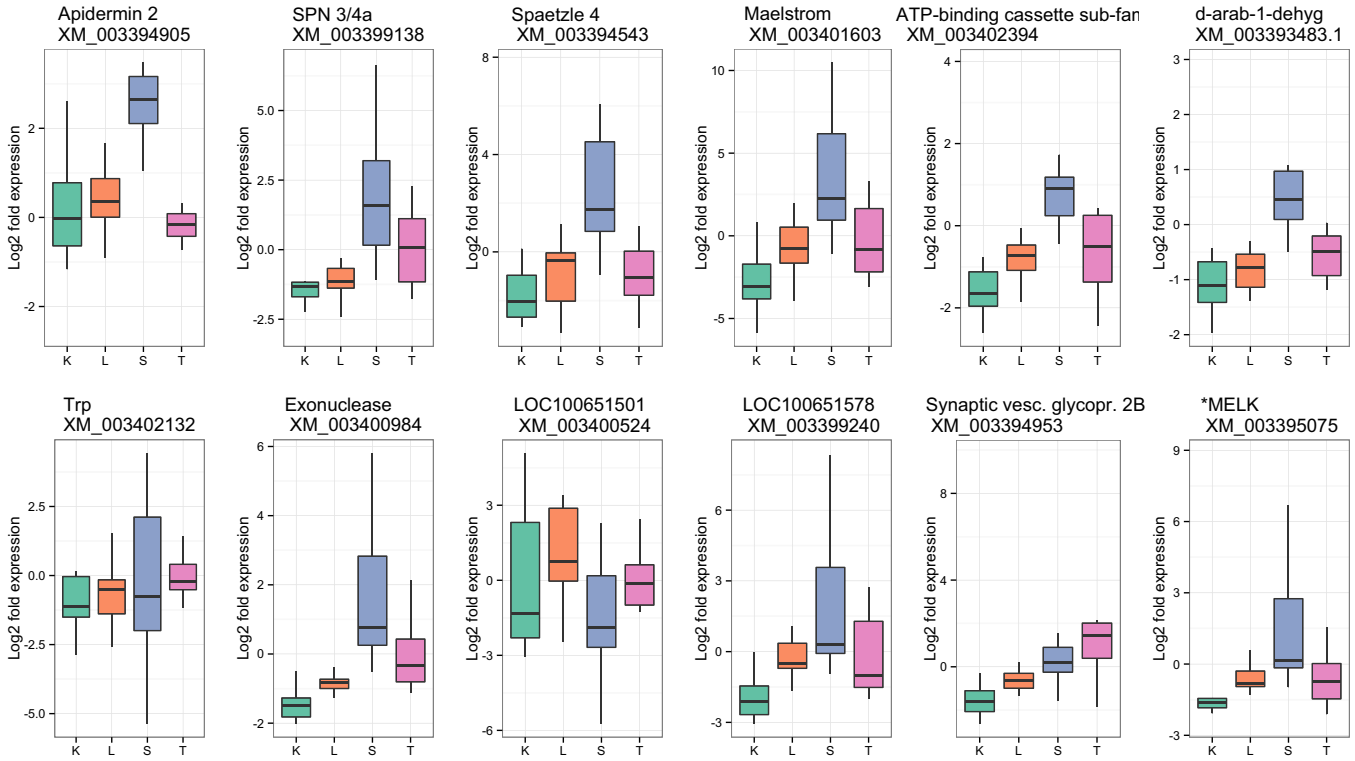

Fig. S3. Logfold change in expression of genes that differ by host genotype [G_H: $F_{3,42} = 4.82$**, $F_{3,42} = 3.30$*, $F_{3,42} = 3.03$*, $F_{3,42} = 5.00$**, $F_{3,42} = 9.20$***, $F_{3,42} = 7.33$***, $F_{3,42} = 4.95$**, $F_{3,42} = 8.99$***, $F_{3,42} = 3.11$*, $F_{3,42} = 3.97$*, $F_{3,42} = 2.65^{\dagger}$, $F_{3,42} = 2.29^{\dagger}$ (reading from left to right and top to bottom); *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, $^{\dagger}P < 0.1$]. In each panel, the *x* axis lists the colonies (K, L, S, and T; and differently colored). Genes and their accession numbers are indicated at the top of each panel. MELK, maternal embryonic leucine zipper kinase; sub-fam, subfamily; Synaptic vesc. glycopr. 2B, synaptic vesicle glycoprotein 2B; Trp, tryptophan.

Table S1. Overrepresented (+) and underrepresented (−) GO terms for bees infected with the parasite genotype no. 68

Root node	Node name	Node ID	Genes	P	Over- or underrepresentation
BP	Negative regulation of transcription from RNA polymerase II promoter	GO:0000122	20	0.019	+*
BP	Aminoglycan metabolic process	GO:0006022	13	0.0083	+
BP	Chitin metabolic process	GO:0006030	9	0.0039	+*
BP	Amino sugar metabolic process	GO:0006040	15	0.011	+
BP	Cellular metabolic process	GO:0044237	1,524	0.015	−
BP	Cellular protein metabolic process	GO:0044267	630	0.020	−*
BP	Cellular localization	GO:0051641	262	0.050	−*
BP	Glucosamine-containing compound metabolic process	GO:1901071	12	0.0071	+
MF	Nucleotide binding	GO:0000166	634	0.023	−*
MF	Protein binding transcription factor activity	GO:0000988	28	0.035	+
MF	Transcription factor binding transcription factor activity	GO:0000989	28	0.035	+
MF	Transcription cofactor activity	GO:0003712	28	0.035	+*
MF	Chitin binding	GO:0008061	5	0.0011	+*
MF	Transcription factor binding	GO:0008134	32	0.0044	+*
MF	Peptidase activity	GO:0008233	132	0.012	+
MF	Serine-type peptidase activity	GO:0008236	29	0.037	+*
MF	Hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds	GO:0016810	30	0.040	+*
MF	Serine hydrolase activity	GO:0017171	29	0.037	+
MF	Small-molecule binding	GO:0036094	645	0.021	−
MF	Anion binding	GO:0043168	492	0.024	−*
MF	Peptidase activity, acting on L-amino acid peptides	GO:0070011	108	0.026	+
MF	Carbohydrate derivative binding	GO:0097367	8	0.0030	+
MF	Nucleoside phosphate binding	GO:1901265	635	0.023	−
CC	Extracellular region	GO:0005576	80	0.031	+*
CC	Cell	GO:0005623	1,776	0.011	−
CC	Cytoplasm	GO:0005737	923	0.012	−
CC	Organelle	GO:0043226	1,196	0.031	−
CC	Intracellular organelle	GO:0043229	1,194	0.031	−*
CC	Intracellular part	GO:0044424	1,511	0.032	−
CC	Cytoplasmic part	GO:0044444	700	0.028	−*
CC	Cell part	GO:0044464	1,775	0.011	−

GO at its coarsest level breaks gene function into three basal root nodes (BP, biological process; CC, cellular component; and MF, molecular function). Root nodes provide the core classification, and the node name gives the finer scale presumed function of genes categorized to these groups.
*Categories that are significant after refinement by FUNC, which tests for overrepresentation or underrepresentation after removing daughter nodes.

Table S2. Overrepresented (+) and underrepresented (−) GO terms for bees infected with the parasite genotype no. 75

Root node	Node name	Node ID	Genes	P	Over- or underrepresentation
BP	Transition metal ion transport	GO:0000041	7	0.028	+*
BP	Meiotic spindle organization	GO:0000212	5	0.020	+*
BP	Assembly of actomyosin apparatus involved in cytokinesis	GO:0000912	8	0.032	+
BP	Cytokinesis, actomyosin contractile ring assembly	GO:0000915	8	0.032	+*
BP	Nucleobase-containing compound metabolic process	GO:0006139	708	0.036	−*
BP	Cellular aromatic compound metabolic process	GO:0006725	743	0.030	−
BP	Nitrogen compound metabolic process	GO:0006807	818	0.020	−
BP	Cellular metal ion homeostasis	GO:0006875	8	0.032	+*
BP	Response to bacterium	GO:0009617	12	0.048	+
BP	Cellular process	GO:0009987	2,412	0.0020	−
BP	Polyol metabolic process	GO:0019751	5	0.020	+*
BP	Cytokinetic process	GO:0032506	9	0.036	+
BP	Meiotic cytokinesis	GO:0033206	5	0.020	+*
BP	Cellular nitrogen compound metabolic process	GO:0034641	752	0.029	−
BP	Hemocyte proliferation	GO:0035172	6	0.024	+*
BP	Defense response to bacterium	GO:0042742	9	0.036	+*
BP	Cellular metabolic process	GO:0044237	1,524	0.014	−
BP	Cellular biosynthetic process	GO:0044249	672	0.044	−*
BP	Cellular macromolecule metabolic process	GO:0044260	1,061	0.036	−*
BP	Heterocycle metabolic process	GO:0046483	736	0.031	−
BP	Anatomical structure development	GO:0048856	683	0.042	−*
BP	Metal ion homeostasis	GO:0055065	10	0.040	+
BP	Organic cyclic compound metabolic process	GO:1901360	754	0.028	−
MF	Carboxylesterase activity	GO:0004091	5	0.028	+*
MF	Binding	GO:0005488	1,852	0.030	−
MF	Iron ion binding	GO:0005506	21	0.0059	+*
MF	Serine-type peptidase activity	GO:0008236	29	0.011	+*
MF	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0016701	5	0.028	+*
MF	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0016705	32	0.013	+*
MF	Serine hydrolase activity	GO:0017171	29	0.011	+
MF	Organic cyclic compound binding	GO:0097159	993	0.049	−*
MF	Heterocyclic compound binding	GO:1901363	992	0.049	−*
CC	Extracellular region	GO:0005576	80	0.0001	+*
CC	Intracellular	GO:0005622	1,645	0.022	−*
CC	Cell	GO:0005623	1,776	0.0059	−
CC	Macromolecular complex	GO:0032991	750	0.033	−*
CC	Organelle part	GO:0044422	679	0.048	−*
CC	Cell part	GO:0044464	1,775	0.0060	−

GO at its coarsest level breaks gene function into three basal root nodes (BP, CC, and MF). Root nodes provide the core classification, and the node name gives the finer scale presumed function of genes categorized to these groups.

*Categories that are significant after refinement by FUNC, which tests for overrepresentation or underrepresentation after removing daughter nodes.

Table S3. Overrepresented (+) and underrepresented (−) GO terms for bees infected with the parasite genotype 161

Root node	Node name	Node ID	Genes	P	Over- or underrepresentation
BP	Negative regulation of transcription from RNA polymerase II promoter	GO:0000122	20	0.015	+*,†
BP	M phase	GO:0000279	9	0.0032	+*
BP	Cellular protein modification process	GO:0006464	340	0.028	−*
BP	Smoothened signaling pathway	GO:0007224	22	0.019	+
BP	Zygotic determination of anterior/posterior axis, embryo	GO:0007354	5	0.048	+
BP	Terminal region determination	GO:0007362	5	0.048	+*
BP	Metabolic process	GO:0008152	1,894	0.0093	−
BP	Regulation of smoothened signaling pathway	GO:0008589	10	0.0040	+
BP	Wnt receptor signaling pathway	GO:0016055	35	0.046	+
BP	Dendrite development	GO:0016358	30	0.034	+
BP	Cell cycle phase	GO:0022403	31	0.037	+
BP	Regulation of Wnt receptor signaling pathway	GO:0030111	17	0.012	+
BP	Negative regulation of Wnt receptor signaling pathway	GO:0030178	7	0.0019	+
BP	Positive regulation of Ras GTPase activity	GO:0032320	5	0.048	+
BP	Positive regulation of Rab GTPase activity	GO:0032851	5	0.048	+*
BP	Protein modification process	GO:0036211	340	0.028	−
BP	Macromolecule modification	GO:0043412	357	0.023	−
BP	Cellular metabolic process	GO:0044237	1,524	0.0069	−*
BP	Primary metabolic process	GO:0044238	1,503	0.023	−
BP	Cellular macromolecule metabolic process	GO:0044260	1,061	0.023	−
BP	Cellular protein metabolic process	GO:0044267	630	0.0009	−
BP	Single-organism metabolic process	GO:0044710	540	0.021	−*
BP	Cell–cell signaling involved in cell fate commitment	GO:0045168	55	0.016	+
BP	Mitotic cell cycle, embryonic	GO:0045448	5	0.048	+*
BP	Negative regulation of smoothened signaling pathway	GO:0045879	7	0.0019	+
BP	Lateral inhibition	GO:0046331	54	0.015	+
BP	Dendrite morphogenesis	GO:0048813	29	0.032	+
BP	Organic substance metabolic process	GO:0071704	1,546	0.016	−
MF	DNA binding	GO:0003677	192	0.012	+*,†
MF	Transcription cofactor activity	GO:0003712	28	0.018	+*,†
MF	Nucleotide binding	GO:0000166	634	0.0038	−
MF	Nucleoside binding	GO:0001882	406	0.033	−
MF	Purine nucleoside binding	GO:0001883	403	0.034	−
MF	Endopeptidase activity	GO:0004175	59	0.010	+
MF	Serine-type endopeptidase activity	GO:0004252	16	0.0066	+
MF	Polypeptide N-acetylgalactosaminyltransferase activity	GO:0004653	6	0.046	+*
MF	Small GTPase regulator activity	GO:0005083	25	0.016	+
MF	Ras guanyl-nucleotide exchange factor activity	GO:0005088	6	0.046	+*
MF	Rab GTPase activator activity	GO:0005097	6	0.046	+*
MF	Transcription factor binding	GO:0008134	32	<0.0001	+*
MF	Peptidase activity	GO:0008233	132	0.0031	+
MF	Serine-type peptidase activity	GO:0008236	29	0.0014	+*
MF	Acetylgalactosaminyltransferase activity	GO:0008376	6	0.046	+
MF	Purine nucleotide binding	GO:0017076	406	0.033	−
MF	Serine hydrolase activity	GO:0017171	29	0.0014	+
MF	GTPase regulator activity	GO:0030695	45	0.048	+
MF	Ribonucleoside binding	GO:0032549	406	0.033	−
MF	Purine ribonucleoside binding	GO:0032550	403	0.034	−*
MF	Ribonucleotide binding	GO:0032553	409	0.032	−
MF	Purine ribonucleotide binding	GO:0032555	405	0.033	−*
MF	Purine ribonucleoside triphosphate binding	GO:0035639	403	0.034	−*
MF	Small-molecule binding	GO:0036094	645	0.0035	−
MF	Anion binding	GO:0043168	492	0.015	−
MF	Nucleoside-triphosphatase regulator activity	GO:0060589	46	0.049	+
MF	Peptidase activity, acting on L-amino acid peptides	GO:0070011	108	0.0013	+*
MF	Nucleoside phosphate binding	GO:1901265	635	0.0038	−
CC	Chromosome, centromeric region	GO:0000775	13	0.0060	+*
CC	Cytoplasm	GO:0005737	923	0.0017	−

Table S3. Cont.

Root node	Node name	Node ID	Genes	P	Over- or underrepresentation
CC	Intracellular part	GO:0044424	1,511	0.017	–
CC	Chromosomal part	GO:0044427	70	0.025	+
CC	Cytoplasmic part	GO:0044444	700	0.021	–*

GO at its coarsest level breaks gene function into three basal root nodes (BP, CC, and MF). Root nodes provide the core classification, and the node name gives the finer scale presumed function of genes categorized to these groups.

*Categories that are significant after refinement by FUNC, which tests for overrepresentation or underrepresentation after removing daughter nodes.

†Categories that are only over- or under-represented after refinement.

Table S4. Primer details and ANOVA results for each gene

Analysis 1			Analysis 2								
G_H (3,64)	Exposure (1,64)	$G_H \times$ Exp (3,64)	G_H (3,42)	G_P (2,42)	$G_H \times G_P$ (6,42)	Description	Identifier	Transcriptome pattern	Forward primer	Reverse primer	Product
				2.96†		Histone H3-like LOC100645858	XM_003392921	down161	TCGTACTGTTTGAAAGGATGGC	CCTTAGTAGCCAACTGCTTACG	90
						Major royal jelly protein 2-like LOC100651804	XM_003396655	down161	TCTAACAACCTCTGAGCTGCTG	TCTGCATCCGCTATGTACACG	150
6.46***			4.95**			Transient receptor potential protein-like LOC100651056	XM_003402132	down161	CAGATTCTGGGCGCTTCTTATG	CATTCAGTGTCAGCTCTTTCCG	126
2.55†		2.72†	5.00**			ATP-binding cassette subfamily G member 1-like LOC100644985	XM_003402394	down161	ATCGCGGAAAGTATGGCATTAG	GCCCAACAAACGTACAATTCAC	67
			2.26†	10.28***		Maternal embryonic leucine zipper kinase-like LOC100647257 MELK	XM_003395075	down68	CAATTACGTCGTGCTCTTCGTC	CGTTTCTCCTTGTAGAATGAACCC	72
		3.35*	3.30*	6.41**		Hypothetical protein LOC100651557 spaetzle 4	XM_003394543	down68	CCGCGAAAGATCAACAGGAAC	ACGGGACAAGCATTTACTCCTC	61
				2.47†		Homeobox protein Nkx-2.1-like LOC100642447	XM_003395361	down68	CAAGCAGCAGAAATACCTGAGC	TTTCACCTGAGTGGGCGTAAG	79
						Hypothetical protein LOC100642500	XM_003399329	down68	AGGGAGACTTTCGATCACACG	AACAACAGTGCCAACAGACAC	95
			3.11*	3.99*		Hypothetical protein LOC100651501	XM_003400524	down68	TGGTGATGTGTTTGTGGATTGC	ACACGAAGAACGAGTCTGTACG	120
5.64**			7.33***	7.00**		LOC100652273 synaptic vesicle glycoprotein 2B-like	XM_003394953	down68_161	CAGAGCACTCAGTGGATTCTTC	TATCAACCACGATAGGGTCCAG	136
		3.48*	3.03*	12.87***		Maelstrom LOC100644702	XM_003401603	down161	GACGAATGGAGAGTAAAGTGGAC	GGCGCATTGGCAAATTTAGAG	90
		2.77*	2.65†	10.47***		LOC100644009 cytochrome P450 315a1	XM_003394564	down68	CCGCGGTTTACTGTTCATGG	TCTAAGTCCAATGGCCACCTC	130
			3.97*	11.61***		LOC100651578 uncharacterized	XM_003399240	down68_161	AAGACGTTCGTCATCATCTTGG	CTTTGCTCGATGAGGTAACGG	101
			2.39†	8.11**		LOC100648144 uncharacterized	XM_003400332	shared_68_161	CGATAAAGACAAGGTCGAGATGC	TTACCGATCTGCTTCGTCTCTG	73
				5.88**		LOC100649557 uncharacterized	XM_003402887	shared_68_161	GCACGTTTAGCACAACAAATGC	TCCTGAGCACGTTGTAACTGAG	83

Table S4. Cont.

Analysis 1			Analysis 2								
G_H (3,64)	Exposure (1,64)	$G_H \times$ Exp (3,64)	G_H (3,42)	G_P (2,42)	$G_H \times G_P$ (6,42)	Description	Identifier	Transcriptome pattern	Forward primer	Reverse primer	Product
		2.73†	3.15*	7.51**	2.09†	LOC100648226 limkain-b1-like	XM_003400820	shared_68_161	CCAGATTCTCCACCTGAGGAAG	GGTAAAGTAAACGGAGGAACGTG	131
		5.44**	8.99***	8.44***		LOC100647912 exonuclease 3′-5′ domain-containing protein 2	XM_003400984	shared_68_161	CGCACCTTTAGTTGGTCCATTG	AAATCTTTGCGTCGTGCATCAG	126
3.11*			5.67**	5.75**	1.95†	LOC100650150 leucine-rich repeat-containing G protein coupled receptor 4 (Toll-like receptor)	XM_003395506	shared_68_75	GAGAACATCGACGCAATGGAG	TTAGCCTGTTCATGCCTTTGTG	115
				3.30*		Hypothetical protein LOC100644966 (putative AMP)	XM_003396598	up75	TCCTCGACACATCATCAACGAC	GCTGTTTGCGGTTGTATACTCG	106
		2.46†		3.41*	2.75*	Esterase FE4-like LOC100644683	XM_003397252	up75	CGTTGGGCTCCTTATTCGATTG	GAACCTGATAGAATCTCCTTTGCG	141
			3.31*	5.62**	2.73*	Apidaecin LOC100649867	XM_003402966	up75	CCACCATGTTCACCATATCTGC	CATCTGCATCAGCTCCATGAC	130
					2.25†	Serine protease inhibitor 3-like LOC100651307	XM_003402976	up75	CACAGAAAGACGTACAGTAACACG	TTCATAAACAGCAGCACCAAGC	104
3.99*	3.30†	2.34†	4.82**	3.64*		Apidermin 2 LOC100645985	XM_003394905	shared_75_161_up	TCATCAGTCGCTTGCTATTTCG	GATGGCGAAGAGGATCAACAG	83
5.43**	8.25**	6.64***	9.20***			D-arabinose-1-dehydrogenase–like LOC100647407	XM_003393483	down68_161, sharedall	TGGAAGCCGTTAAGGCTATGG	CGTACCATAATGACAACCAAGCG	104
				2.55†	2.32*	Abaecin	XM_003394653		GCCACAATATGTGGAATCCT	ATGACCAGGGTTTGGTAATG	141
3.87*		3.17*	8.40***		2.11†	Serine protease inhibitor 3/4a LOC100648482	XM_003399138	shared_68_161	GCAGAGACAAATGTTGAAGCAC	CACAGTCTGGGATAATGAAGAACC	78
3.12*						Defensin	NM_001280909	shared_68_75	GTCTGCCTTTGTCGCAAGAC	GACATTAGTCGCGTCTTCTTCG	139
				2.94†		Hymenoptaecin LOC100631061	XR_132450	shared_68_75	TTCATCGTACTGGCTCTCTTCTG	AGCCGTAGTATTCTTCCACAGC	85
						Arginine kinase	AF_492888		CTGGACTCTGGTGTCGGTAT	GTCTTTTGGTGGATGCTTGT	129
						Elongation factor α	XM_003401944		GCTGGTGACTCGAAGAACAATC	GGGTGGTTCAACACAATAACCTG	74
						Phospholipase A2	FN_391388		TATCTTTCAATGCCCAGGAG	GTCGTAACAAATGTCATGCG	129

Analysis 1 treated expression as a dependent variable of exposure (exposed or unexposed) and host genotype (G_H). Analysis 2 treated expression as the dependent variable of both the genotype of the parasite (G_P) and of the host (G_H). The *F* statistics are given for each of the two model factors and their interaction in the first six columns, with the degrees of freedom found in the header. *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$; $^{\dagger}P < 0.1$.