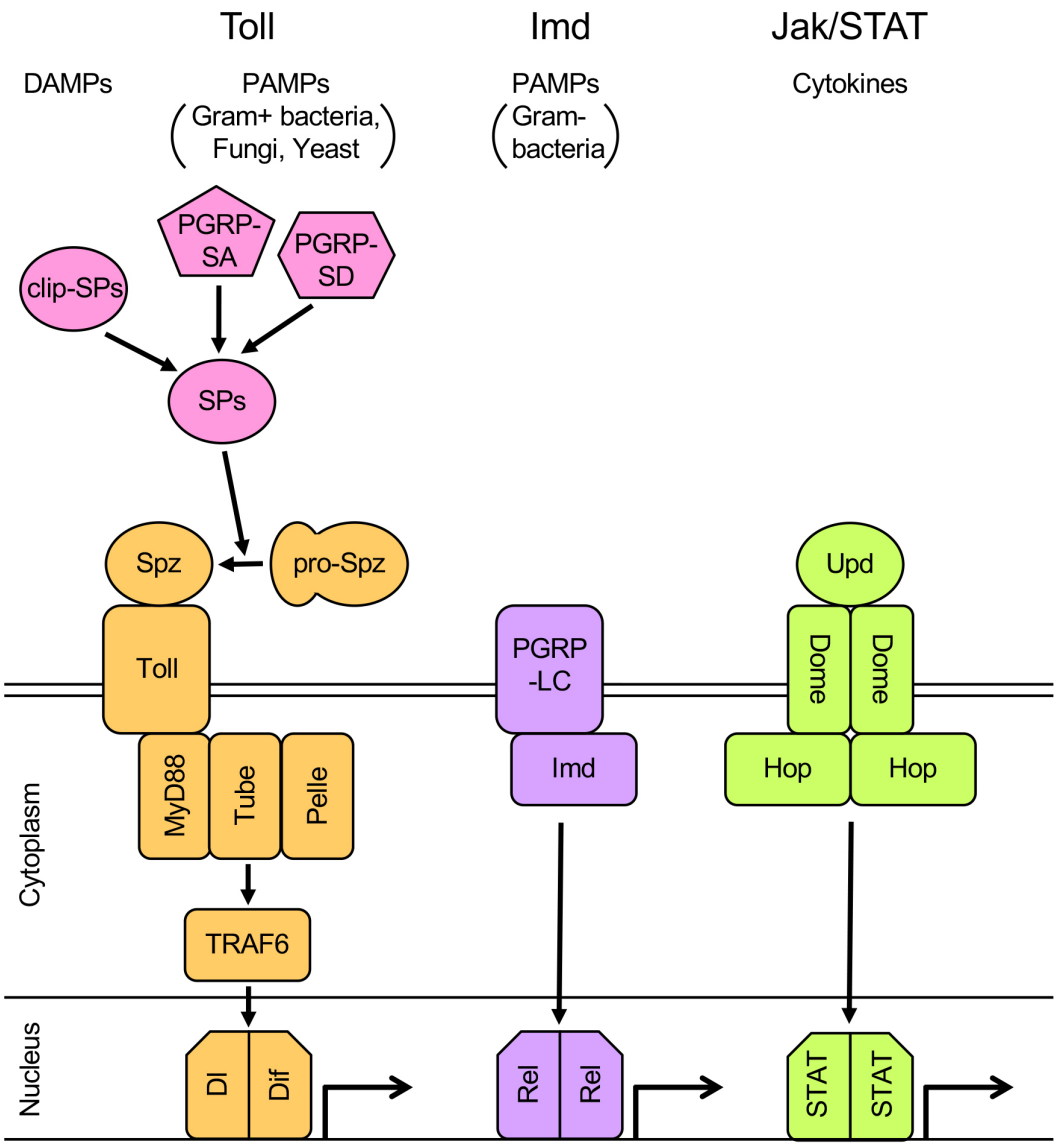
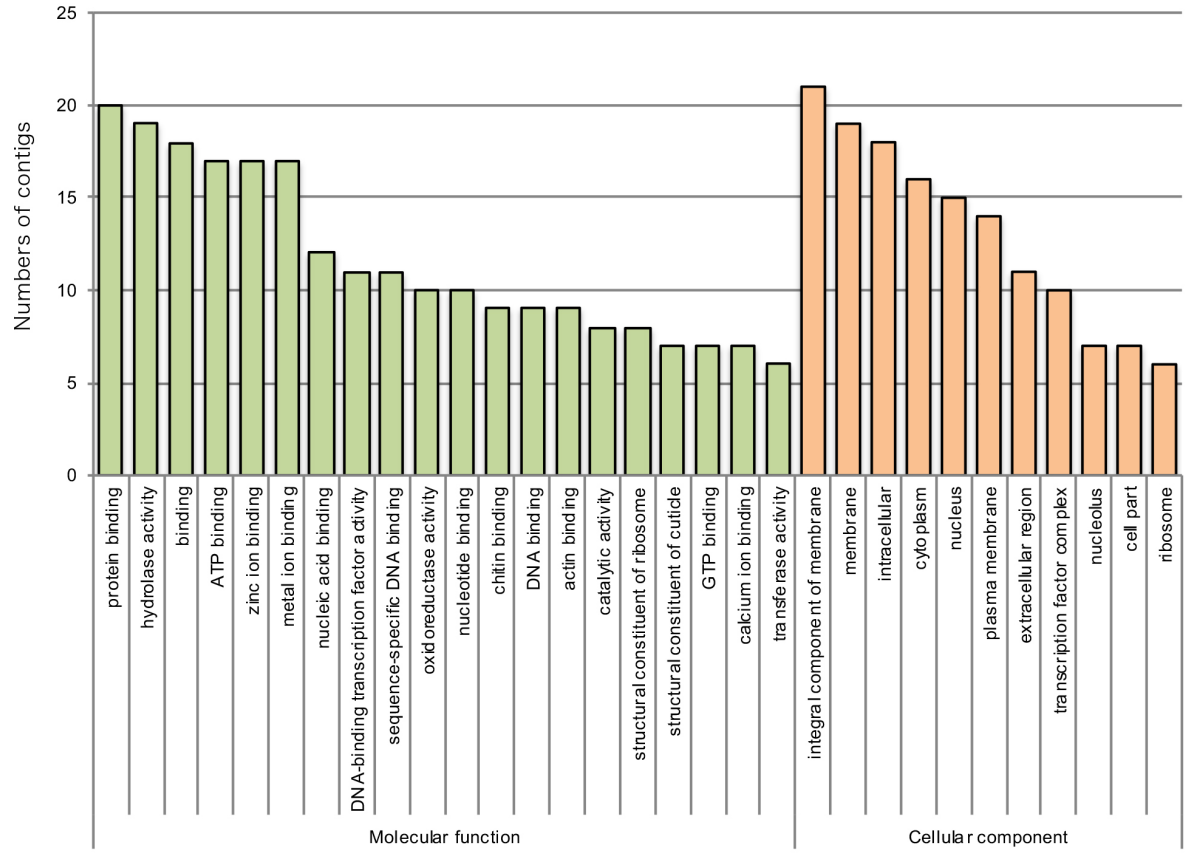



**Fig. S1. Signalling pathways of insect immunity, after Hillyer (2016), Lindsay and Wasserman (2014) and Anthoney et al. (2018).**
Schematic diagram of Toll, Imd, and JAK/STAT signalling pathways for insect immunity. Infectious pathogens, including gram-positive bacteria, fungi, and yeasts, are recognised by PGRP-SA and PGRP-SD, which activate clip-domain serine proteinases (clip-SPs) to catalyse pro-Spz to Spz. Matured Spz binds to Tolls and activates NF-κB transcription factors Dl and Dif via MyD88, Tube, Pelle, and TRAF6. DAMPs released from injured cells activate clip-SPs. Gram-negative bacteria are recognised by PGRP-LC via Imd and activate NF-κB transcription factor Rel. Insect cytokine Upd binds to interleukin receptor Dome and activates transcription factor STAT via Janus kinases Hop (Anthoney et al., 2018; Hillyer, 2016; Lindsay and Wasserman, 2014).
Abbreviations: JAK/STAT, Janus kinase/signal transducer and activator of transcription protein; NF-κB, nuclear factor kappa-B; Dl, dorsal; Dif, dorsal-related immunity factor; Dome, Domeless; MyD88, myeloid differentiation primary response 88; TRAF6, TNF receptor-associated factor 6; DAMPs, damage-associated molecular patterns; Psh, Persephone; PGRP, Peptidoglycan recognition protein; Spz, Spatzle; Hop, Hopscotch; Imd, Immune deficiency; Rel, Relish; Upd, Unpaired.

**A**




**B**

| contig_ID | Sequence description | Length | 0 hpa 595,425 reads in total # Reads | 0 hpa RPKM | 3 hpa 519,961 reads in total # Reads | 3 hpa RPKM | RPKM Ratio 3h/0h |
|---|---|---|---|---|---|---|---|
| Transcription factors | | | | | | | |
| isotig04802 | kayak | 2,559 | 23 | 15.09 | 101 | 75.91 | 5.03 |
| isotig11345 | dna-binding protein d-ets-4 | 2,174 | 16 | 12.36 | 38 | 33.62 | 2.72 |
| isotig06051 | ets homologous factor-like | 2,648 | 24 | 15.22 | 54 | 39.22 | 2.58 |
| isotig16044 | ap-1 | 1,030 | 38 | 61.96 | 72 | 134.44 | 2.17 |
| VEGF signalling | | | | | | | |
| isotig15859 | Platelet-derived and vascular endothelial growth factors | 1,060 | 2 | 3.17 | 25 | 45.36 | 14.31 |
| isotig13937 | pvf3 cg34378-pd | 1,380 | 3 | 3.65 | 17 | 23.69 | 6.49 |
| isotig18768 | vascular endothelial growth factor a-a-like | 705 | 5 | 11.91 | 15 | 40.92 | 3.44 |
| isotig03363 | vascular endothelial growth factor receptor 1-like | 6,760 | 29 | 7.2 | 71 | 20.2 | 2.81 |
| isotig14929 | vascular endothelial growth factor receptor 1 isoform x2 | 1,200 | 15 | 20.99 | 34 | 54.49 | 2.6 |
| isotig14209 | pdgf vegf receptor | 1,325 | 7 | 8.87 | 13 | 18.87 | 2.13 |
| IGF signalling | | | | | | | |
| isotig09133 | tribbles homolog 2 | 4,891 | 136 | 46.7 | 254 | 99.88 | 2.14 |
| FGF signaling | | | | | | | |
| isotig11083 | dual specificity protein phosphatase mpk3-like | 2,311 | 10 | 7.27 | 25 | 20.81 | 2.86 |
| isotig11152 | fgfr1 oncogene partner 2 homolog | 2,269 | 10 | 7.4 | 21 | 17.8 | 2.41 |
| TGF-β signalling | | | | | | | |
| isotig14196 | transforming growth factor beta regulator 1 | 1,328 | 6 | 7.59 | 18 | 26.07 | 3.43 |
| isotig03246 | smad nuclear-interacting protein 1 | 2,945 | 17 | 9.69 | 30 | 19.59 | 2.02 |
| Wnt signalling | | | | | | | |
| isotig12204 | disheveled-associated activator of morphogenesis 2 | 1,823 | 10 | 9.21 | 34 | 35.87 | 3.89 |
| Toll signalling | | | | | | | |
| isotig06664 | Toll2-5 | 2,309 | 17 | 12.37 | 35 | 29.15 | 2.36 |
| isotig12616 | unc93-like | 1,697 | 11 | 10.89 | 22 | 24.93 | 2.29 |
| isotig05588 | Relish | 4,770 | 27 | 9.51 | 52 | 20.97 | 2.21 |
| isotig09244 | Toll8 (slit homolog 2) | 4,522 | 43 | 15.97 | 82 | 34.87 | 2.18 |
| isotig17867 | Toll2-2 | 814 | 9 | 18.57 | 17 | 40.17 | 2.16 |
| isotig11861 | serine protease easter | 1,956 | 45 | 38.64 | 79 | 77.68 | 2.01 |

**Fig. S2. GO annotations of RNA-seq results.**
(A) Graphs show 20 and 11 most frequently counted GO terms of molecular function and cellular components by annotations of the transcripts with upregulated expression in RLs. (B) Selected signalling pathway genes upregulated in RLs (3 hpa) compared with NLs (0 hpa). Note that contigs are assembled sequences of reads obtained from RLs and NLs, and isotigs are assembled sequences of contigs.

**A**

| Gene name | Contig | Region (bp) |
|---|---|---|
| *Toll* | Contig34 | 815164 - 803187 |
| *Toll2-1* | Contig175 | 1629363 - 1615808 |
| *Toll2-2* | Contig590 | 2211452 - 2224860 |
| *Toll2-3* | Contig7 | 597224 - 621200 |
| *Toll2-4* | Contig79 | 4071160 - 4076220 |
| *Toll2-5* | Contig175 | 2955568 - 2942763 |
| *Toll6-1* | Contig285 | 4448827 - 4452034 |
| *Toll6-2* | Contig330 | 781359 - 783951 |
| *Toll7* | Contig330 | 7144339 - 7140837 |
| *Toll8* | Contig285 | 7182752 - 7187271 |
| *Toll9* | Contig121 | 18924776 - 18926973 |

**B**

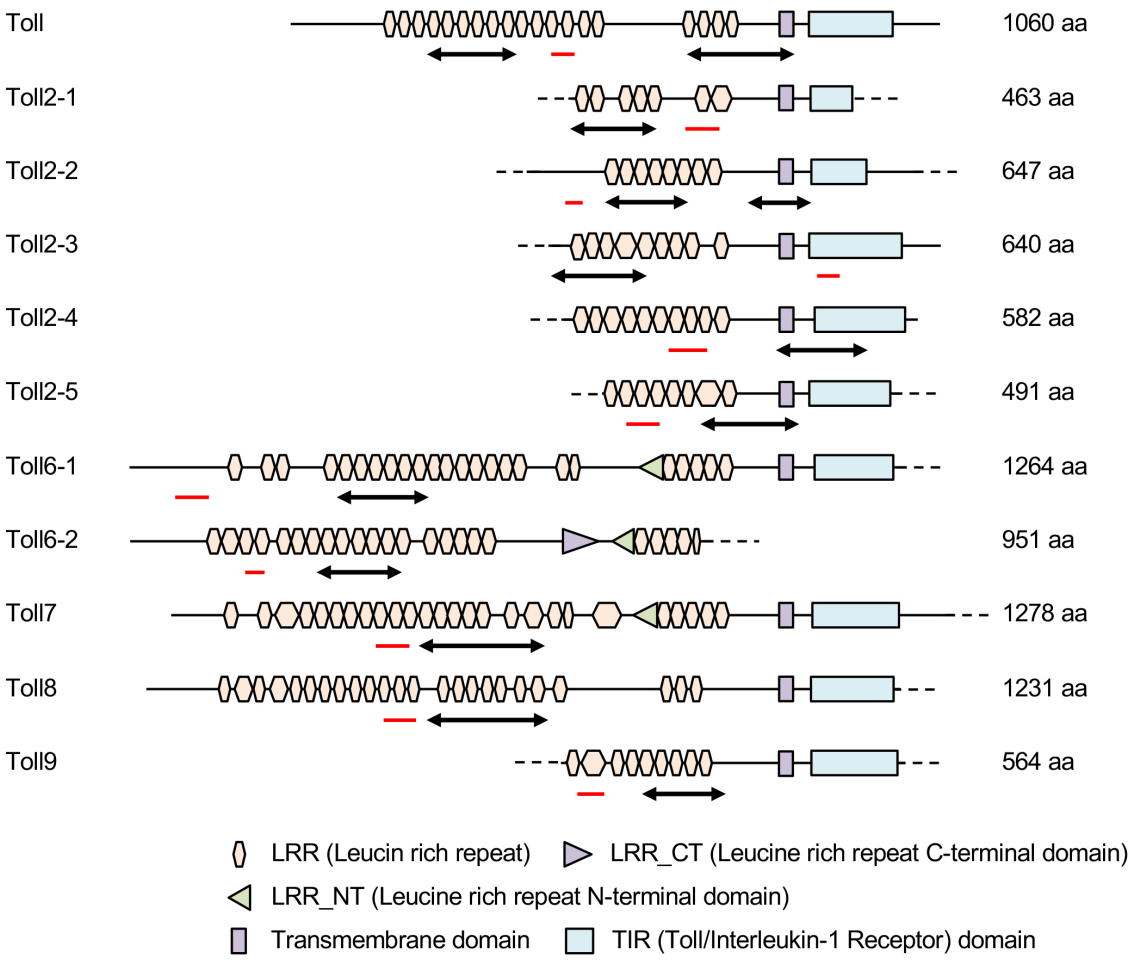



**Fig. S3. Genomic loci of *Gryllus* Toll genes and their domain structures.**

(A) Physical positions of *Gryllus* Toll genes spanning the genome contigs. Note that three pairs of Toll genes (*Toll2-1* and *Toll2-5*, *Toll6-1* and *Toll8*, and *Toll6-2* and *Toll7*) are located at the different regions of same contigs. (B) Schematic diagram of *Gryllus* Toll proteins is shown. Domains were predicted by Protein BLAST at NCBI web BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) and SMART website (http://smart.embl-heidelberg.de/). Dotted lines indicate regions that we have not cloned. Double-headed arrows and red lines indicate regions for RNAi and qPCR, respectively. To verify the specificity of RNAi against *Toll* or *Toll2-2*, we compared the phenotype using dsRNAs corresponding to two independent regions of each gene. The phenotypic effects by RNAi against *Toll(5')*, which correspond to an extracellular LRR region, and *Toll(3')*, which corresponds to an extracellular region and transmembrane domain were not significantly different ($p>0.05$, Fisher's exact test) (see Fig. S4B). The similar results were obtained for *Toll2-2*$^{RNAi}$. We therefore used the *Toll(5')* and *Toll2-2(5')* fragments for all subsequent analyses.

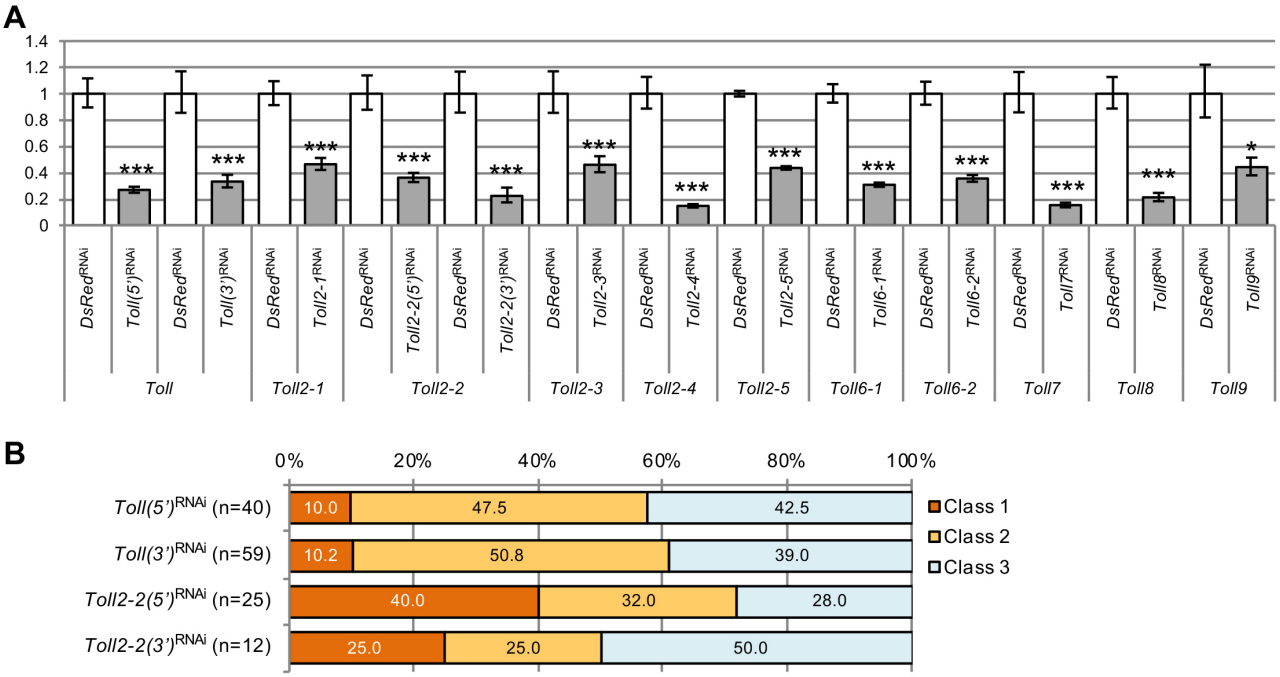



**Fig. S4. Efficiencies of RNAi for *Gryllus* Toll genes.**

(A) RNAi efficiencies to endogenous on-target genes, revealed by qPCR. Two independent regions of *Toll* (*Toll(5')* and *Toll(3')*) and *Toll2-2* (*Toll2-2(5')* and *Toll2-2(3')*) were used for RNAi experiments to observe phenotype reproducibility. The y-axis indicates normalized expression of *Gryllus* Toll genes in the *DsRed*$^{RNAi}$ samples and relative expression levels in the RNAi samples against the corresponding Toll genes. Asterisks indicate significance between *DsRed*$^{RNAi}$ and RNAi against Toll genes (*$p < 0.05$, ***$p < 0.001$ by Student's t-test). (B) Graph shows the percentage of class 1, class 2, and class 3 phenotypes obtained by RNAi against two independent regions of *Toll* and *Toll2-2* genes. Numbers of RNAi-treated individuals are shown by *n*. The phenotype ratios of *Toll(5')*$^{RNAi}$ and *Toll(3')*$^{RNAi}$ were similar ($p = 0.954747$, Fisher's exact test) and those of *Toll2-2(5')*$^{RNAi}$ and *Toll2-2(3')*$^{RNAi}$ were also similar ($p=0.462691$, Fisher's exact test).

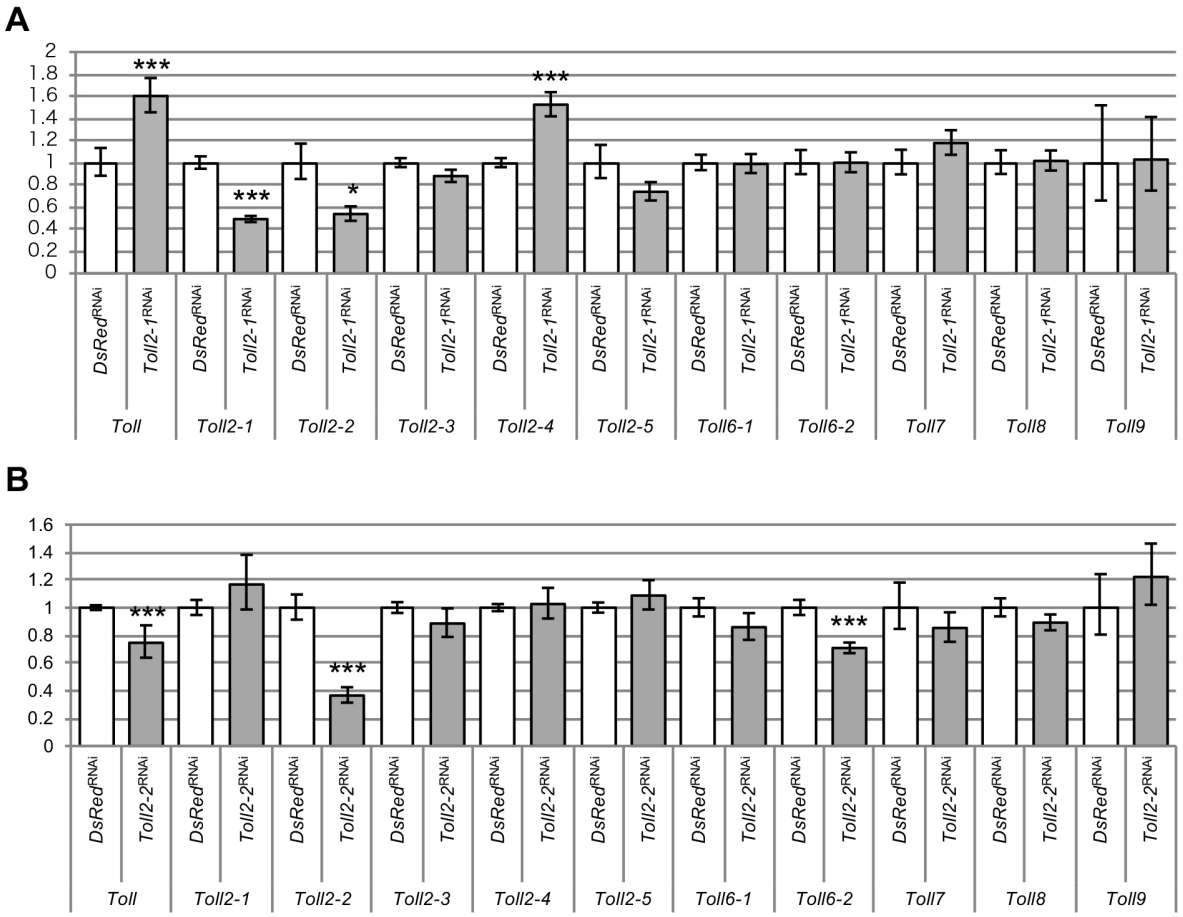



**Fig. S5. Efficiencies of RNAi for *Toll2-1* and *Toll2-2* genes.**

(A,B) RNAi efficiencies to on-target and off-target genes by *Toll2-1*$^{RNAi}$ (A) and *Toll2-2*$^{RNAi}$ (B). The y-axes indicate normalized expression of *Gryllus* Toll genes in the *DsRed*$^{RNAi}$ samples and relative expression levels in the RNAi samples against the corresponding Toll genes. Asterisks indicate significance between *DsRed*$^{RNAi}$ and RNAi against each Toll gene (*$p < 0.05$, ***$p < 0.001$ by Student's t-test). (C) The nucleotide sequence homology between the dsRNA region of *Toll2-1* and the most homologous region of *Toll2-2*. The homology score was 49.46% between them. We could not find the homologous region that spans more than 21 bp, which would work as siRNA to inhibit *Toll2-2* expression, when we injected *Toll2-1* dsRNA.

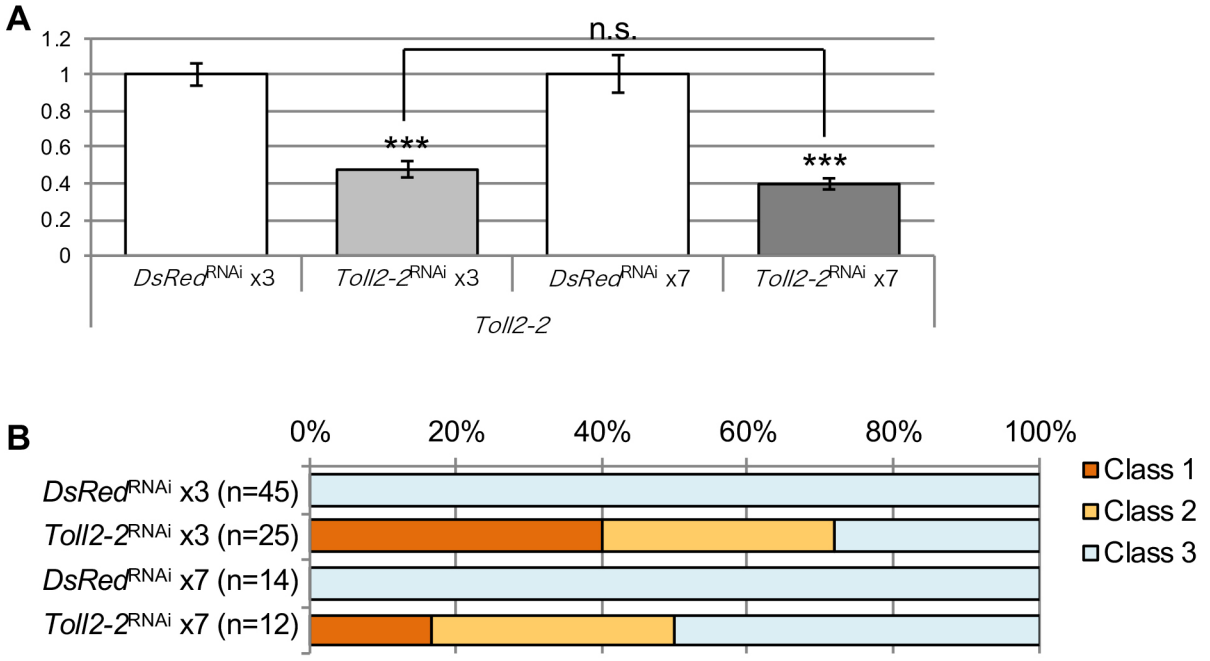



**Fig. S6. RNAi efficiency and phenotype ratio of *Toll2-2*$^{RNAi}$ in different dsRNA dose.**

(A) Relative expression levels of *Toll2-2* after *Toll2-2*$^{RNAi}$ x3 (207 nL dsRNA injection) or *Toll2-2*$^{RNAi}$ x7 (483 nL dsRNA injection) to see RNAi efficiencies. The y-axis indicates normalized expression of *Toll2-2* in the *DsRed*$^{RNAi}$ samples and relative expression levels in the *Toll2-2*$^{RNAi}$ samples. 207 nL or 483 nL of *DsRed* dsRNA were injected into control nymphs. Relative expression levels of *Toll2-2* in *Toll2-2*$^{RNAi}$ x3 and *Toll2-2*$^{RNAi}$ x7 were significantly reduced compared with respective control experiments (***$p < 0.001$ by Student's t-test), but reduction of *Toll2-2* expression by *Toll2-2*$^{RNAi}$ x7 was not significant to that by *Toll2-2*$^{RNAi}$ x7 (n.s.; not significant). (B) Phenotypic ratios of RNAi by *Toll2-2*$^{RNAi}$ x3 or *Toll2-2*$^{RNAi}$ x7. Ratios of class 1 and class 2 were not significantly changed by *Toll2-2*$^{RNAi}$ x7 compared with *Toll2-2*$^{RNAi}$ x3 ($p>0.05$, Fisher's exact test).

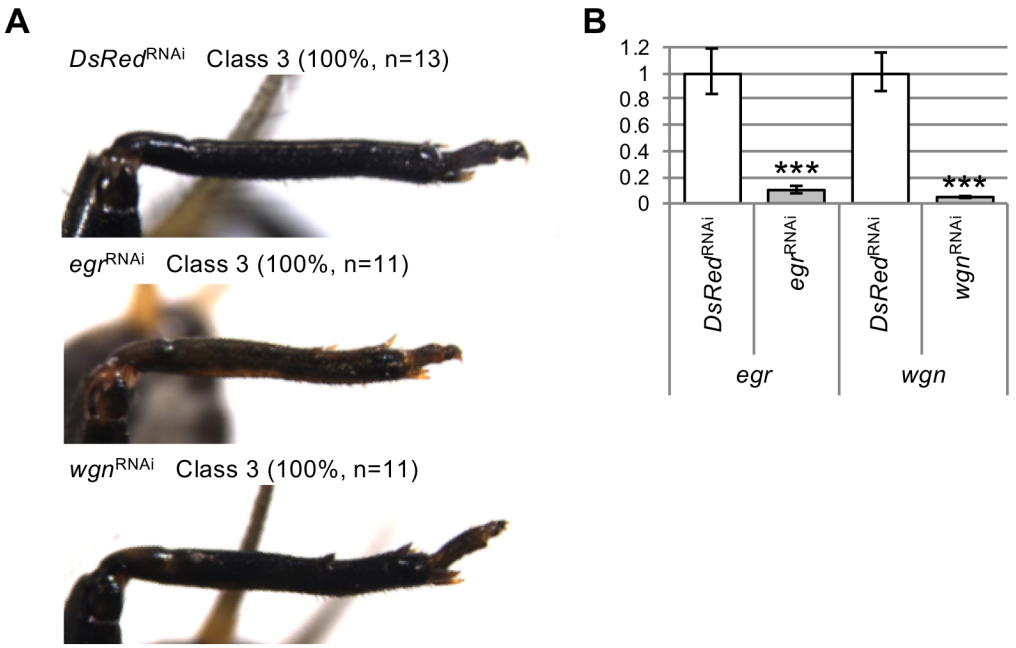



**Fig. S7. Phenotypes of RNAi for *egr* and *wgn*.**

Typical morphology of regenerating legs of *DsRed*$^{RNAi}$, *egr*$^{RNAi}$, or *wgn*$^{RNAi}$ crickets at the fifth instar. Note that these RNAi crickets regenerated the lost part normally, and no RNAi crickets showed class 1 or 2 phenotypes. (B) Efficiency of RNAi against *egr* and *wgn*. The y-axis indicates normalized expression of *egr* and *wgn* in the *DsRed*$^{RNAi}$ samples and relative expression levels in the *egr*$^{RNAi}$ and *wgn*$^{RNAi}$ samples. Asterisks indicate significance between *DsRed*$^{RNAi}$ and RNAi against *egr* or *wgn* (***$p < 0.001$ by Student's t-test).

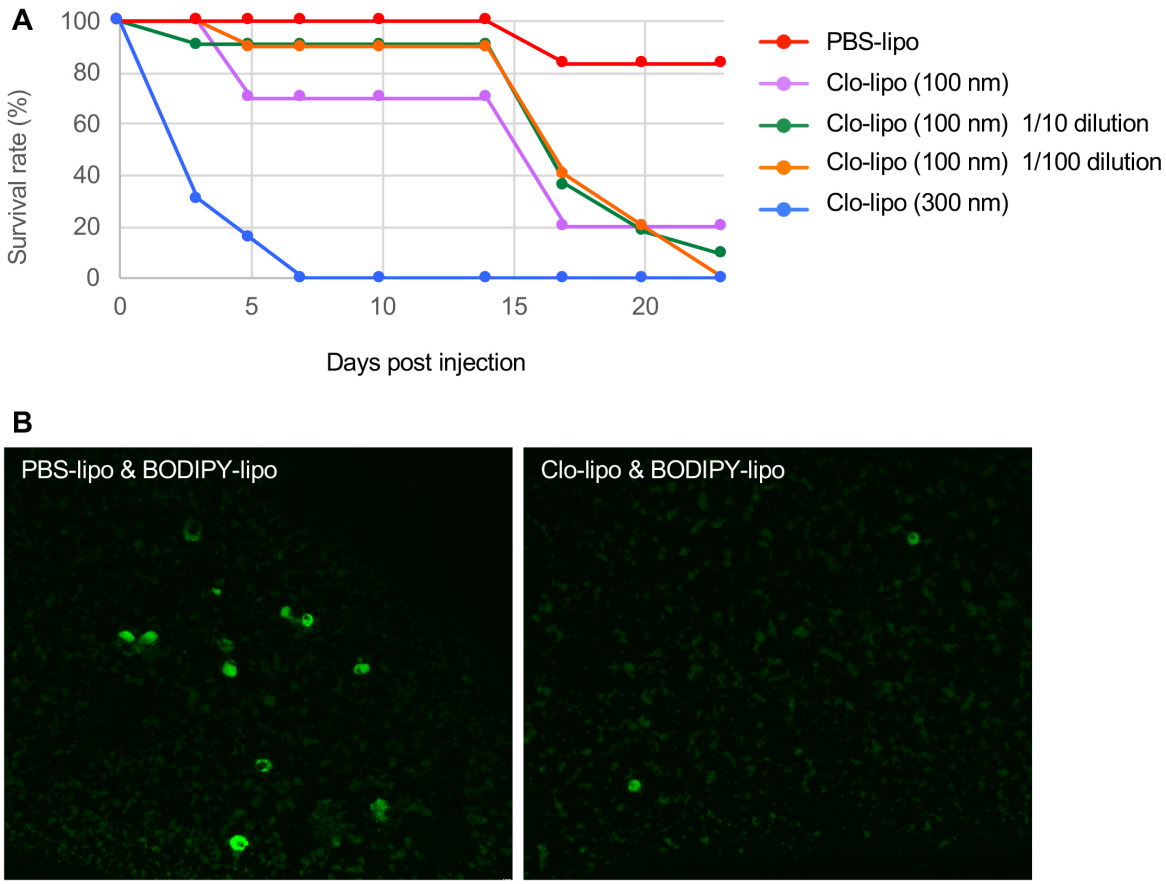



**Fig. S8. Effects of plasmatocyte depletion.**

(A) Survival curve of PBS-lipo, Clo-lipo (100 nm) or Clo-lipo (300 nm) injected cricket nymphs. The mean lifespan of Clo-lipo (100 nm) injected crickets was 15 days, which was longer than that of Clo-lipo (300 nm) injected crickets (2.5 days). The short lifespan of Clo-lipo (300 nm) injected crickets was an obstacle to observing regeneration processes. Thus, we used Clo-lipo (100 nm) to deplete the plasmatocytes in this study. PBS was used as the diluent. (B) Plasmatocytes in the haemolymph were visualised by BODIPY-lipo incorporation in the PBS-lipo injected or Clo-lipo injected crickets.

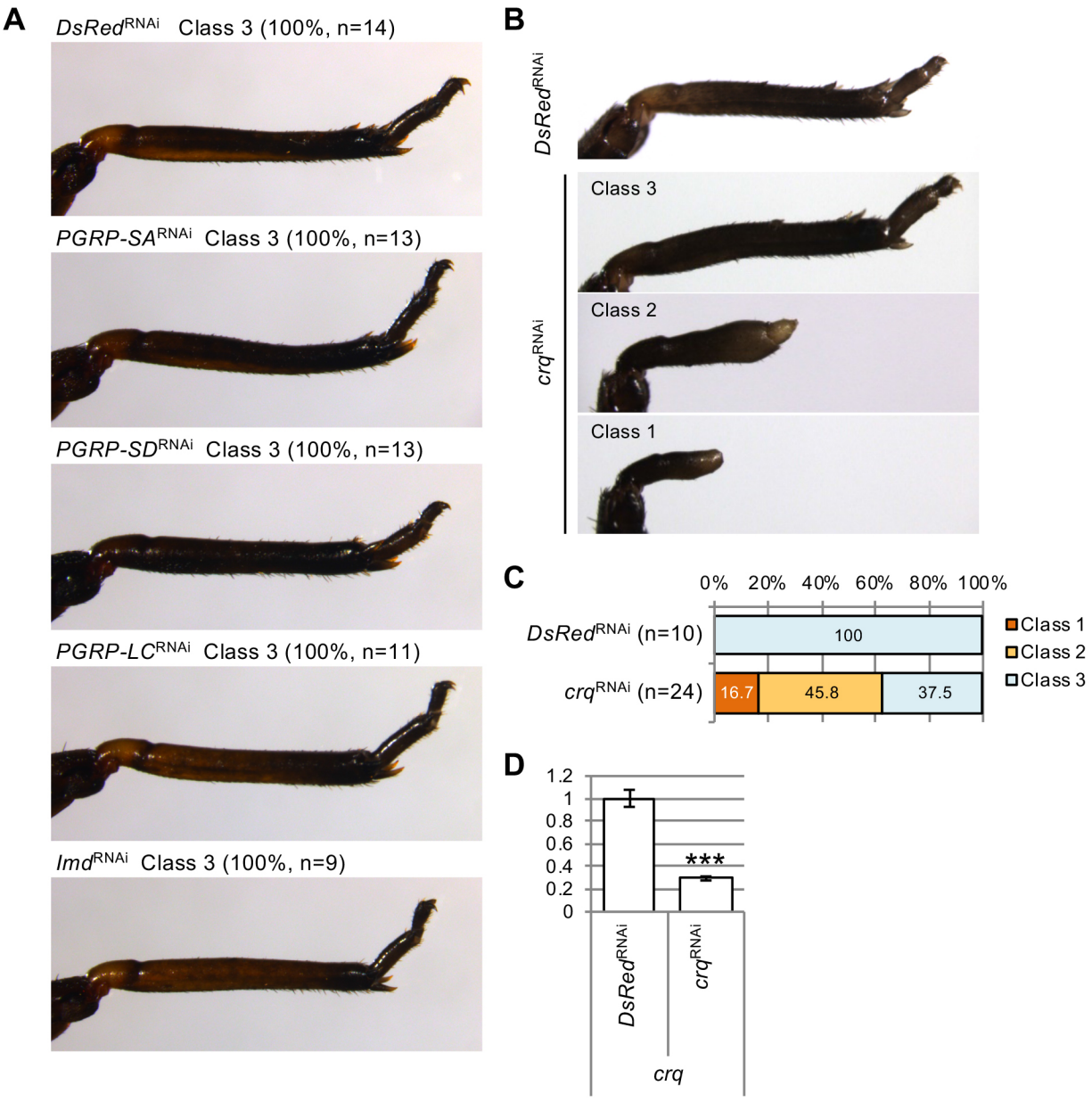



**Fig. S9. Phenotypes after RNAi to PAMPs and cellular debris recognising molecule genes.**
(A) Typical morphology of regenerating legs of *DsRed*$^{RNAi}$, *PGRP-SA*$^{RNAi}$, *PGRP-SD*$^{RNAi}$, *PGRP-LC*$^{RNAi}$, or *imd*$^{RNAi}$ crickets at fifth instar. Note that all of *PGRP-SA*$^{RNAi}$, *PGRP-SD*$^{RNAi}$, *PGRP-LC*$^{RNAi}$, or *imd*$^{RNAi}$ crickets show normal leg regeneration. (B-D) Phenotypes and efficiency of RNAi for *crq*. (B) Morphology of regenerating legs of *DsRed*$^{RNAi}$ and *crq*$^{RNAi}$ crickets at fifth instar. (C-D) Phenotype ratio (C) and efficiencies (D) of *DsRed*$^{RNAi}$ and *crq*$^{RNAi}$. *crq*$^{RNAi}$ significantly decreased the amount of *crq* transcripts to 29.4% in regenerating legs at 48 hpa. The y-axis indicates normalized expression of *crq* in the *DsRed*$^{RNAi}$ and a relative expression level in the *crq*$^{RNAi}$. Asterisks indicate significance between *DsRed*$^{RNAi}$ and *crq*$^{RNAi}$ samples (***$p < 0.001$ by Student's t-test).

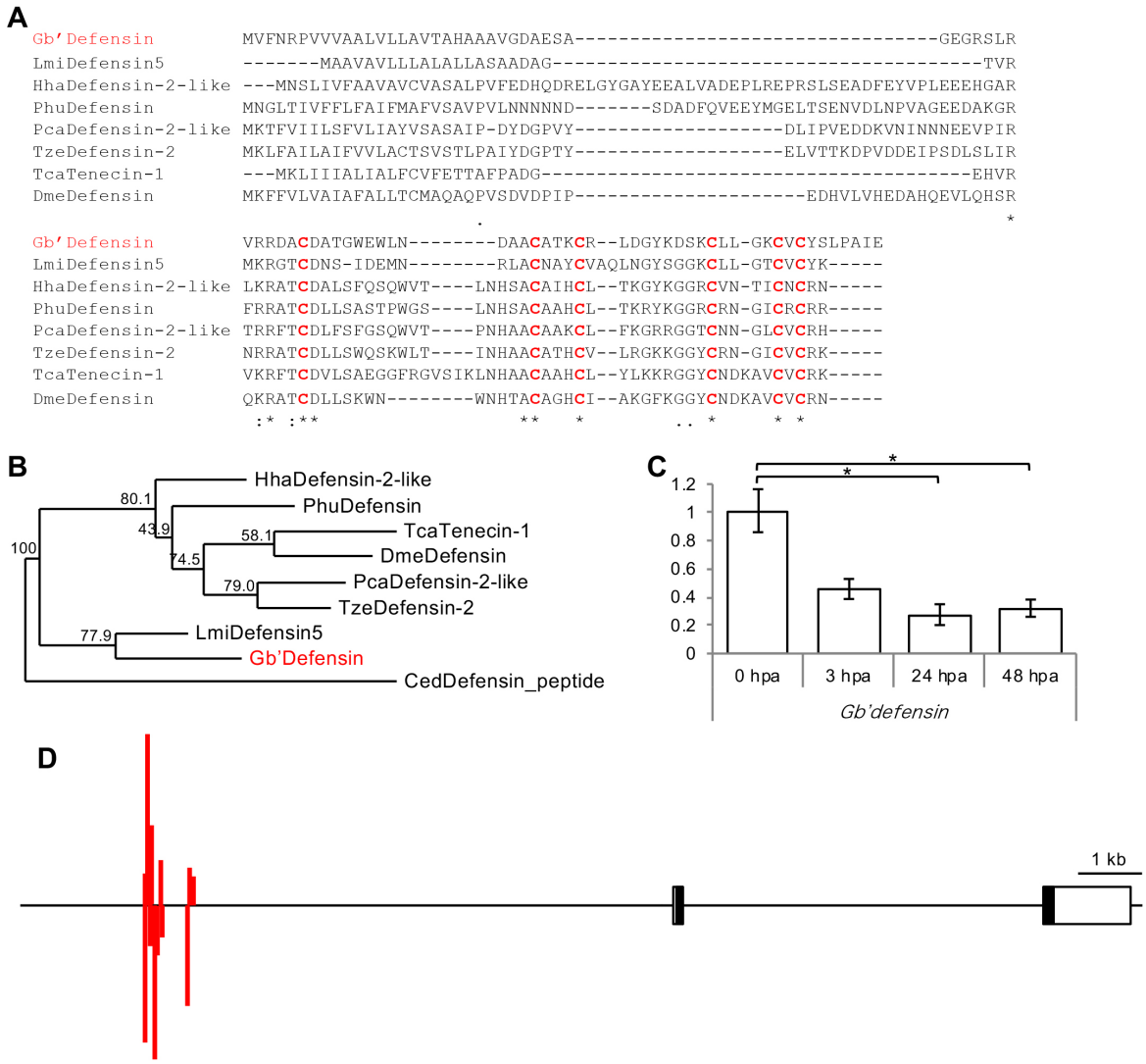



**Fig. S10. Amino acid homology, phylogenetic tree and expression of *Gb' defensin*.**
The *Gryllus bimaculatus* genome contains a single *defensin* gene. (A) *Gb' defensin* encodes 84 amino acids, with six evolutionarily conserved cysteine residues, shown in red. The N-terminal region of *Gb'* Defensin has diverged from the Defensins of other insects, but the C-terminal domain contains six evolutionarily conserved cysteine residues. (B) The phylogenetic tree indicates that *Gb'* Defensin is evolutionarily close to the grasshopper *Locusta migratoris* Defensin. *Centruroides edwardsii* was selected as the outgroup. (C) Temporal expression changes of *Gb' defensin* during leg regeneration, as revealed by qPCR. The y-axes indicate normalized expression at the 0 hpa and relative expression levels at 3, 24 and 48 hpa. Asterisks indicate significance of expression changes (*$p < 0.05$) by Tukey's test. (D) Spatial distribution of NF-κB binding sites (dl(var.2)) in the upstream region of *Gb' defensin*, by using Cister website (http://www.ijdb.ehu.es/web/), are indicated by red lines. Black boxes and white boxes represent coding and non-coding regions, respectively. Red bar lengths indicate probabilities. Gb, *Gryllus bimaculatus*, Lmi, *Locusta migratoria*, Tze, *Trachymyrmex zeteki*, Pca, *Polistes canadensis*, Hha, *Halyomorpha halys*, Phu, *Pediculus humanus*, Tca, *Tribolium castaneum*, Dme, *Drosophila melanogaster*. CedDefensin_peptide (*Centruroides edwardsii*) was selected as an outgroup.

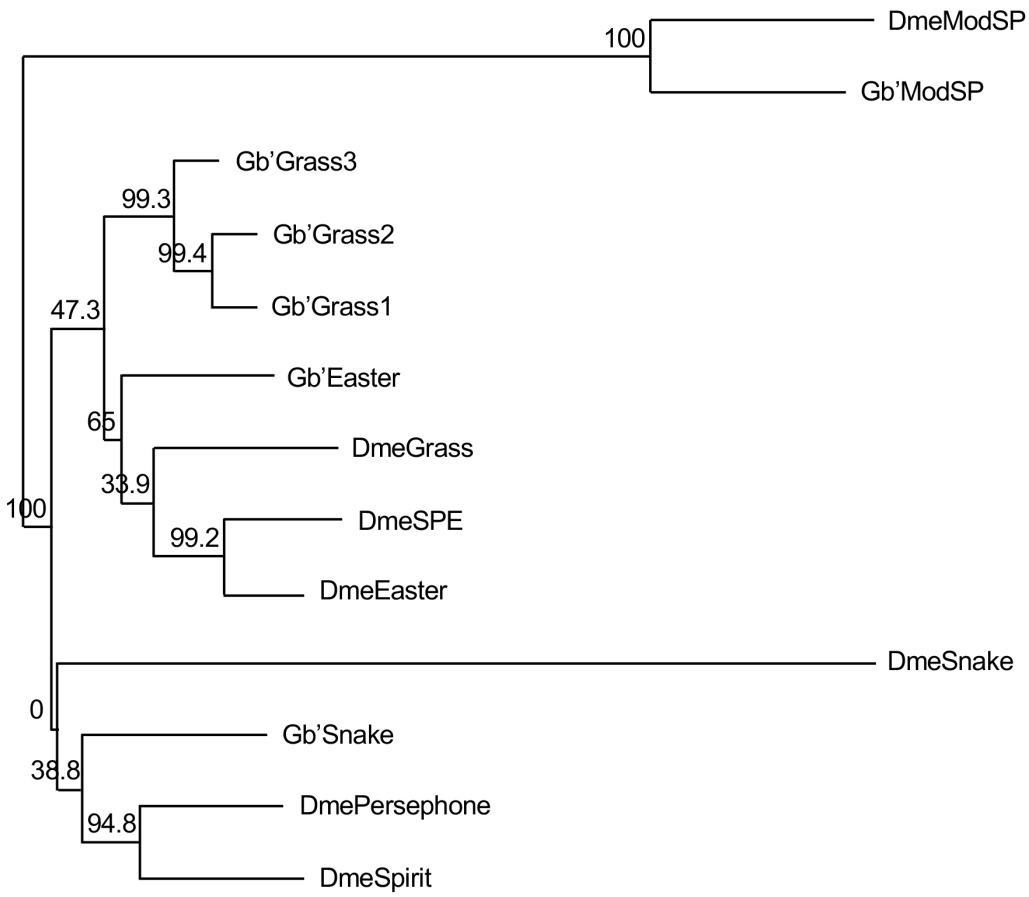



**Fig. S11. Phylogenetic tree of Toll signalling-related proteinases**

Phylogenetic tree of Toll signalling-related serine proteinases in *Gryllus* and *Drosophila*. *Gryllus* genome contains ModSP, Easter, and Snake homologues, and three Grass paralogues (Grass1, Grass2 and Grass3). We could not find *Drosophila* SPE and Persephone homologues in the *Gryllus* genome.

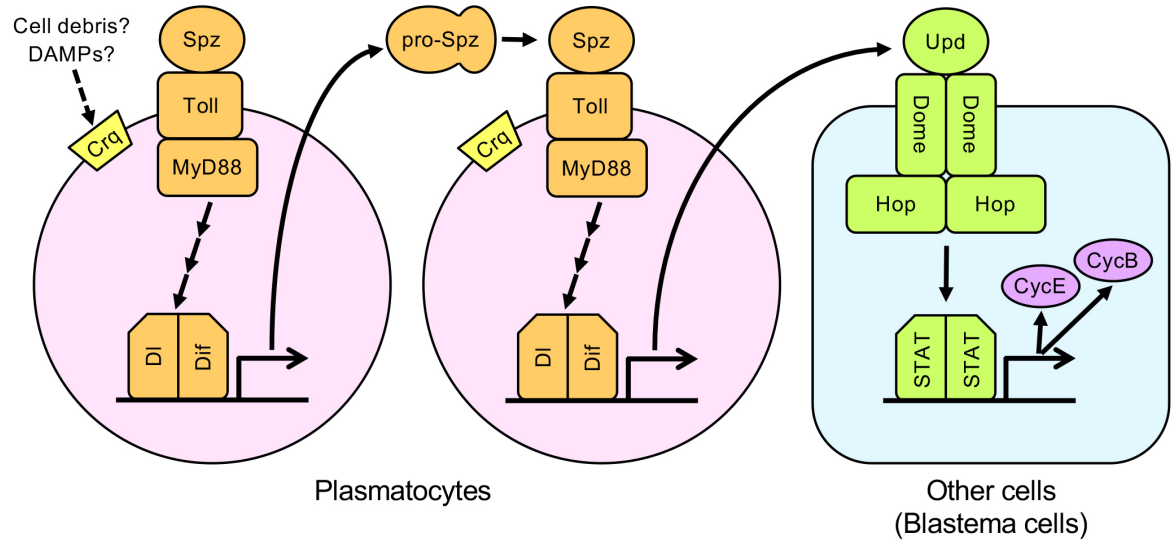



**Fig. S12. Roles of Toll signalling during leg regeneration.**

Schematic representation of Toll signalling during regeneration. In the plasmatocytes, Crq, and probably also Toll2-2, recognises apoptotic cells and cell debris caused by amputation and activates Toll signalling. Activated Toll signalling induces the *spz/spz2* expression that activates Toll signalling in surrounding plasmatocytes to lead accumulation of plasmatocytes in regenerating leg, and *upd* expression that activates JAK/STAT signalling in other cells including blastema cells mediated by the expression of Cyclin E and Cyclin B, which promote cell proliferation during regeneration.

**Table S1. Comparison of expressed contigs between regenerating legs (3 hpa) and non-regenerating legs (0 hpa).** Comparison of RPKM values of contigs between regenerating legs and non-regenerating legs. Contigs are ordered by RPKM values of regenerating legs.

Click here to download Table S1

**Table S2. Blast results of contigs only expressed in or upregulated in the regenerating legs.** Blast annotations are listed. Contigs are ordered by ratios of RPKM values of between regenerating legs and non-regenerating legs.

Click here to download Table S2

## Table S3. Primer sequences for gene cloning

| Targeted gene | Forward primer (5' -> 3') | Reverse primer (5' -> 3') | Amplicon size |
|---|---|---|---|
| *spz* | CATGAATGGAGAGAAATCATTA | CATAACAAACACAACACGATG | 302 |
| *spz2* | GTATCGCACTATAATCCTGACGAAT | GTGTGATTTGACACACACAACAGT | 436 |
| *Toll(5)* | GGAAACAAAATCTCAAATCTAACAAAA | AAGCTCTTTTAGATACTCTGTGTCTCG | 426 |
| *Toll(3)* | TCAAGAATTACTTAATCCAACATTTCC | ACCAAACTTTGACTTCATTTTGATAAC | 524 |
| *Toll2-1* | AATTATTGAATACCTGGATCTATCACG | TTTGTTTTGAGACATGTTCAGTACTTC | 520 |
| *Toll2-2(5)* | ATAGGATTGAAATTGCTGATTATTACG | AGTTTGTTTAGACCTTTAAATGCAATG | 434 |
| *Toll2-2(3)* | ACAACACTGGTTAGACGTCACAAAA | AAGCCTTTCTTTCAGTCTCCTTCTC | 302 |
| *Toll2-3* | CAACTTCCTACTGGGCTACCTG | GGATATGTTGCAAGTACTCACGTC | 472 |
| *Toll2-4* | CTTACATTATAGTAGGCGTGGTCCTC | AAAGAATAAACTGTAATGTTCCGCTAA | 449 |
| *Toll2-5* | GTTGAAATTACAGAACAATCTGTAGCA | ATGTTTTGAGAGATAAAAGAACCAAGA | 545 |
| *Toll6-1* | GAAGTTTTCGATCTGTCGAATAATAAA | AACTAAGTACGTACAAACCGTTGAGAG | 445 |
| *Toll6-2* | AGATATCAAAGAAGTGTACCTGCAGAA | AGGTCTTTGATTCGATTGTTAGAGAG | 411 |
| *Toll7* | ACGATTAGCAATAATCTTCTCATTAGC | GTAGTCGAACCACACTAAATGGTTATT | 462 |
| *Toll8* | AATCAGTTCCTAGATGTTCCTGAAGTA | AAGTATACGACTGCACCTTGTTGAT | 598 |
| *Toll9* | ACAATAATTTAAGAGAGCATTTAGGCA | AAAGAACTCAATCATTGGACAACTATC | 407 |
| *MyD88* | CAGTACCGAATTTATATGACATTCCTC | CAACACATCATCTCTCGTTAATATTTC | 404 |
| *tube* | AAAAGATTAAAGAATGATGCTGTCAGT | TAAGCTGATGTTCCAAATACTGTAGTG | 431 |
| *pelle* | CGGCATGATAATATACTTCCTTTGTAT | ACTTTTGTAGACAACTGTTTGTTCCTT | 389 |
| *TRAF6* | AAATGAAGAGACTGACTTATTTCCAGA | TATATCACTCACAGTCCAAACAAGAAC | 559 |
| *dl* | AGCCAGTAGTACTCCAGATAACAAGAC | AGAAGCGAACTTGGATATCTTCTTTAG | 548 |
| *Dif* | TCATCATCATCAATGAGTAATAAAAGC | TCCTTCTAAAAAGACTTGGAAACATAA | 486 |
| *Rel* | ACAATGAATAGAGAAGAGCCATTTTTA | CAGTCAAAGCACTTTTCATATTGTTTA | 625 |
| *upd* | GAGAACTTCAAAGAGAAATATGTCCAG | CCATTCATGTAGTCACGGTAGATTAG | 455 |
| *egr* | ACTTCGAAGGTAACGGAAAGC | CAGTGTGACCCAGTTTGACAAG | 414 |
| *wgn* | ACTAAGTTTGATGGTACCAGAACTCG | TTTATTGTTTTAACAAACATATTTACTCCT | 322 |
| *Imd* | GATCCTCCCAGAGTTGAAATACAC | CAGTAACATCTGATACACCACCTCTTT | 537 |
| *PGRP-SA* | AGAATCGATTATATGGTGATTCCACT | GGATCTCCTGGAAGAGTGCTAGT | 424 |
| *PGRP-SD* | GTCTGGTGGAAATATGAATCAGATAAT | CCTTCTTCTAAGAACTTCTGACACACT | 418 |
| *PGRP-LC* | TTTGGTAACAAAACTTTTTATAATGGC | ATGATAACATATGGCACTGGTGTAGTA | 566 |
| *crq* | TATGTTACAAAGACAGTGAAGGAGTTG | AGTGGTGTTAAGTATGATGAATTAGCC | 566 |

**Table S4. Primer sequences for qPCR**

| Targeted gene | Forward primer (5' -> 3') | Reverse primer (5' -> 3') | Amplicon size |
|---|---|---|---|
| *actin* | TTGACAATGGATCCGGAATGT | AAAACTGCCCTGGGTGCAT | 64 |
| *spz* | GCCAATTCAAACCACGCTTC | CATCCACGCCTCCTTCACA | 81 |
| *spz2* | GATACCCCGACCGTCGATAC | GCAGCAGGGTGGTGTAGAGA | 81 |
| *Toll* | ATCACTCATCTCCTCCTACCC | AACCCAGCTAATTCACCGTTT | 134 |
| *Toll2-1* | CGGAAGTGGGTGATGCGT | GATGACCTTCCTGCTGTGCT | 147 |
| *Toll2-2* | ATTCGATGATGGACTCTTTGTAGGA | CGTGGAGATGAAAAGCGGTAAAG | 121 |
| *Toll2-3* | GCCCTCCCACCAAACCTC | TGACCATCTCAGATAAACATCACACA | 145 |
| *Toll2-4* | TGGAACCGTGGATTGAAGAGG | CAACATGACTGGGCTGAGGT | 101 |
| *Toll2-5* | TCCAAGACACTCATCACATCACT | TTGAATTGAAGGCAGTTGACACTC | 105 |
| *Toll6-1* | ACACCACCAACTTCAGCGT | GCGGGTCAGGTGGTAGAAG | 119 |
| *Toll6-2* | CCGCGATGACCATGGAGTT | GGTTGCGCGTGAGGTTG | 150 |
| *Toll7* | CAGAACTCCATCGGCTACATC | GTTAAACATCAACGGCCCTATTTC | 111 |
| *Toll8* | AACACCTTTGCCTCTCTTTACAATC | AATGCTTCGGATGTTGTTGTTATCT | 138 |
| *Toll9* | GCCACTCCAAACCTTCAAACA | ACTTTTGTTCCTTCTAATGTTCCTCA | 117 |
| *cycE* | AGCAACAGGAGGAAGGAGCA | CCAGGGCAGCATAAGGAAAC | 144 |
| *cycB* | CCCAGGTGGAGGTCAAGAGA | GGAAATTCGTGGTCGGAAAA | 132 |
| *upd* | AGGTGCAAGTGCTGATGGTG | GCGACGTGCTGTTGTTTTGT | 99 |
| *dome* | CAGTGACGGAAGTTACCAATTCAT | TGTAAAAGCGAAGTACACCATTCATT | 81 |
| *hop* | CCTCCTTCAGAATATGATCGTTCA | ACGATCCCAGGCCAGAAAA | 91 |
| *STAT* | TGGGCCAAGGGTTATCACTAGT | CCTGTGTGCGTCTGCGTAAA | 81 |
| *egr* | GATTCATACATATTCAAAGCTCCTACAATC | ACTGTTGTACCATGAAGAAAGCAA | 100 |
| *wgn* | TGAACTGCTAATTTGATGTTTACGAATG | GCCATTAACCACGCACATGAA | 119 |
| *crq* | ATTGCTGGTCTCGGTGCTTT | GTTCGTGGTCCTGGGTCTCT | 88 |
| *Gcm* | CGGTCTGTGTTGTGTCCTTTG | ATGCTGGAACTGGGGATTGT | 150 |

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