

Figure S1: Partial protein alignment of Dicer-2. The partial sequence of *G. sigillatus* Dicer-2 was aligned with Dicer-2 and Dicer 1 sequences from a representative set of insects. Gs = *Gryllobates sigillatus*, Sg: *Schistocerca gregaria*, Lm: *Locusta migratoria*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Zn: *Zootermopsis nevadensis*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Sg Dicer3: BAX36479.1, Sg Dicer2: QVD39336.1, Sg Dicer1: BAX36477.1, Lm Dicer3: BAW35366.1, Lm Dicer1: BAW35364.1, Lm Dicer2: BAW35365.1, Dm Dicer1: NP_524453.1, Dm Dicer2: NP_001286540.1, Bm Dicer2: NP_001180543.1, Bm Dicer1: XP_037869731.1, Zn Dicer1: XP_021929007.1, Zn Dicer2: XP_021927098.1, Aa Dicer2: QXE98924.1, Aa Dicer1: XP_001659747.2,

Am Dicer1: NP_001116485.2, Am Dicer2: XP_016773223.2, Tc Dicer1: EFA11550.2, Tc Dicer2:
NP_001107840.1.



Figure S2: Protein alignment of Argonaute-2. The sequence of *G. sigillatus* Argonaute-2 was aligned with homologous sequences from a representative set of insects. Gs = *Grylodes sigillatus*, Sg: *Schistocerca gregaria*, Lm: *Locusta migratoria*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Zn: *Zootermopsis nevadensis*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Lm Ago2b: QUP51772.1, Lm Ago2a: QUP51773.1, Sg Ago2b: QVD39218.1, Sg Ago2a: QVD39219.1, Tc Ago2a: EFA11590.1, Tc Ago2b: EFA04626.2, Am Ago2: XP_395048.4, Bm Ago2: NP_001036995.2, Dm Ago2: NP_730054.1, Aa Ago2: XP_011493002.2, Zn Ago2: XP_021934925.1

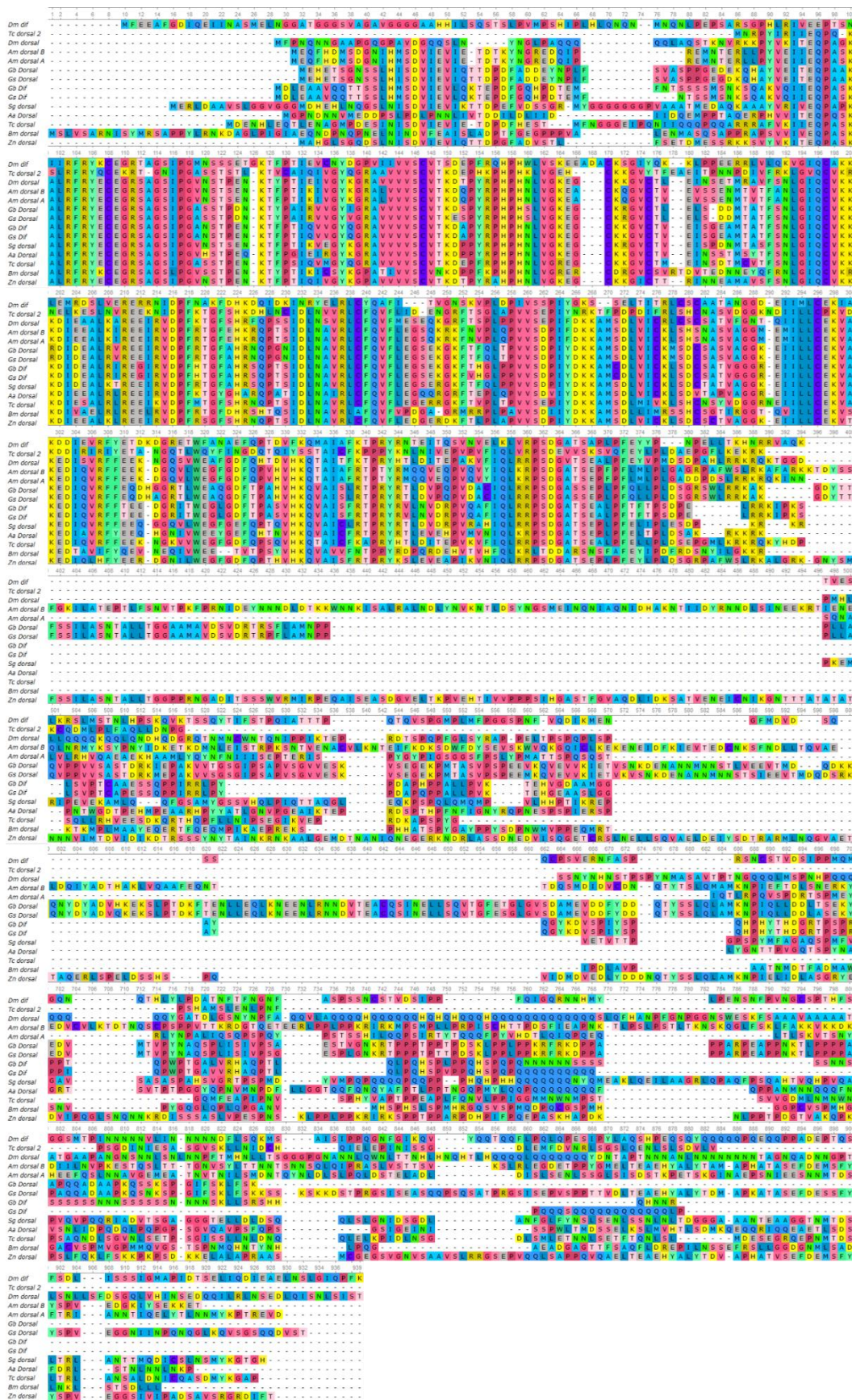


Figure S3: Protein alignment of Dorsal. The sequences of *G. sigillatus* Dorsal and Dif were aligned with homologous sequences from a representative set of insects. Gs = *Gryllodes sigillatus*, Gb: *Gryllus bimaculatus*, Sg: *Schistocerca gregaria*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Zn: *Zootermopsis nevadensis*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Dm Dorsal: NP_724052.1, Dm Dif: AAA28465.1, Am Dorsal B: NP_001164477.1, Am Dorsal A: NP_001011577.1, Gb Dorsal: BBG28463.1, Gb Dif: BBG28464.1, Sg Dorsal: XP_049833658.1, Aa Dorsal: AAW67214.1, Tc Dorsal 2: EFA02885.1, Tc Dorsal: EFA02850.1, Bm Dorsal: XP_037870194.1, Zn Dorsal: KDR23857.1

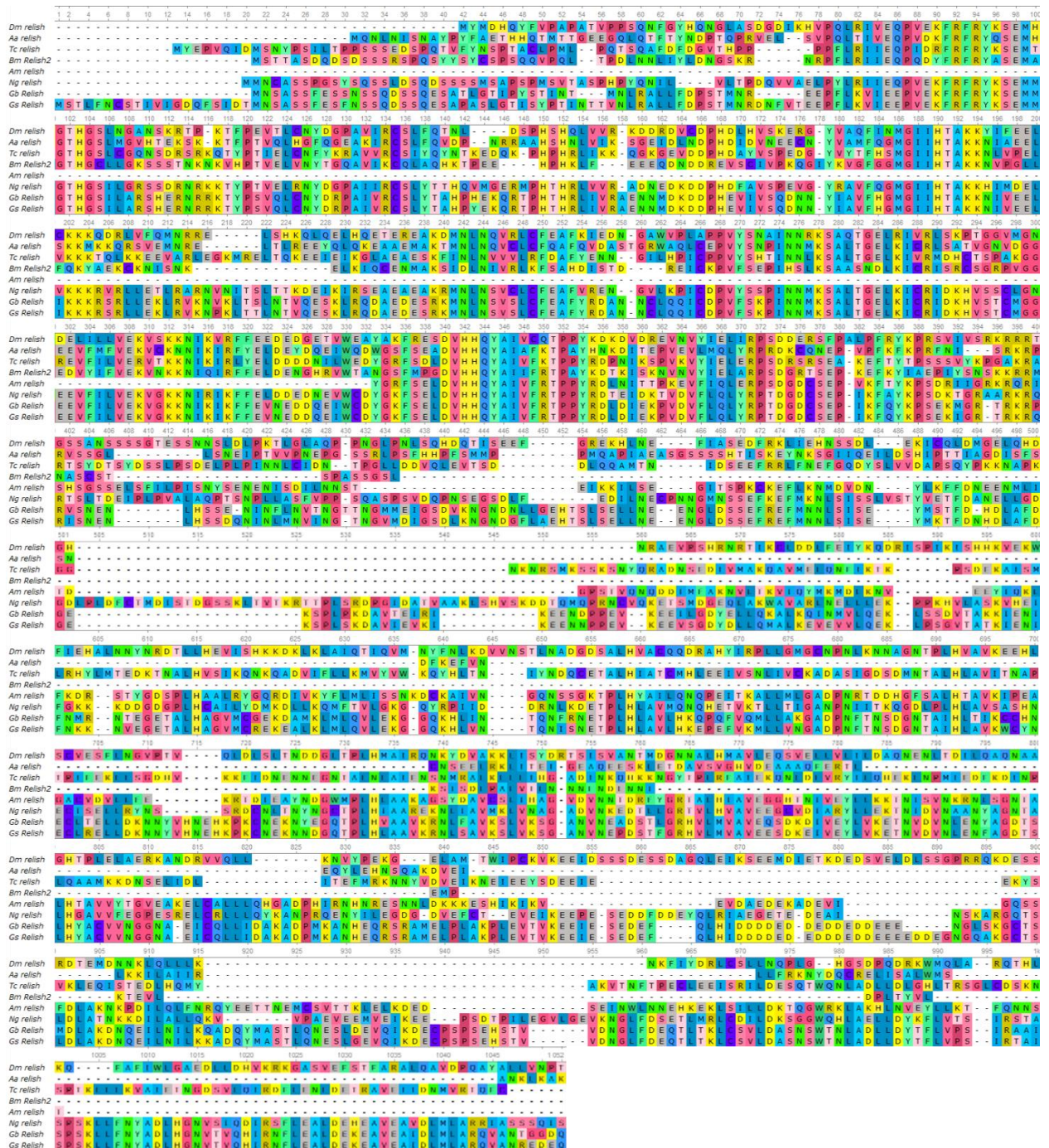


Figure S4: Protein alignment of Relish. The sequences of *G. sigillatus* Relish were aligned with homologous sequences from a representative set of insects. Gs = *Gryllodes sigillatus*, Gb: *Gryllus bimaculatus*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Aa: *Aedes aegypti*, Am: *Apis mellifera*, Ng: *Nasutitermes graveolus*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Ng Relish: AAZ08468.1, Bm Relish2: BAF74126.1, Tc Relish: EEZ97717.1, Aa Relish: AAM97894.1, Dm Relish: NP_996187.1, Am Relish: ACT66913.1, Gb Relish: BBG28465.1

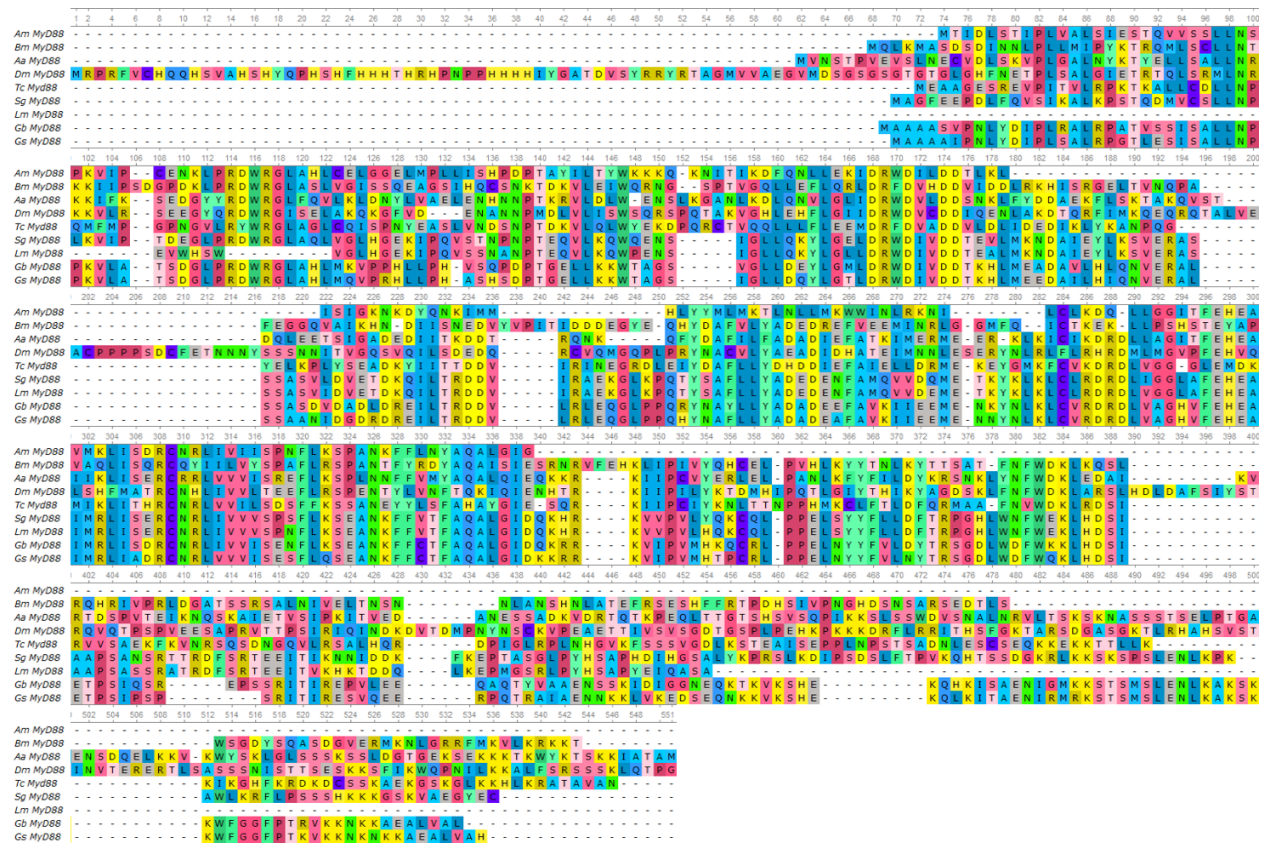


Figure S5: Protein alignment of MyD88. The sequence of *G. sigillatus* MyD88 was aligned with homologous sequences from a representative set of insects. Gs = *Gryllobates sigillatus*, Gb: *Gryllus bimaculatus*, Sg: *Schistocerca gregaria*, Lm: *Locusta migratoria*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Am MyD88: AGM19319.1, Tc MyD88: EFA01304.1, Bm MyD88: XP_004921573.1, Sg MyD88: XP_049839790.1, Lm MyD88: AWW58420.1, Gb MyD88: BBG28459.1, Aa MyD88: XP_001658635.1, Dm MyD88: NP_610479.1

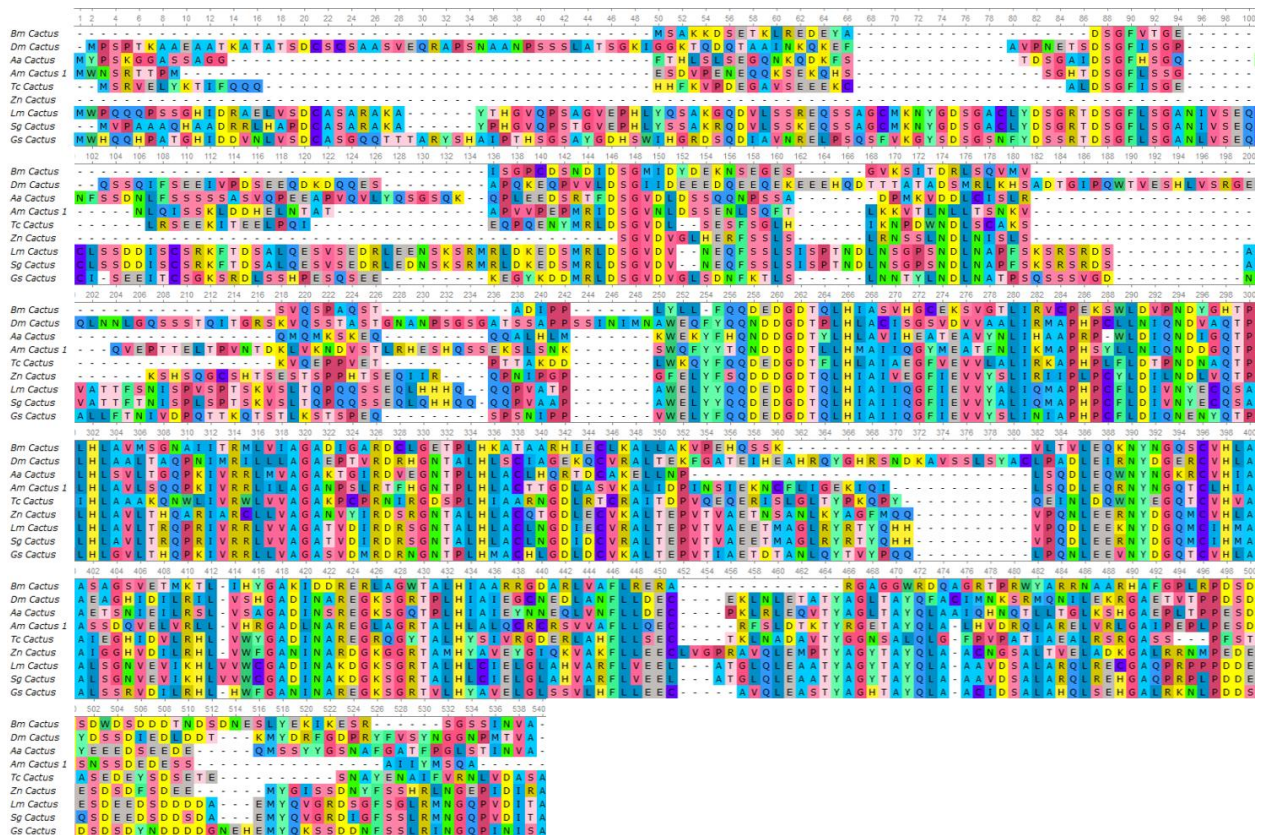


Figure S6: Protein alignment of Cactus. The sequence of *G. sigillatus* Cactus was aligned with homologous sequences from a representative set of insects. Gs = *Gryllobates sigillatus*, Sg: *Schistocerca gregaria*, Lm: *Locusta migratoria*, Tc: *Tribolium castaneum*, Zn: *Zootermopsis nevadensis*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Am Cactus: NP_001157184.1, Dm Cactus: AAA85908.1, Bm Cactus: BAI67121.1, Lm Cactus: AZP56667.1, Sg Cactus: XP_049833628.1, Aa Cactus: XP_001650267.3, Tc Cactus: KYB24622.1, Zn Cactus: XP_021919362.1

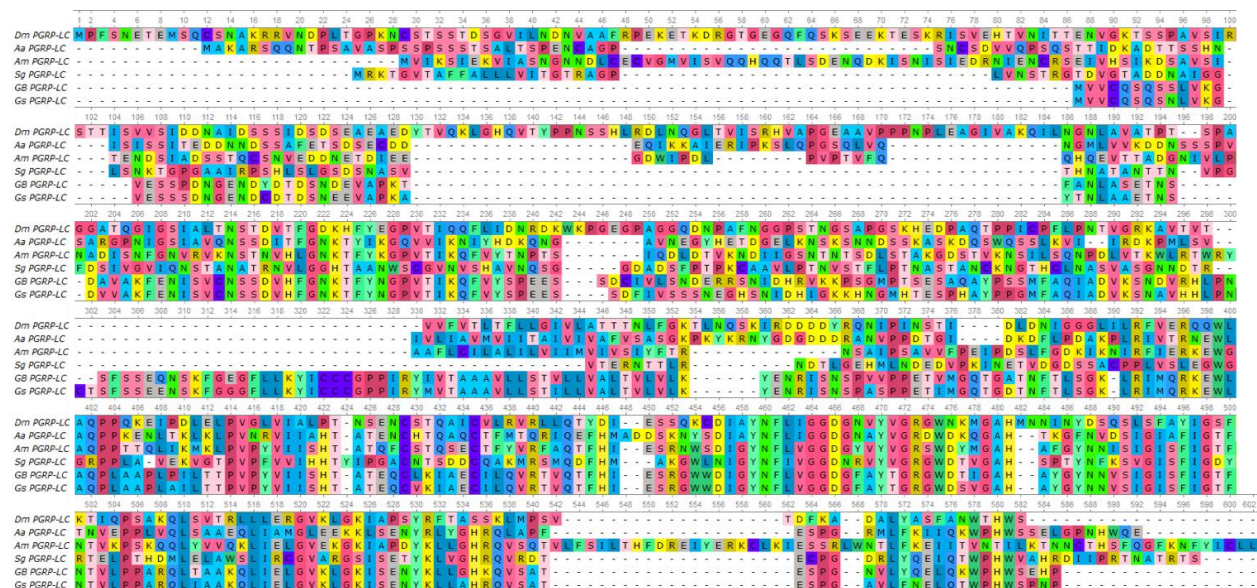


Figure S7: Protein alignment of PGRP-LC. The sequence of *G. sigillatus* PGRP-LC was aligned with homologous sequences from a representative set of insects. Gs = *Gryllobates sigillatus*, Sg: *Schistocerca gregaria*, Gb: *Gryllus bimaculatus*, Dm: *Drosophila melanogaster*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Dm PGRP-LC: NP_648298.1, Am PGRP-LC: KAG9434435.1, Gb PGRP-LC: BBG28440.1, Sg PGRP-LC: XP_049839352.1, Aa PGRP-LC: XP_021698612.1

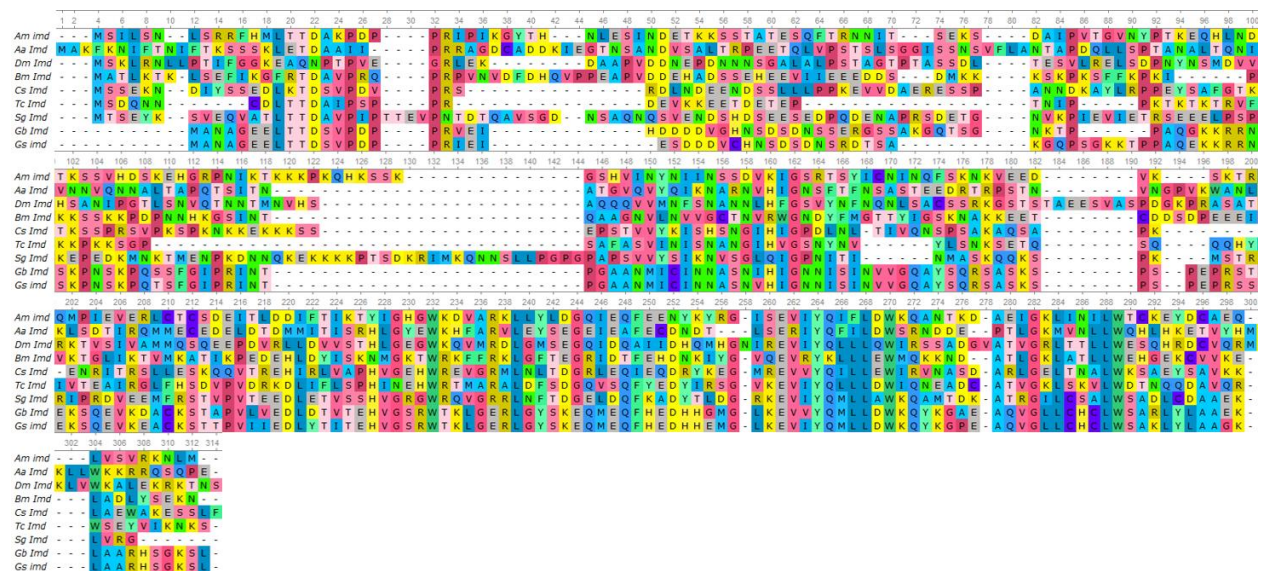


Figure S8: Protein alignment of Imd

The sequence of *G. sigillatus* Imd was aligned with homologous sequences from a representative set of insects. Gs = *Gryllobates sigillatus*, Sg: *Schistocerca gregaria*, Gb: *Gryllus bimaculatus*, Cs: *Cryptotermes secundus*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Gb Imd: BBG28437.1, Sg Imd: AFK75938.1, Am Imd: NP_001157189.2, Bm Imd: XP_037866830.1, Cs Imd: XP_023727856.1, Dm Imd: NP_573394.1, Aa Imd: EAT37980.1, Tc Imd: EFA11587.1

Dm Dome
Aa Dome
Fo Dome
Tc Dome
Hh Dome
Gs dome
Gb Dome

Figure S9: Protein alignment of Domeless

The sequence of *G. sigillatus* Domeless was aligned with homologous sequences from a representative set of insects. Gs = *Grylodes sigillatus*, Gb: *Gryllus bimaculatus*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Aa: *Aedes aegypti*, Fo: *Frankliniella occidentalis*, Hh: *Halyomorpha halys*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Dm Dome: NP_523412.1, Aa Dome: EAT35350.1, Gb Dome: BAN10236.1, Tc Dome: EFA12822.1, Fo Dome: KAE8744265.1, Hh Dome: KAE8573886.1



Figure S10: Protein alignment of PIAS

The sequence of *G. sigillatus* PIAS was aligned with homologous sequences from a representative set of insects. Gs = *Gryllosigillatus*, Zn: *Zootermopsis nevadensis*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Am PIAS: XP_623571.3, Zn PIAS: XP_021928824.1, Dm PIAS: AAF58984.1, Aa PIAS: XP_021700150.1, Bm PIAS: XP_004922440.1, Gb PIAS: BAN10244.1



Figure S11: Protein alignment of STAT5B

The sequence of *G. sigillatus* STAT5B was aligned with homologous sequences from a representative set of insects. Gs = *Gryllos sigillatus*, Sg: *Schistocerca gregaria*, Lm: *Locusta migratoria*, Tc: *Tribolium castaneum*, Zn: *Zootermopsis nevadensis*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Aa: *Aedes aegypti*, Am: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Am STAT5B: XP_397181.1, Lm STAT5B: QTE34030.1, Sg STAT5B: XP_049827783.1, Tc STAT5B: XP_969477.2, Bm STAT5B: NP_001157388.1, Dm STAT92E: AAC46984.1, Aa STAT92E: EAT38424.1, Zn STAT5B: XP_021921231.1



Figure S12: Protein alignment of R2D2

The sequence of *G. sigillatus* R2D2 was aligned with homologous sequences from a representative set of insects. *Gs* = *Grylodes sigillatus*, *Sg*: *Schistocerca gregaria*, *Lm*: *Locusta migratoria*, *Tc*: *Tribolium castaneum*, *Zn*: *Zootermopsis nevadensis*, *Dm*: *Drosophila melanogaster*, *Bm*: *Bombyx mori*, *Aa*: *Aedes aegypti*, *Am*: *Apis mellifera*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: *Am* TARP2: XP_006560091.1, *Sg* tarbp2-like: XP_049859483.1, *Lm* R2D2: UEP55409.1, *Zn* tarbp2-like: XP_021919678.1, *Dm* R2D2: ABB77175.1, *Bm* R2D2: BAJ11654.1, *Tc* R2D2: NP_001128425.1, *Aa* R2D2: AJF11544.1, *Dm* Loquacious: NP_723813.1, *Bm* Loquacious: NP_001182008.1, *Aa* R3D1: AJF11546.1



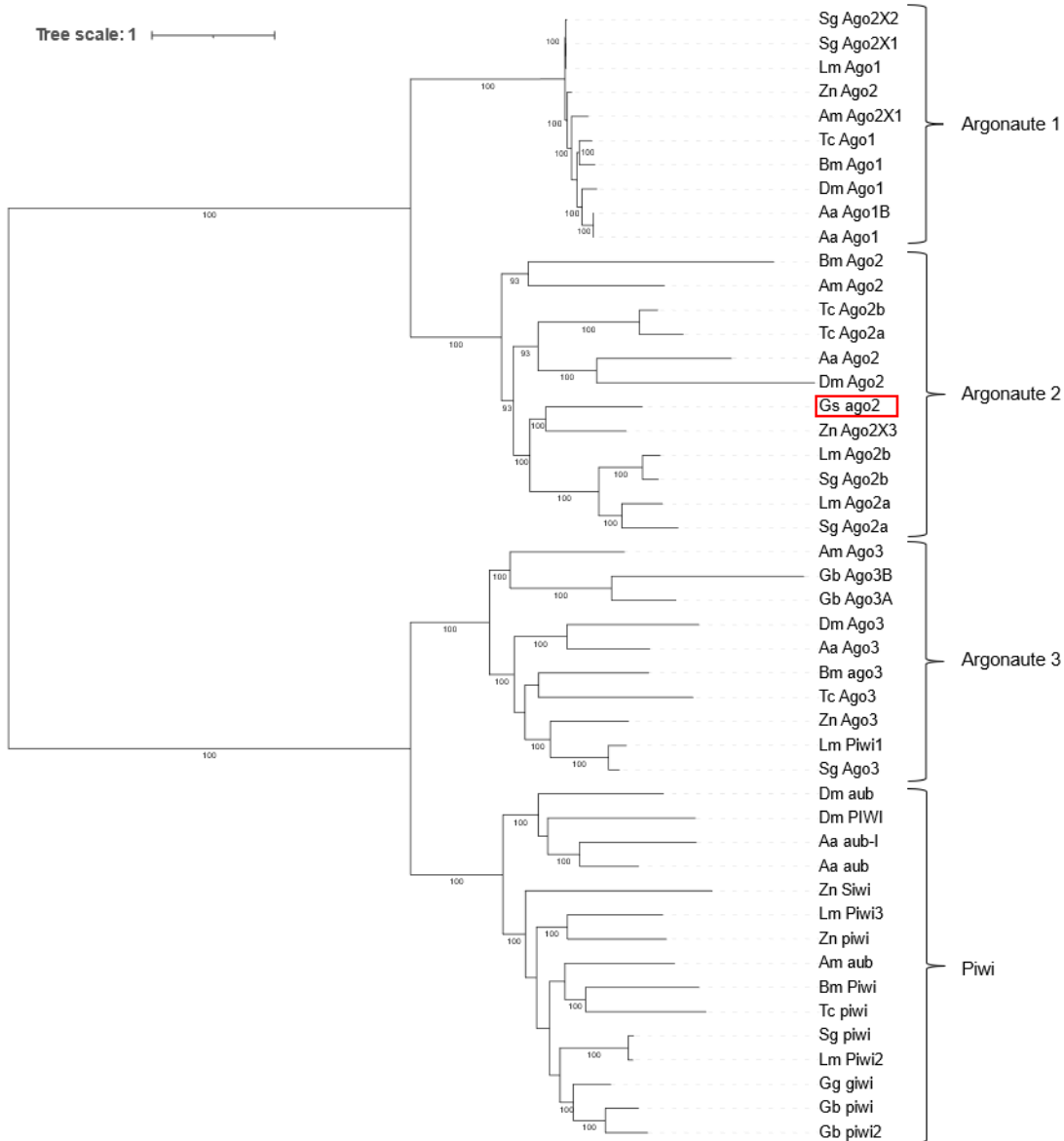


Figure S15: Maximum likelihood tree of Argonaute and piwi proteins. A Maximum Likelihood tree of Argonaute and piwi proteins from a representative set of insects is shown, showing the position of *G. sigillatus* Argonaute-2 within the clade of Argonaute-2 proteins. Bootstrap support values above 90, obtained from 1000 bootstraps, were added to each branch. Gs = *Gryllodes sigillatus*, Sg: *Schistocerca gregaria*, Lm: *Locusta migratoria*, Tc: *Tribolium castaneum*, Dm: *Drosophila melanogaster*, Bm: *Bombyx mori*, Zn: *Zootermopsis nevadensis*, Aa: *Aedes aegypti*, Am: *Apis mellifera*, Gg: *Gampsocleis gratiosa*. All proteins were obtained from the ncbi protein database, and represent the following accession numbers: Lm Ago2b: QUP51772.1, Lm Ago2a: QUP51773.1, Sg Ago2b: QVD39218.1, Sg Ago2a: QVD39219.1, Tc Ago2a: EFA11590.1, Tc Ago2b: EFA04626.2, Am Ago2: XP_395048.4, Bm Ago2: NP_001036995.2, Dm Ago2: NP_730054.1, Aa Ago2: XP_011493002.2, Zn Ago2: XP_021934925.1, Lm Piwi3: BAW35371.1, Lm Piwi2: BAW35370.1, Lm Piwi1: BAW35369.1, Lm Ago1: BAW35367.1, Sg Ago2X2: XP_049830024.1, Sg Ago2X1: XP_049830023.1, Sg Siwi: XP_049864520.1, Sg Ago3: XP_049857113.1, Gb piwi: AFW31611.1, Gb piwi2: AGJ83080.1, Gg giwi: AFW04603.1, Gb Ago3A: AGJ83081.1, Gb Ago3B: AGJ83082.1, Tc Ago1: EFA09197.2, Tc Ago3: EFA02921.1, Tc piwi: EFA07425.1, Am Ago2X1: XP_026300412.1, Am aub: XP_026300661.1, Am Ago3: XP_026300549.1, Bm Ago3: BAF73717.2, Bm

Ago1: NP_001095931.1, Bm Piwi: BAF98574.1, Dm Ago1: NP_725341.1, Dm Ago3: NP_001036628.2, Dm PIWI: AAD08704.1, Dm aub: NP_476734.1, Aa Ago1B: EAT32599.1, Aa Ago1: QPA18337.1, Aa Ago3: XP_001652945.1, Aa aub: XP_001653082.1, Aa aub-l: XP_021712346.1, Zn piwi: KDR24114.1, Zn Siwi: XP_021936690.1, Zn Ago3: XP_021933458.1.

