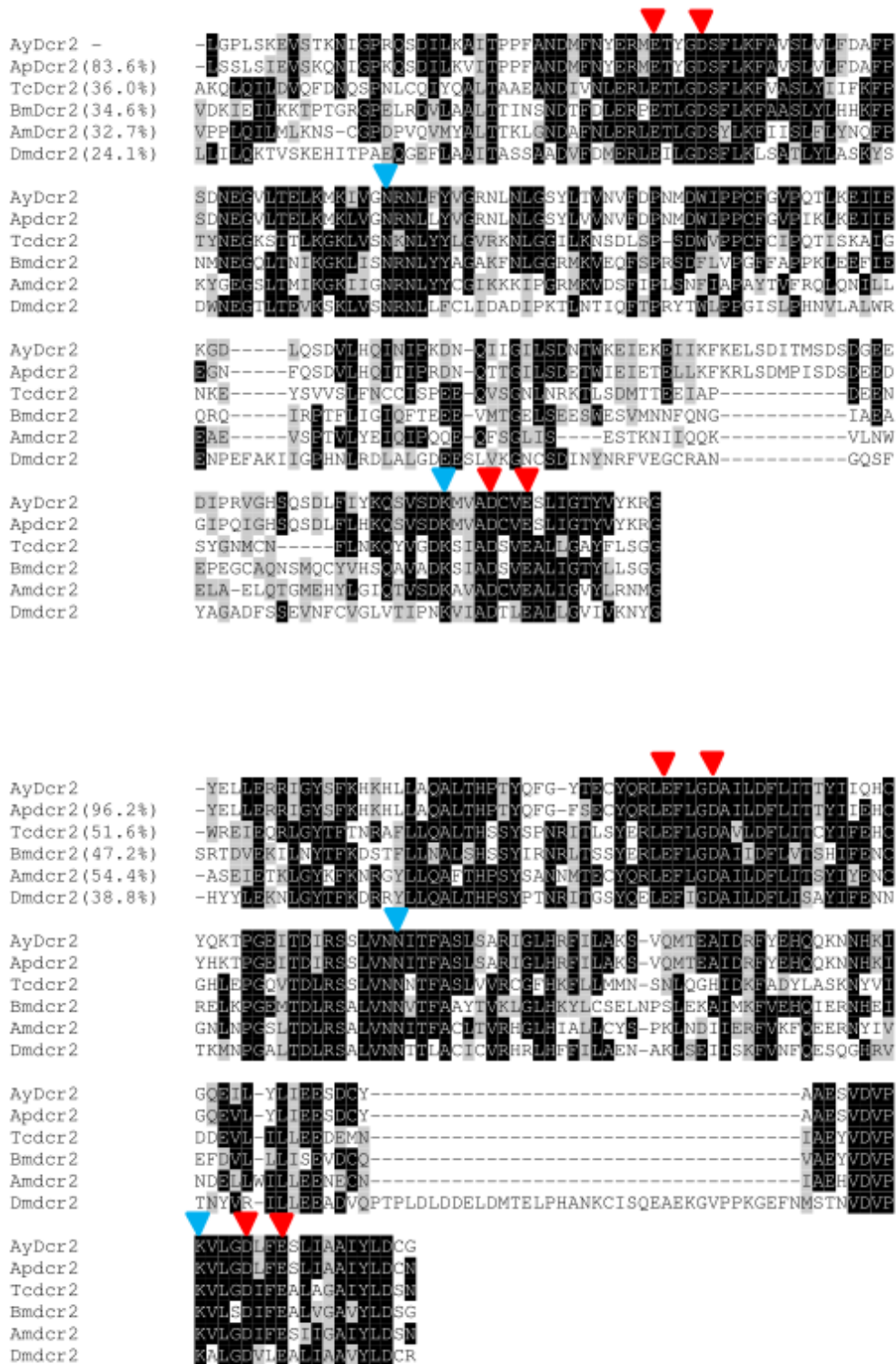
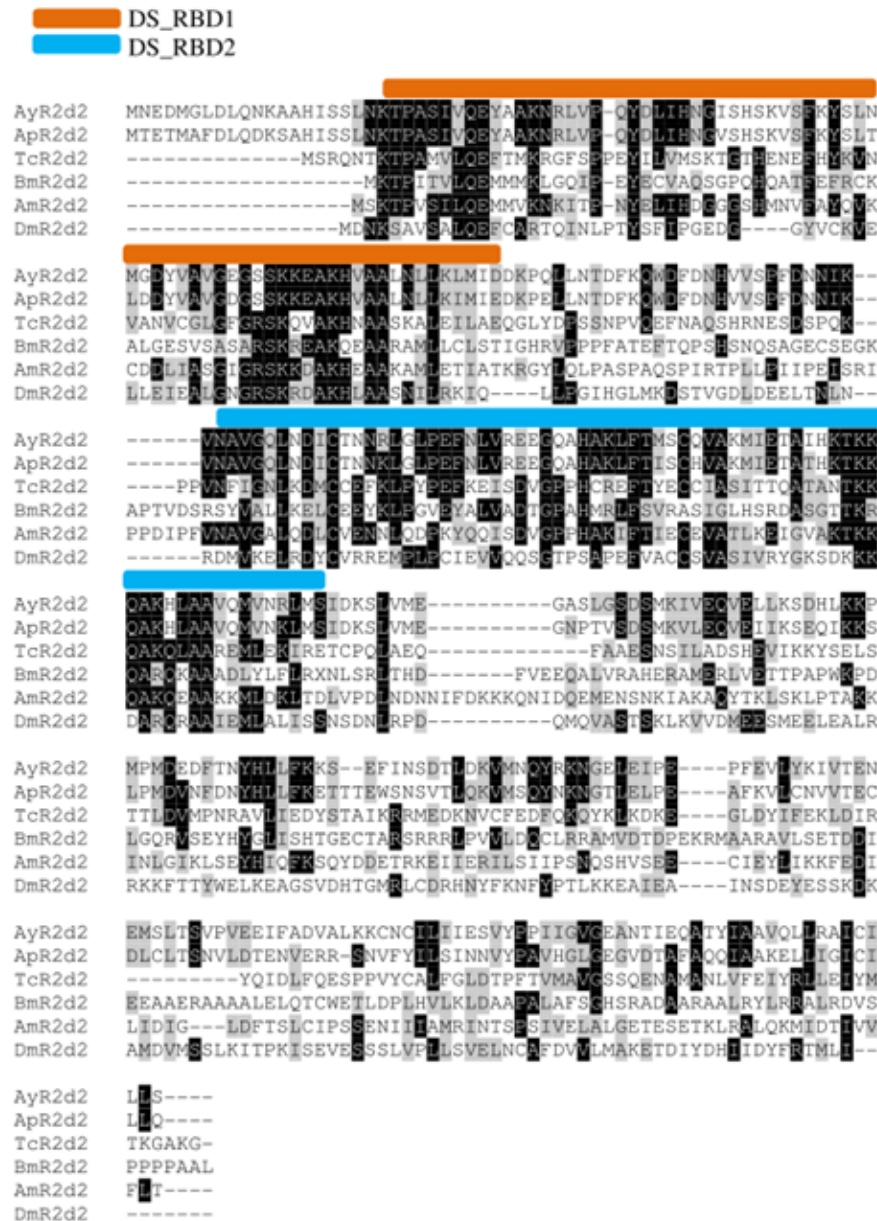


## Supplementary Information

**Figure S1.** Alignment of amino acids sequences from RNase IIIa (top) RNase IIIb (bottom) domains of insect Dcr2 proteins. The conserved and similar amino acid residues are labeled in black and grey backgrounds respectively. Red and blue arrowheads indicate catalytic residues of Dcr2 proteins. The figures in the parentheses indicate the percent identity of that protein to the respective domain of AyDcr2. The accession numbers for various protein sequences used in the alignment are provided in Table S2.



**Figure S2.** Alignment of amino acids sequences from insect R2d2 proteins. The conserved and similar amino acid residues are labeled in black and grey backgrounds respectively. The accession numbers for various protein sequences used in the alignment are provided in Table S2.



**Figure S3.** Alignment of amino acids sequences from insect Ago2 proteins. The conserved and similar amino acid residues are labeled in black and grey backgrounds respectively. The accession numbers for various protein sequences used in the alignment are provided in Table S2.

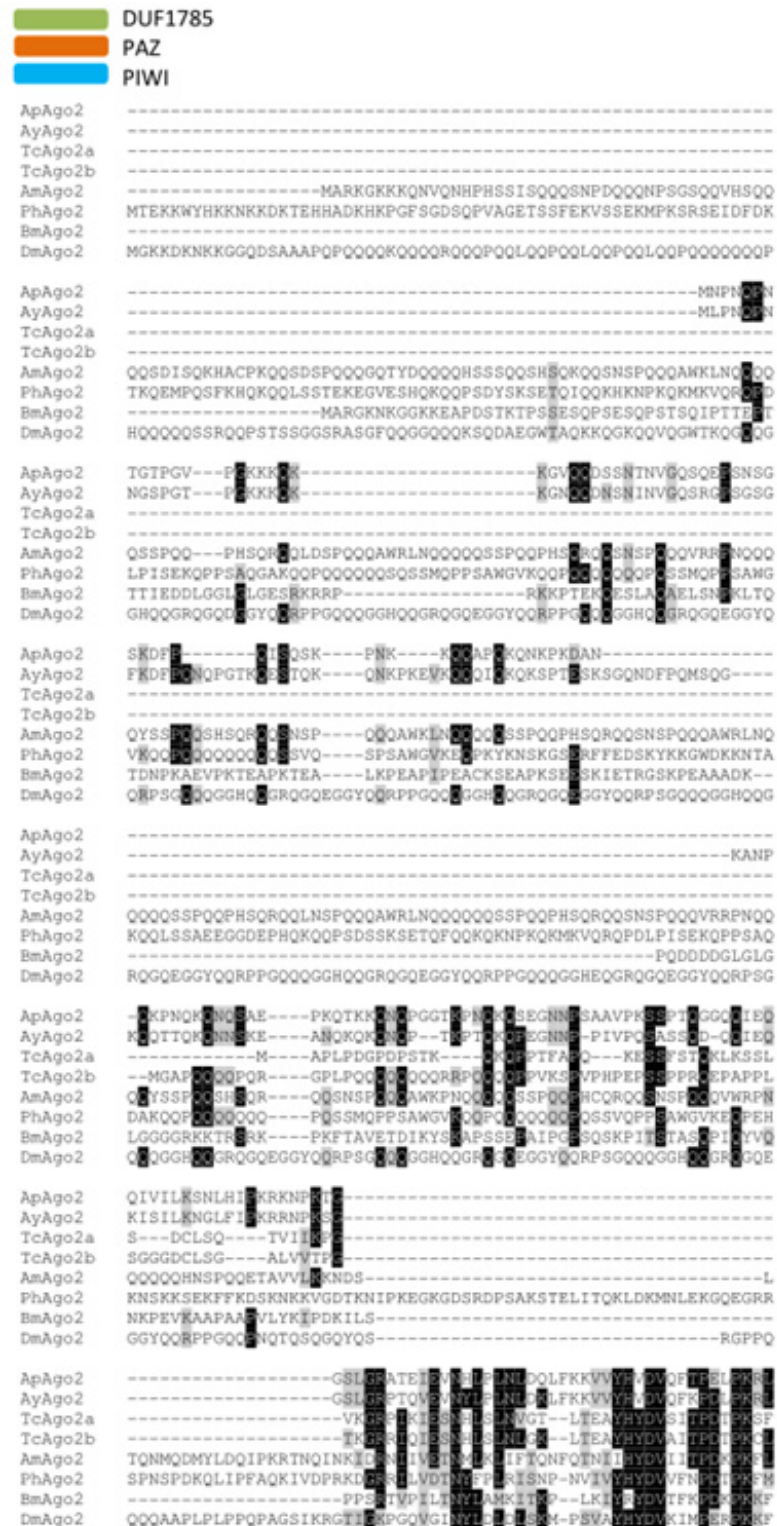


Figure S3. Cont.

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ApAgo2  LRNALDEENNHNYPKVNFAFDGRNNYTIKEI----KGKSDTVSVNDENNRTIDFGIST
AyAgo2  LRNALDEENNHNYPKLLFAFDGRNNYTIKEI----KGKSDLINVNDENNRTIDFTITT
TcAgo2a  LRDMVNLPAKHYPKNHPAFDGRKNLYSPKRLFLPNDTMSDITIEEGENKKRG--FKVVV
TcAgo2b  LRDMVNLPAKHYPKNHPAFDGRKNLYSPKRLFLPNDTMSDITIEEGENKKKE--FKVEV
AmAgo2  LRTVFEERKRKQCCKRYPAFDGRKNAYSAKLLFFGDKSNEEDINQFDVNTKRKERNKIYL
PhAgo2  LRLAWNKYASDNFKNRIITVFDGRKNAYSGELISNGNCHSAGVSIWNPSGKIREFSVSI
BmAgo2  IAQVFKLVKSKEFFKEILAFDQTKNYSLTFLFKITTEYRGVKVILKDMNGKMPFEVSF
DmAgo2  YRQAFECRVDQLGGAVLANDGKASCVGVDRFLFNSQNPE---VTVTDRNGRTLRYTIEI

ApAgo2  SIVNTIHMNKIED-YLKSGSSNTFFGDAFCALDIVLKNRFALRFINVGRSFFFPVR--I
AyAgo2  SVNVVIQMNKIED-YLKSGSSNATPGDAFCALDIVLKNRFALRFINVGRSFFFPVR--I
TcAgo2a  KLARTVLLSPLR----DILQTRQSPDQALQCLDIVLRNAP-SNSCISSGRCTFTPPRE-G
TcAgo2b  KLARTVLLSPLH----DIMRTTQSPDQALQCLDIVLRNAP-SNACIAGRCFTFTPPRE-G
AmAgo2  NKVACLILSWLTNLKCDMMDSERN-QKCIACALDILRHGP-AYQYTVVGRSLQPPPEP-G
PhAgo2  QEVRODYKQSLH-----NVKLPEAEISVLEIILKNRF-SNTLVPCGRSFFPKSQMGI
BmAgo2  KASGIVLYNNVLKHMATGGSSLNAPTDTIQCTDIVLKGQT-LESYVKAGRQYEMRFAS--
DmAgo2  KETGDSITDLKSLTTYMNDRIFDKPMRAMQCVFVLASPC-HNKAIRVGRSFFKMSDP-N

ApAgo2  TPVDLGGEMELMKCFQSPVMGNKP-YNLDVAHKGFPKQPLINFTNEMN-----
AyAgo2  TPVDLGGEMELMKCFQSPVMGNKP-FLNLDVAHKGFPKQPLINFTNEMN-----
TcAgo2a  QILRLGDMEMYYGCVQSAIRGNKQPLNVDVVAHKAFKALNVLDLVCELGSDYRNTMTR
TcAgo2b  QIILRLGDMELYYGCVQSAIRGNKQPLNVDVVAHKAFKASNVLDIVCEIGSDFRNTMTR
AmAgo2  RIVSLNGLDLVWGVFQSVVIGSKP-YNLDVAHKGFPKQSVIETLMKELCN-----V
PhAgo2  RARSISSCLDYRAGHYCAATLQRI-YNLGLAKAFYKSLPVIDWAYSFTS-----
BmAgo2  -PIDLGGLEMTITGLSQAFTSKA-FINVDVAHKGFPKQEMICAFTRDFR-----LDP
DmAgo2  NRHELDGGEALVGLYQAFMLGDRF-FLNVLTIHSHKSFISMFWIYLERFSLK-----A

ApAgo2  CDLNSEMDQRSYNTLASVYKGLKIDFTVPCNPNTK---RSYKVVGLLDTASRFREFMEDP
AyAgo2  CDLNSEMDQSFNALSNVYKGLKIDFMVPCNPNTK---RSYKVVGLLDTAAKRFREFMEDP
TcAgo2a  CDLNQPLTDFVQKALEKFLKQLKVTHYEIFGASGSR---RIHRVNGLRAPPSQARFTHJD-
TcAgo2b  ANLSQPLREFVQDFEKEIKQLKVYKYEIPNQSSEK---RIHRVNGLGEPFSQAKFKLDD-
AmAgo2  QDLTPKNIEYNLVNINKFLKGLKQLVELEPGPTSK---RTYRVNKLVDGARENKFRLED-
PhAgo2  ----SYNNRINLDSLYNFKGAKVEYKLPSSDPG---KIPRVNGLVGNAAEETFEKDT-
BmAgo2  NRPVDRQPGRAAEAFNEEIRGLKVVSKEILGTGSPQGLREHICNGVDFPSPRGTFTLEND
DmAgo2  KINNNTNLDYSRRFLPEFLAGINVVYTFQSFQAP---RVYRVNGLSRAPASSETFEHD-

ApAgo2  VRGKQTLNVQCFRITRNYVIRKENLPCLHVGNVNKK--TAIFIELCHVQKGGQLRLKKLS
AyAgo2  VRGKQSLNVQCFKITRNYSIKYNLPCLEHVGNVNKK--TAIFIELCIQVQGGQLRLKKLS
TcAgo2a  ---GKVTIWEKYYQEVKRCRLQYHPLFTLVVGSQRQRE--VLIPLEFCTVWVGQVNVNKKM
TcAgo2b  ---GRMTIWEKYYQEVKRCRLQYHPLFTLVVGSREERESKILPLPEFCTVWVGQAINKKM
AmAgo2  ---QTLCSVEKYFLQIKKTIKYNLPCLEHVGNSQKNS--IYLPALCTVWAGQVINKEMN
PhAgo2  ----ITMTWATYFAKDKKPLKHSHELNVVGSQQRK--IYLPMEFCRIVEDQVFMGEMS
BmAgo2  KGPPVRMTVYKYEYKMKKKYRIKYEDLNLVVGPKDKN--IYLPMELEVWAGQVARKQLN
DmAgo2  ---GKKVTEASYFHS-RNYPLKEFQLECLNVGSSIKS--IILPIELCSIEEGQALNRKDG

ApAgo2  ELYTAAMVNNAARPPGERQTIENCLRDIAYNKQEVVLK-DFGHEVKEHFAASIPARVLQPF
AyAgo2  EMQTASMVNNAARPPSERQTIENCLRDIXNQDEVLN-EFGVNVTEQFASIPARVLQPF
TcAgo2a  ENQTSVMTKKAATSTQVRKKIMQVLRKANYNSDPCVR-EFGFSVNNSFEKLDGRVLQPF
TcAgo2b  ENQTSAMIRKAATSTQVRKKIMQTLRTANYNDECIR-EFGFSVNNSFEKLDGRVLNPF
AmAgo2  KIOTSKMVRETATNTQKRKEKIMNGFARMNDNOCETLMNEHFHSVNTFEKVPARVLKAP
PhAgo2  PDETRMVKLATSDAKTRKDIYVFNKANFESNNIYMK-EFGLSVDKDMERIOARTHEFP
BmAgo2  DRCLSTMVREAATPPDVRKKKIEEVIQKYNYSKNOFFK-TYGLEIANEFYQVPAKILEAF
DmAgo2  ATGVANMIRYAATSTQVRKKIMNLLQYFQHNLDETIS-RFGIRIANDIVVSTRVLSEF

ApAgo2  SLAYAQNKRETKRAGVWRPDR--FSKAVHINKWVVLNLDQR-----TNIASIKNFEKSLM
AyAgo2  FLAYAQNRETRERGGVWKPDR--FSKAVHINKWVVLNLDGR-----TNMGSIKNLERNLI
TcAgo2a  TLLYARKAEVTEPSKGVWRADMNREFVGAIVKWTIVSCTRH-----PER--GEQLADMIF
TcAgo2b  SLLYADNAQIKESKGVWRADNRRLVGATINKWTIASGTRY-----PSRD-ADKLADMIF
AmAgo2  KLOPKER-EITVSKGTNRADKFFSPCVLPKRLWTILNLDKF-----VNAHDLNHNKLL
PhAgo2  SLR--TKGSVEVVKDGANKIRD--FTPTVLDNMCLLYFDNC-----VRKENLNDFQNLK
BmAgo2  TLEVGPQPTFVKKGVMQANC--LLKPEALNSGFIATELD-----PRGCNYEDIVSKLM
DmAgo2  QVEHSHKRFMTVKNKSNRMDGMKLELPKPKAHKCAVLYCDPRSGRKMNYTQLNDFGNLII

ApAgo2  MSARDLNVVMSPMDPVINIFLRSS-LADIKTSIGNVSTKQACNTELIWVWTFDYPAGI
AyAgo2  MSSKELNVVNPMDPPINCLLQRNMRVAEIKTLVGNNSRKLQVNTIELIWWTFDAPAGV
TcAgo2a  RMASNGMQITSKATGEFQHLGGRQNIRDLI----DYER--RKQDHDLIIVVWNSGP-Q
TcAgo2b  RMASNGMQITSKAT-ESTHIGGRQGNIRDLI----DYER--GKQDYDLIIVVWNSGP-Q

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Figure S3. Cont.

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AmAgo2  HSKFLNMKIEEACH--FTNLTITQTNINNI-----EYKDKKKKONILVVVILENLND-A
PhAgo2  RKSTEFNMQVKDAIRNEVGGNSHPREIARTLQ-----ELQMKLVVVITFETKG-L
BmAgo2  NTSRQNMNVTPQKMACFNIRINDLHKSMTHA-----LEKQVNFVVVSGRGROY
DmAgo2  SCSKAVNISLSDSVTYRPFDDERSLDTIFAD-----LEKQHLIAVITF-QFRIS

ApAgo2  YASVKQKSELEW--GILTQCIKSKTMFMVN---TSISSNILLKINSKLNGLNITLAIRSS
AyAgo2  YGMVKQTSLELEI--GVLTOCIKSRTMFMVN---STSSNILLKINSKLNGLNITLAIRSS
TcAgo2a  YSLVKQAELNV--GCLTQCIKSRITAKLN---PQITANILLKINSKLNGLNITLAIRSS
TcAgo2b  YSLVKQAELNV--GCLTQCIKSRITAKLN---PQITANILLKINSKLNGLNITLAIRSS
AmAgo2  YSLVKQISELDIHBETITQCIKKNCTLKLN---DSTIGNILLKINSKLNGLNITLAIRSS
PhAgo2  YSKIKNICHTQEG--ILTOCVRAETLCODFRKFSTIVENILLKKNAKLGEINVSIDKNEF
BmAgo2  YHKIKQIAELKVG--ILTHVFRELTATRRMN--POTARNILLKINSKLNGLNITLAIRSS
DmAgo2  YDTIKQKAELOHG--ILTOCIKQFTVPERKN--NOTIGNILLKINSKLNGLNITLAIRSS

ApAgo2  PPSMPS--AIIISGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
AyAgo2  PPSMPS--AIIISGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
TcAgo2a  LEMSRP--CIINGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
TcAgo2b  PLIMKRP--CIINGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
AmAgo2  FNCLYQP--CIINGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
PhAgo2  PTLDEL--VMVIGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
BmAgo2  PQLKSGAVMIGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL
DmAgo2  LEWKNNT--MYIGADVTHPSPEQNTIPSVAAVAASHLTGSGSYNMEWRLCSPEKVEITQDL

ApAgo2  EDVHIQLKVKERTKIVKKIFMFRDGVSEGOFLQLLEYELIAIRACRLNI--AYKFE
AyAgo2  EDVHIQLKVKERTKIVKKIFMFRDGVSEGOFLQLLEYELIAIRACRLNI--AYKFE
TcAgo2a  CANTVEQLMFFYRKTRHKPBTIVFFRDGVSEGOFAEVRRATISAIHQACKLQR-EGHFE
TcAgo2b  CNITVEQLMFFYRKTRHKPBTIVFFRDGVSEGOFAEVRRATISAIHQACKLQR-EGHFE
AmAgo2  EEMIIQLKYPYVVTGQKPKLIFMFRDGVSEGOFLVIMHKLISAIKRAIARLEKSNELRI
PhAgo2  ENITCEHLAKYQIRQNYPEKIFMFRDGVSEGOFLVIMHKLISAIKRAIARLEKSNELRI
BmAgo2  EEMVDFHFAKKSQGLPKKVFVFRDGVSEGOFAEVMKSELTGLHRAVQSVAG-LNAKF
DmAgo2  FSTITLHLVYKKEYRNAYSDHIIYYRDGVSEGOFLVIMHKLISAIKRAIARLEKSNELRI

ApAgo2  SVTFLVQKRHHTRMFFKFSYDMDGKFSNVPSSTIIDTQITHFELDFYLCSHASIQGTS
AyAgo2  SVTFLVQKRHHTRMFFKFSYDMDGKFSNVPSSTIIDTQITHFELDFYLCSHASIQGTS
TcAgo2a  RITFLVQKRHHTRMFFINPRSEDKNNVFAGTQVDTHITNPRMODFYLVSHASIQGTA
TcAgo2b  KITFLVQKRHHTRMFFINPRSEDKNNVFAGTQVDTHITNPRMODFYLVSHASIQGTA
AmAgo2  PITFLVQKRHHTRMFFIDAKNSDDKNFVQASTQVDTEITHFTHIDFYLVSHASIQGTA
PhAgo2  KITFLVQKRHHTRMFFVNDADAIGRMFNVFAGTQVDTHITNPRMODFYLVSHASIQGTA
BmAgo2  EWLILVQKRHHTRMFFLP---GNNARFNVDPGTQVDRTIWHFELDFYLVSHASIQGTA
DmAgo2  KITCCVIVQKRHHTRMFFSGDVTISNRFNVDPGTQVDRTIWHFELDFYLVSHASIQGTA

ApAgo2  RPTKYHLIWDNNFTEDOLELTLYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
AyAgo2  RPTKYHLIWDNNFTEDOLELTLYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
TcAgo2a  RPTKYCTIWDNNMNDITBELTYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
TcAgo2b  RPTKYCTIWDNNMNDITBELTYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
AmAgo2  RPTKYRCHNENOMPENITBELTYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
PhAgo2  RPTKYRCHNENOMPENITBELTYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
BmAgo2  RPTKYRCHNENOMPENITBELTYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK
DmAgo2  RPTKYRCHNENOMPENITBELTYLCHMFVRCITRSVSPAPTYAHAAAFARAYTENK

ApAgo2  TINLNNLEDECTRNQLNHSFTVNTPMFFV
AyAgo2  TIDLNLDEDECTRNQLNHSFTVNTPMFFV
TcAgo2a  KDLTLQLKTHQKQCIQESTVREKPMFFV
TcAgo2b  KLDSQLKTHQKQCIQESTVREKPMFFV
AmAgo2  PLNIDNLQESCKK-KMTLRINKSSPMFFV
PhAgo2  NLKSNDD-LKSIQAKLKDVLSQKNPMFFV
BmAgo2  IFNNNLKSNDD-LKSIQAKLKDVLSQKNPMFFV
DmAgo2  TNRFLLKSNDD-LKSIQAKLKDVLSQKNPMFFV

```

**Figure S4.** Sid1 protein in *A. glycines*. Italicized and underlined residues at amino-terminal indicate the secretion signal peptide (SignalP). Amino acid residues in black background indicate transmembrane domains (total 11).

```

MWKPIFVIIFGLSSVWSELFSENVERYGSNDLIPVLKGNYSQNYPQIINNMTSYLFLYD
YLPNSTFEPPRVKVTLIEPEDNSIVDPLIVVVRHRSVGVISQWLPYIEKQKEIKYKAAHI
LCPLLASANNESRIVVSVSTNSINNITFILRLDIQKSFNVLLNQEVSNLSPSEPYYYY
SFKQNSSMVLHVKSDDSIQSSCPVFDLSLETQYDGLRQTVSKTGIIISKDE
YPLGLFIVFVHSDSACHQGNQAINFRKTSINFVVKPTVDFNYQIINCLIVIVIFIFI
LWDTTFEYYHTKGDDLKTIDIIQEEPSTSICTPVIQPDNVSYDSSLDDETIDILKSPEP
KVDLIRTKACLVSDLSKDKHRLKAKSLYVWNLTITVAVFYSLEPVTQLVFTSQMLIET
GNQDLCCYNFLCSHSFILGPWKFSDFNHIFSNIGYIFFGLLFILITYKRECVNIPNKKFG
IPNHYGLYYAMGSALAMEGLMSACYHVCNHSNFQFDTSPMYVICMLSMIKIYQTRHPDI
NANAYLVFGVLALVILGLTGIMYEGPILFVLFTCLHLIMIFWLSAQIYYMGRWKLDKKT
PKRFLNHIMTAPNCPKPYPNRMVLLSFGILINLGLAVSHWIIKFGNFGNYLLILFMVNL
ILYLSFYIVMKLISKEKLDHFWPLLYILLAVIFWSASLYFYVHKSSSWTLSAAESRTYNT
CTFMDFYDNHDIWHFLSAISLFLSMVLFTLDDDVNSKPTATIPVF

```

**Figure S5.** Alignment of amino acids sequences from insect Sid1 proteins. The conserved and similar amino acid residues are labeled in black and grey backgrounds respectively. The accession numbers for various protein sequences used in the alignment are provided in Table S2.

```

AySid1 -----MKKPIFVIFGLSSVWSBELFSENVERVGSNDLIPVLKGNYSQNPQIINNIM
AgSid1 -----MKKPIFVIFGLSSVWSBELFSENVERVGSNDLIPVLKGNYSQNPQIINNIM
ApSid1 -----MKKPIFVIFGLSSVWSBELFSGQYASYKSNLIPVLKGNYSQNPQIINNIM
PhSid1 -----MIICDNFNVVKELPVGVKMYT-----IDNTV
AmSid1 -----MANYTAYQEA-----IDNTV
NlSid1 MIFSILFKMRNVLYYYVLSFISTAVLSLNFESILKNSENATVPHYCEFNKLYNFQANNA
BmSid1a -----MMGYRKILLMLLIKISYCFKNSVNLAVNRTFQYNIYNDTWINLQVNNI
TcSid1a -----MIAAAGILLVPLADCAHIALNIEQHGG-----NYSQVMPFFENQT

AySid1 SYLFLYDYLPNSTFEPRVKVILIEPEDNSIVDEPLIVVVRHRSQVSWOLEFIEKQQ---
AgSid1 SYLFLYDYLPNSTFEPRVKVILIEPEDNSIVDEPLIVVVRHRSQVSWOLEFIEKQQ---
ApSid1 SYLFLYDYMLNSTLEPRVKVILIEPENHDIIDPLIVVVRHRSQVSWOLEFIEKQQ---
PhSid1 EYIIETKNLSQNDKVE--PRIFLKCNCENGENELVVMVANKGVLSWOLEFIEKQ---
AmSid1 EYVTSMETVRIEVESN-----ATSNIELIVVVRQKKEFLSWOLEFIEKQSM--Y
NlSid1 TVPVLVFNKTENSTIYF--ARITTSDDAATAENPLFAAWQKSLTTAEVERLVPSN--
BmSid1a IEQILDFTEDSKLLGFPTRHVTNTSLTSDHEFLITATQKGVSSWOLEFLVLQT--D-
TcSid1a TEHVLFEP--TSDSIYFVYKAWSSG-AKLAS--EVLVVRQEREVISWOLEFVVDITMK-

AySid1 --EIKYKAAHILCEPLLSASNNES-----RIVVSVS-----TNSINNIIE
AgSid1 --EIKYKAAHILCEPLLSASNNES-----RIVVSVS-----TNSINNIIE
ApSid1 --EIKYKAAHILCEPLLSASNNES-----GLVVSVS-----TNSPNNIIE
PhSid1 EHYSIYKETERLTCEYNIINSLLNFDY----SENNNSVIPTAPVKLTLSFELKKLOV
AmSid1 FNNSEYKETSRTLCSTNYNHGKLG-----QEKEFMILSVS-----ITNHQNIIE
NlSid1 -KNLLRNVRITLCPHYVNIINSTAH-----MDSFFITVS-----IDASNIIE
BmSid1a DYFLMLNDMERTLCFHDAGSDIRRESPP-----TVOLIT-----SSANVSV
TcSid1a DGVVHEHNTSRTLCHNDMPRIAKAKATSRILPIQLSQNFILALST-----SLANVDI

AySid1 ILRLDIKSENVLLNQEVSNLSPSEFWYIYYSFK-----QNS
AgSid1 ILRLDIKSENVLLNQEVSNLSPSEFWYIYYSFK-----QNS
ApSid1 ILRLDIKSENVLLNQEVSNLSPSEFWYIYYSFK-----QNA
PhSid1 ELIWNLYDELIDNESKTVNMTPTSTFYFLVEEQ-S-----EEV
AmSid1 ILNWTKEHNEYLSTGENKTVEISPSQENHYGYTESGQ-----VES
NlSid1 TIRAQLVDFEVDVVGKPISTFTVSHAHQEYSEFEP-----DYL
BmSid1a DIKLRVDEDFYIELGKVNEIVNPSSEFYIYYSFEDQNPWNVSHAAGGLDGTQRYNNYIP
TcSid1a SVMVEEERDEYLOEGRPYEVSVSPSESKYIYYSFEDHK-----KN

AySid1 SMVLLHVKSDDSIICMTLSIONSSCPVFDLSLETVOYDGLRQTVSKTGGIILSKDEYPLGLF
AgSid1 SMVLLHVKSDDSIICMTLSIONSSCPVFDLSLETVOYDGLRQTVSKTGGIILSKDEYPLGLF
ApSid1 SMVLLHVKSDDSIICMTLSIONSSCPVFDLSLETVOYDGLRQTVSKTGGIILSKDEYPLGLF
PhSid1 NSULLHWITSDDDTCLIVSTIONVSCPIFDLEENVOYRSHFQDITRCGGILITRDAPFNGFY
AmSid1 SSVTVHVKSDDSIICMTVSTIONVSCPVFDLEENIEFSCYQWTVIROGGITVKEEFPLOFE
NlSid1 SSGVLRKISDINSVQMSLEWQNFSCPVDQENNLKETGYWETIRGGMLLTRAFPIPRVE
BmSid1a KSVILVIESDDDBICATVSTIONVSCPVFDNREIKYAGYHLTSSQGGITLTQAMFPGFY
TcSid1a TSAMIEINSDDDVCLIVSTIQSFCPVFDLQKDTYSGKWOTINRKGGITRQREFFPGFE

AySid1 IVFVVSDDSAACH-----CGNYQAINRTKSINEVVRKPTV---DFNYQIINCLIV
AgSid1 IVFVVSDDSAACH-----CGNYQAINRTKSINEVVRKPTV---DFNYQIINCLIV
ApSid1 IVFVVSDDNSAACH-----CGNYQAINRTKSINEVVRKPTV---DFNYQIINCLIV
PhSid1 IVLIVTGEENYCF-----SKFLGNEYDRKSVTVQLSKSISSSDYHIAVLLTILV
AmSid1 VVLVVSDDTDCY-----GTPT-MIPSENKRVILTINASTIKROYTHASGIVVCOV
NlSid1 IVFVVSDDSGDQSGHI-----PSSGSGPADRIKRVLEHIFESTIYQDYDIAMAAVILIA
BmSid1a VVLIVRQSDADCTGAS---ETEDAPKSFPAKSKTIFRLKIATISYQENLVGALVSAAL
TcSid1a IVFVAKADNYQCSQKHSVLLVEHRKQHLILANRTSTTETITNKGNGKENGASLATILGA

AySid1 IVIEIFILFTFTFFYHTRGDDLKIDITQEEPSTSTCSFE-----VNIC
AgSid1 IVIEIFILFTFTFFYHTRGDDLKIDITQEEPSTSTCSFE-----VNIC
ApSid1 TFHISITILVLTFFYHAKRDNLKIDITQEEPSTSTCSFE-----VNIC
PhSid1 LSLSECTLMFTVFYIYNKKEKNFIPDDCFIISSENEVSASVSNVLPALSPSSPGPFITGTD
AmSid1 IFSECTITYVFSVISKVRNRQMKETILNCESEHINEPIIS-----SPST-----VEESG
NlSid1 FALMYTGAFGVFVNAKRRKER---NELSEFYDSFCGEAS-----VVTG
BmSid1a VLLVALFVLALLPCPCRCTEEVLVVVEESSPSTREDSEA-----
TcSid1a LLSFCIVSTIMIAETRWG-----TISKFRPSGDELDADW-----

AySid1 EDNVSYDSSLDETDIDILKSPPEPKDLIRTKACLYVSDLSKKDHRILKAKSRLYVWNLIT
AgSid1 EDNVSYDSSLDETDIDILKSPPEPKDLIRTKACLYVSDLSKKDHRILKAKSRLYVWNLIT
ApSid1 EDNVSYDSSLDETDIDILKSPPEPKDLIRTKACLYVSDLSKKDHRILKAKSRLYVWNLIT
PhSid1 TLSIKTDSSLDETDIDNVSDVFEKDIFFSLKGYMYLCOLARKNQSVLRKSKSEMYLNLIT
AmSid1 EVSIDSSLDETDIDIMEDALSKEIIRTKLVLSLCOLARKDPILIRHKGRLYLYLNLIT
NlSid1 TLSGADVEGVFNSQLSSNTSTLARPREI-IIRKLCNLDAKVNRMVRRRRLYVWNLIT
BmSid1a -----ETDTQPILEAGAADEWSREHALTIGKTRAPPDITARRSDRFEGGALT
TcSid1a -----SEPPEPPIITRELKHELUSRQ-ALTWNLLARAP-EKDRRRSYNLYLHILS

```

Figure S5. Cont.

AySid1	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
AgSid1	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
ApSid1	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
PhSid1	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
AmSid1	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
NlSid1	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
BmSid1a	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
TcSid1a	VAVFYSLPVTQLVFTSQKMLDETGNODLCYYNFLCSHFFILGPWKFSDFNHIFSNIQYIF
AySid1	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
AgSid1	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
ApSid1	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
PhSid1	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
AmSid1	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
NlSid1	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
BmSid1a	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
TcSid1a	FGLLFILLITYKRECVN----IPNKK----FGIPNHYGLYYAMGSAALAMEGLMSACYHVCF
AySid1	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
AgSid1	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
ApSid1	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
PhSid1	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
AmSid1	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
NlSid1	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
BmSid1a	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
TcSid1a	NHSNFOFDTSMFYVLCMLSMIKIYQTRHPDINANAYLVFGVLAALVITLGLTGIVYEGFIL
AySid1	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
AgSid1	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
ApSid1	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
PhSid1	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
AmSid1	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
NlSid1	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
BmSid1a	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
TcSid1a	FVLFTCLHLIMIFMLSAQIYYMGRWKLLKKTPKRFLNHIHTAPN----PCRFRYPNRMV
AySid1	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
AgSid1	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
ApSid1	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
PhSid1	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
AmSid1	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
NlSid1	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
BmSid1a	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
TcSid1a	LLSFGILINLGLAVSHWIIR---FGNFGNYLLILFMVNLILYLSEFYIVMKLISKEKLHFW
AySid1	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
AgSid1	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
ApSid1	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
PhSid1	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
AmSid1	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
NlSid1	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
BmSid1a	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
TcSid1a	PLLYILLANIFMSASLYFYVHKSSSWTLSAASRTYNTPTCFMDFYDNHDIWHFLSAISL
AySid1	FLSFMVLSFLDDVNSKETATIPVE
AgSid1	FLSFMVLSFLDDVNSKETATIPVE
ApSid1	FLSFMVLSFLDDVNSKETATIPVE
PhSid1	FLSFMVLSFLDDVNSKETATIPVE
AmSid1	FLSFMVLSFLDDVNSKETATIPVE
NlSid1	FLSFMVLSFLDDVNSKETATIPVE
BmSid1a	FLSFMVLSFLDDVNSKETATIPVE
TcSid1a	FLSFMVLSFLDDVNSKETATIPVE

Table S1. Scanprosite hit scores for various domains in insect Dcr2 proteins.

Domains	Dcr2 proteins				
	AyDcr2	ApDcr2	TcDcr2	BmDcr2	DmDcr2
Helicase (a)	19.5	19.7	22.2	21.4	18.7
Helicase (b)	14.0	13.6	12.1	12.6	12.1
Dicer_DSRBF	27.0	26.1	24.8	23.5	24.9
PAZ	17.3	18.4	17.2	11.9	8.7
RNase III (a)	20.1	19.6	23.9	21.3	18.4
RNase III (b)	35.5	34.0	36.9	34.7	31.1
DSRBD	10.0	9.6	-	9.1	9.7

**Table S2.** GenBank accession numbers for various protein sequences used in various analyses.

<b>Name</b>	<b>Accession #</b>
ApDcr2	XP_003240110.1
AmDcr2	XR_120636.1
BmDcr2	NP_001180543.1
CeDcr2	NP_498761.1
DmDcr2	NP_523778.2
TcDcr2	NP_001107840.1
ApR2d2	NP_001155644.1
AmR2d2	XP_001121349.2
BmR2d2	NP_001182007.1
CrRde4	NP_499265.1
TcR2d2	NP_001128425.1
DmR2d2	NP_609152.1
PhR2d2	XP_002430935.1
ApAgo2	XP_001944852.2
AmAgo2	XP_395048.4
BmAgo2	NP_001036995.2
CeAgo2	NP_871992.1
DmAgo2	NP_648775.1
PhAgo2	XP_002422648.1
TcAgo2a	NP_001107842.1
TcAgo2b	NP_00107828.1
AgSid1	ABP98803.1
ApSid1	XP_001951907.1
AmSid1	XP_395167.4
BmSid1a	NP_001106735.1
BmSid1b	BAF95807.1
BmSid1c	NP_001106736.1
CeSid1	NP_504382.2
NISid1	ADI88514.1
PhSid1	XP_002430777.1
TcSid1a	NP_001099012.1
TcSid1b	NP_001103253.1
TcSid1c	NP_001099128.1

**Table S3.** qPCR primer sequences and product length.

<b>Name</b>	<b>Primer sequences</b>	<b>Product length (bp)</b>
<i>AyDcr2</i>	GAGATTTCTGACTCTTTAGC CCGATTGCCGAATAACAA	100
<i>AyR2d2</i>	AATCTGAAGACGCACATC TAGCCGCATACTCTTGTA	135
<i>AyAgo2</i>	GAATCGTCAATCGTCATT AACAGAATACTCAGAATATCG	93
<i>AySid1</i>	ACCATCAGAACCAGTGTATT TGTCGTAAGCCATCATATTGTA	165

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