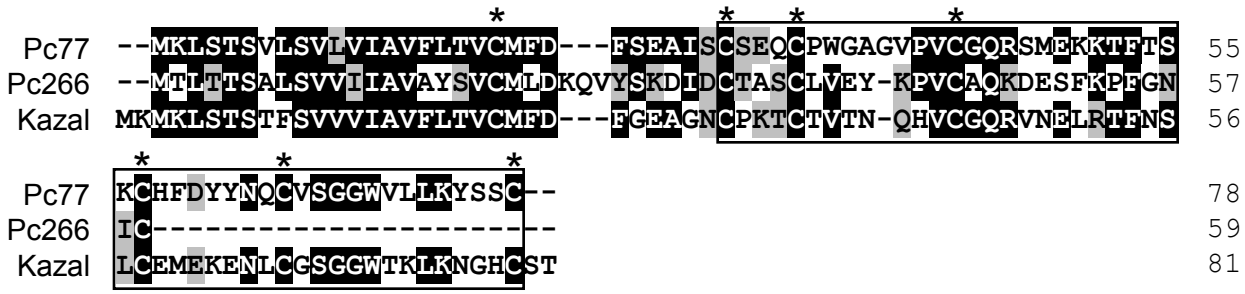
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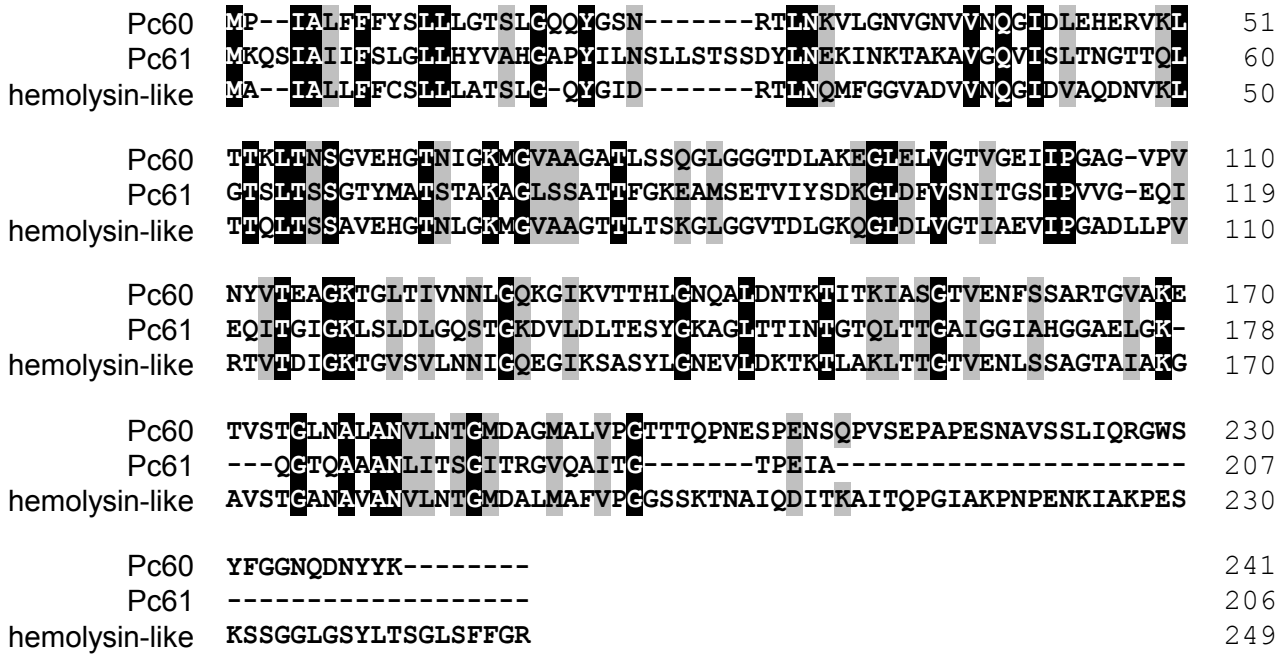
Pc266 --MTLTTSALSVVIIAVAYSVCMLDKQVYSKDIDCTASCLVEY-KPVCAQKDESFKPFGN 57
Kazal MKMKLSTSTFSVVVIAVFLTVCMFD---FGEAGNCPKTCTVTN-QHVCGQRVNELRTFNS 56
Pc77 KCHFDYYNQCVSGGWVLLKYSSC-- 78
Pc266 IC---------- 59
Kazal LCEMEKENLCGSGGWTKLKNGHCST 81

Fig. S1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Pc61 MKQSIAIIFSLGLLHYVAHGAPYILNSLLSTSSDYLNEKINKTAKAVGQVISLTNGTTQL- 60
hemolysin-like MA--IALLFFCSLLLATSLG-QYGID-------RTLNQMFGGVADVVNQGIDVAQDNVKL 50
Pc60 TTKLTNSGVEHGTNIGKMGVAAGATLSSQGLGGGTDLAKEGLELVGTVGEIIPGAG-VPV 110
Pc61 GTSLTSSGTYMATSTAKAGLSSATTFGKEAMSETVIYSDKGLDFVSNITGSIPVVG-EQI 119
hemolysin-like TTQLTSSAVEHGTNLGKMGVAAGTTLTSKGLGGVTDLGKQGLDLVGTIAEVIPGADLLPV 110
Pc60 NYVTEACKTGLTIVNNLGQKGIKVTTHLGNQALDNTKTITKIASGTVENFSSARTGVAKE 170
Pc61 EQITGIGKLSLDLGQSTGKDVLDLTESYGKAGLTTINTGTQLTTGAIGGIAHGGAELGK- 178
hemolysin-like RTVTDICKTGVSVLNNIGQEGIKSASYLGNEVLDKTKTLAKLTTGTVENLSSAGTAIAKG 170
Pc60 TVSTGLNALANVLNTGMDAGMALVPGTTTQPNESPENSQPVSEPAPESNAVSSLIQRGWS 230
Pc61 ---QGTQAAANLITSGITRGVQAITG-------TPEIA---------- 207
hemolysin-like AVSTGANAVANVLNTGMDALMAFVPGGSSKTNAIQDITKAITQPGIAKPNPENKIAKPES 230
Pc60 YFGGNQDNYYK-------- 241
Pc61 ---------- 206
hemolysin-like KSSGGLGSYLTSGLSFFGR 249

Fig. S2

A

```
Pc24   MEMFMLLLVSYLSSVHSGKINECNMKNITMHVVTWNVNGERPT-CLLKLLGQFQEKDEDE  59
Pc29   MKLKILLLFLFVS-LYAK---EAPENPRTVYVVTWNVGEENPPGSVKELLGQISSKDELN  56
Pc31   MKLKILLLFLFVS-LYAK---EAPENPRTVYVVTWNVGEENPPGSVKELLGQISSKDELN  56
Pc32   MKLKILLLFLFVS-LYAK---EAPENPRTVYVVTWNVGEENPPGSVKELLGQISSKDELN  56
IP5P   MNLKILLLFSFAS-LYAKYSKAAEDNPRSVYVVTWNVAEKDPPGSVKELLGQVSDSSEVN  59

Pc24   PDMVIVGLQEVTKSIDTALKDYFLGNRWEASIGDILES-NDYVKVETASLFGMFLNVYVK  118
Pc29   PDIIIVGLQEVTMNPIKALKNKLVGDKWSEDIDDILKSNNNYAKIYSESLLGMLLKVYVR  116
Pc31   PDIIIVGLQEVTMNPIKALKNKLVGDKWSEDIDDILKSNNNYAKIYSESLLGMLLKVYVR  116
Pc32   PDIIIVGLQEVTMNPIKALKNKLVGDKWSEDIDDILKSNNNYAKIYSESLLGMLLKVYVR  116
IP5P   PDIVIIGLQELTMNPVQAVVNNIFKDKWSDDFNEILKSRNNYHKVYSESLLGILLKGIVK  119

                                                  *
Pc24   IQHSWSVADVN-IRHIDTEYFRYYDNKGGVIMKFRLYGRLFCLVHAHL--HGQNKTARIE  175
Pc29   IKYKVTLSKEKDATTVKTGVKGFSGNKGAVIIKFKLNELSYCVVNSHLPAHDEKLEERID  176
Pc31   IKYKV--SKEKDATTVKTGMKGFSGNKGAVIIKFKLNEQSYCVVNSHLPAHDEKLNERIE  174
Pc32   IKYKVTLSKEKDATTVKTGMKGFSGNKGAVIIKFKLNEQSYCVVNSHLPAHDEKLKERID  176
IP5P   IKYKDSINKKADATTVKTGLGGMSGNKGAVILKFQLNNRWFCIVNSHLAAHDEKLQERIE  179

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Pc24   DYKEIEQIRTVFCENPSDYVFFLGDLNFHIRKVENLKTPEEIHALIKDEKYDELLKEDEL  235
Pc29   DYKTINRERGKFCGN-SDYVFWLGDLNFRLD--ESLKD-EKIRELVKQKKFNELLQKDQL  232
Pc31   DYKTINKERGKFCGN-SDYVFWLGDLNFRLD--ESLPD-QKIRELVNQKKFPELLQKDQL  230
Pc32   DYKTINRERGKFCGN-SDYVFWLGDLNFRLD--ESLKD-EKIRELVKQKKFNELLQKDQL  232
IP5P   DYKTINNKRVDFCNKPSDFIFWLGDLNFRLQ--EDVED-EKIRNWVQQRKYADLLKLDQL  236

Pc24   LYYKNANKIFRNYTEQPIKFPPTYKFLLKRNKSEYNLKRRPAWTDRILYKTESEREITPI  295
Pc29   KVNHETKEIFGTFNEQEIKFAPTFK--LEKGKGEYSKQRRPAWTDRVLYKSDTSKIIKPT  290
Pc31   KVNHKTKEIFSTFKEQEIKFAPTFK--LEKGKGEYSKQRRPAWTDRVLYKSGTSKIITPT  288
Pc32   KVNHETKEIFGTFNEQEIKFAPTFK--LEKGKGEYSKQRRPAWTDRVLYKSDTSKIIKPT  290
IP5P   KINKQTKEIFTDFNEKEITFAPTFK--LEKGTGTYSTKRRPAWTDRILYKSDTKKNITPT  294

Pc24   SYNSMEDHRKSDHYPVEAI------                                      314
Pc29   LYQSITSYIQSDHYPVQAQFFIANK                                      315
Pc31   LYQSITSYKQSDHYPVQAQFFIANK                                      313
Pc32   LYQSITSYIQSDHYPVQAQFFIANK                                      315
IP5P   LYKSIESYKHSDHYPVQAQFDIKY-                                      318
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B

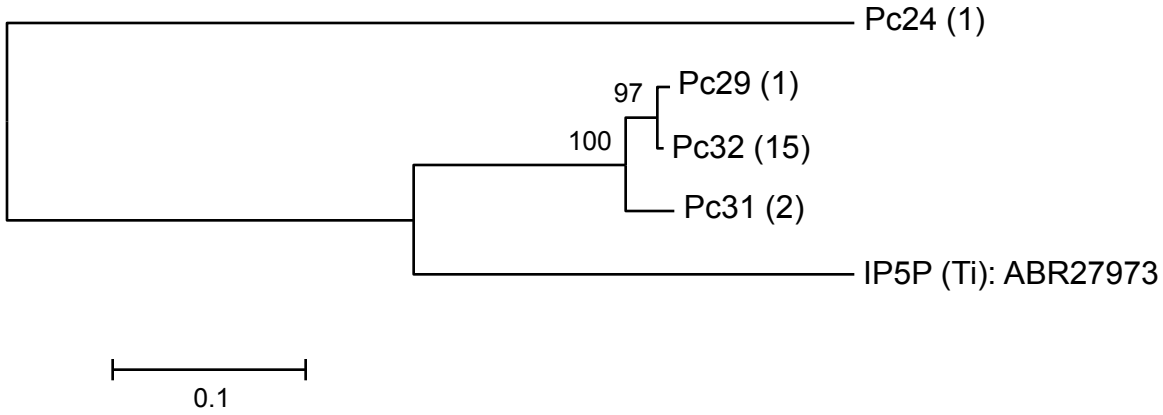


Fig. S3

A

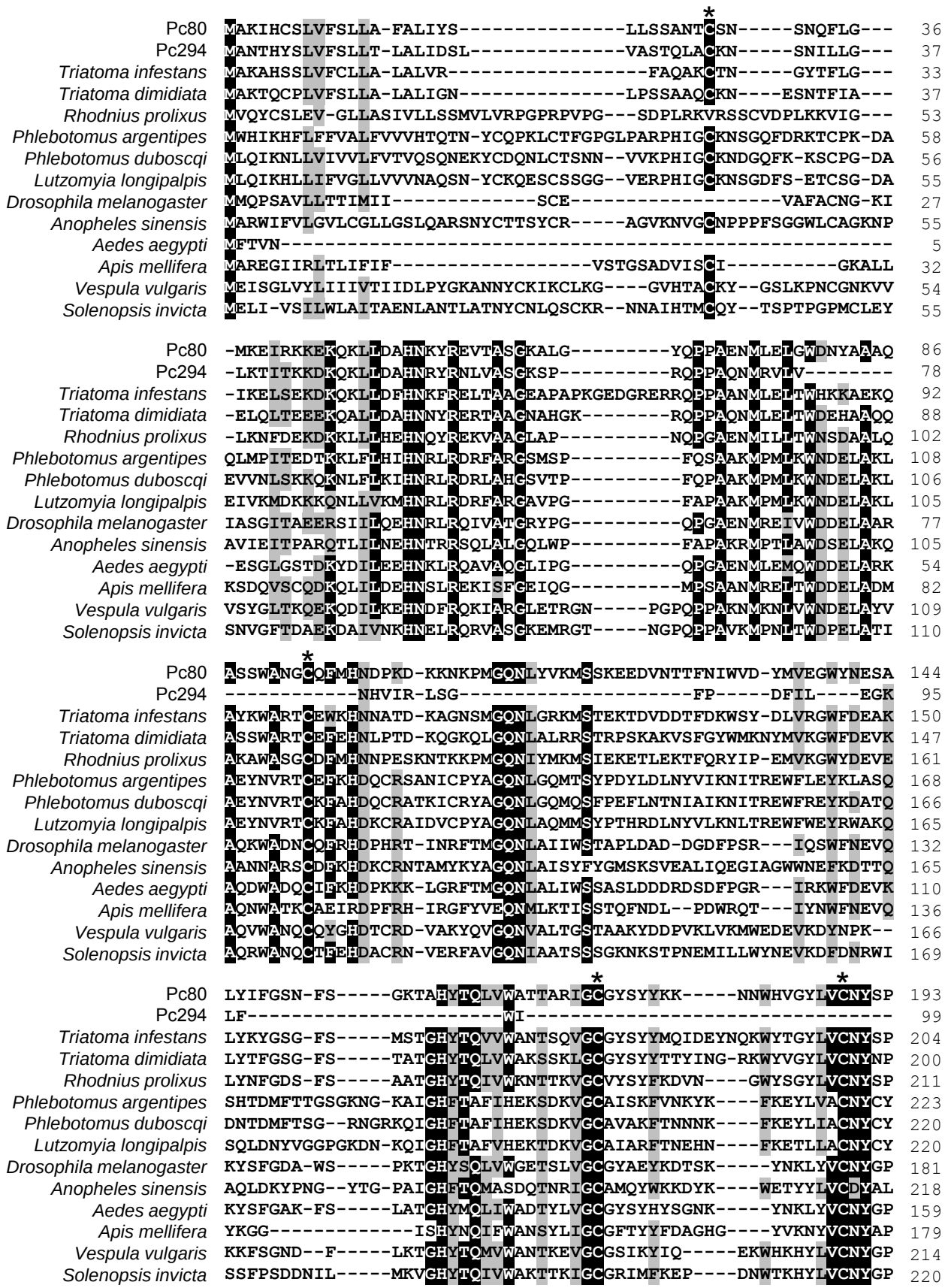

Pc80
Pc294
Triatoma infestans
Triatoma dimidiata
Rhodnius prolixus
Phlebotomus argentipes
Phlebotomus duboscqi
Lutzomyia longipalpis
Drosophila melanogaster
Anopheles sinensis
Aedes aegypti
Apis mellifera
Vespula vulgaris
Solenopsis invicta

Fig. S4

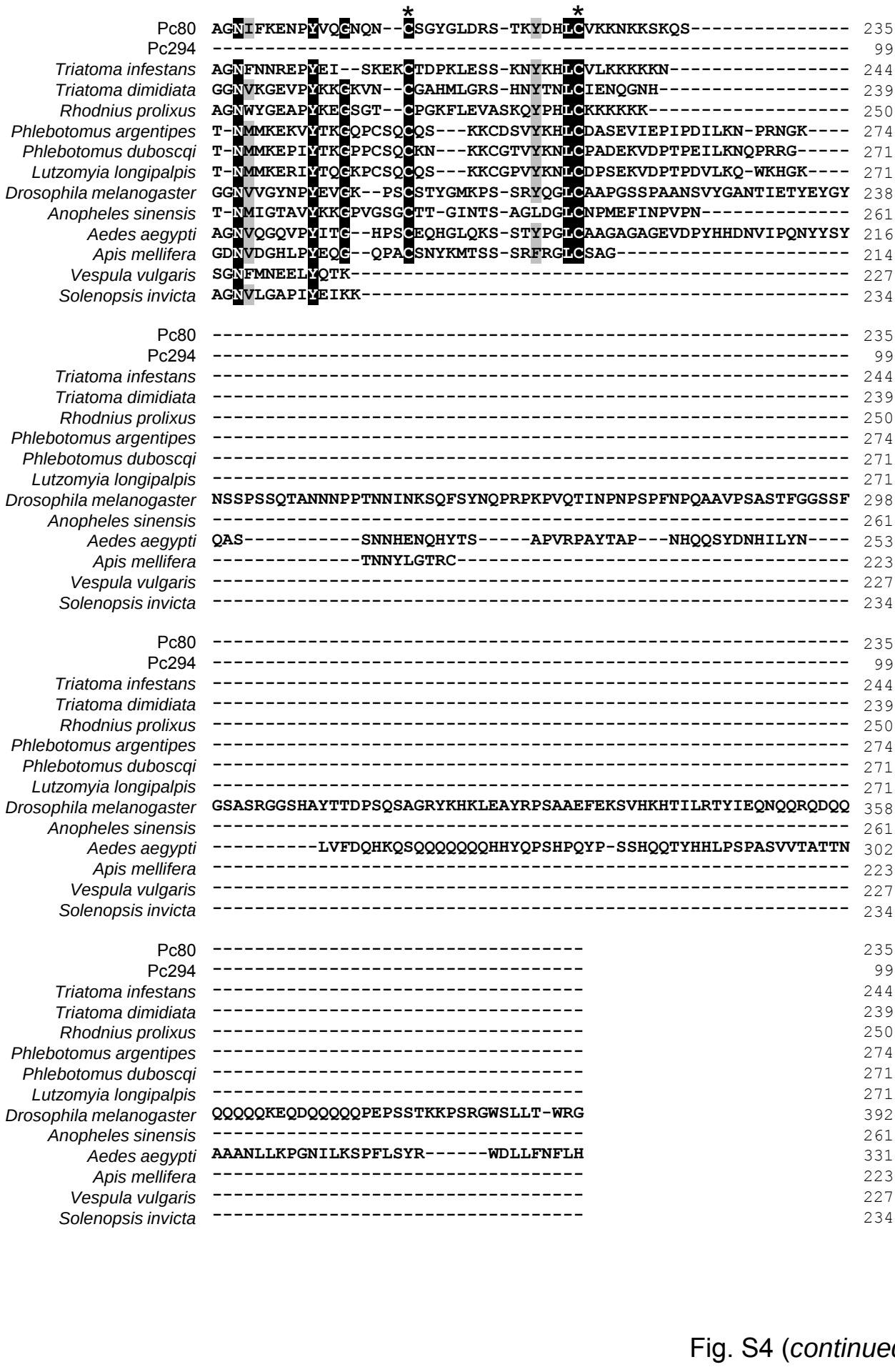


Fig. S4 (*continued*)

B

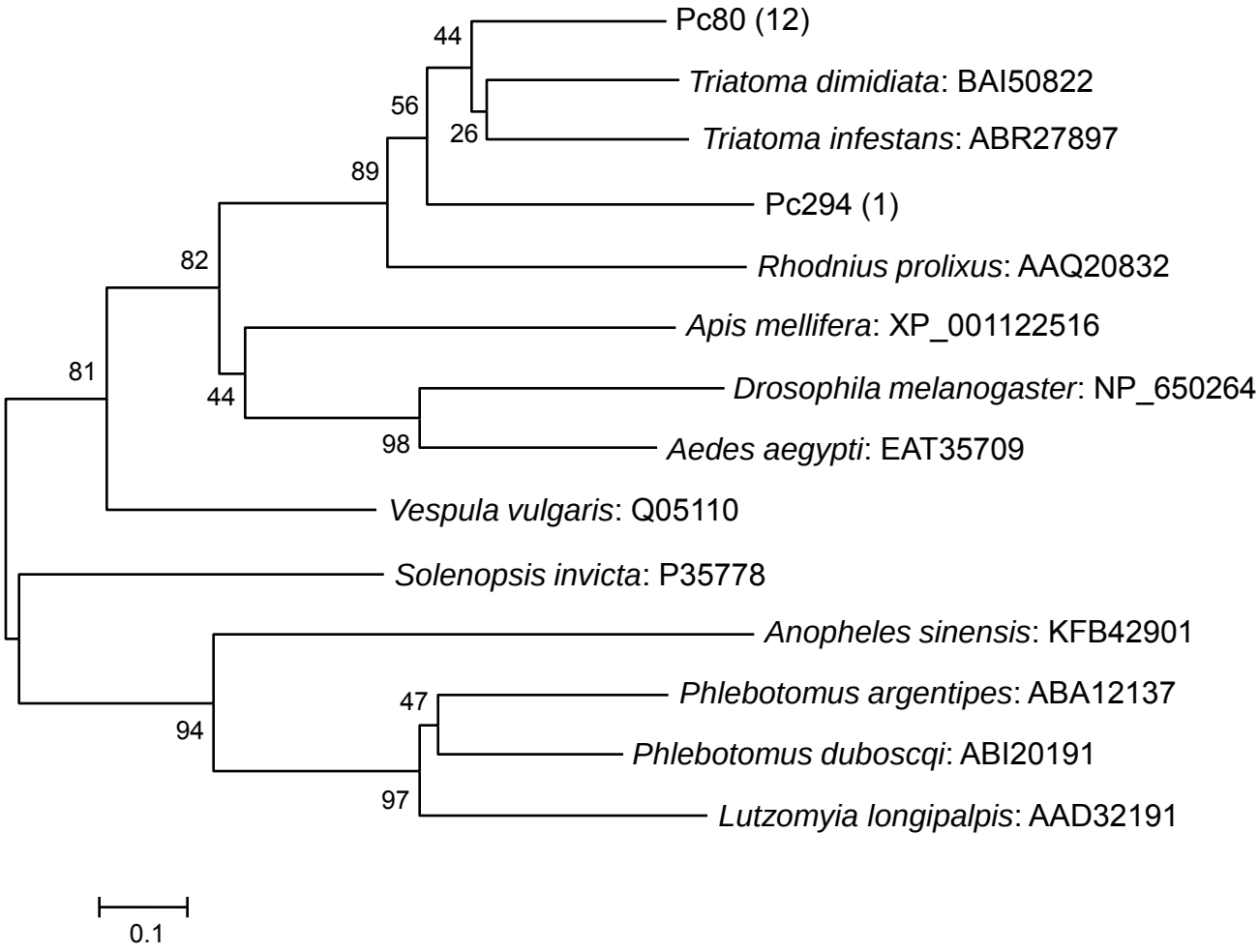
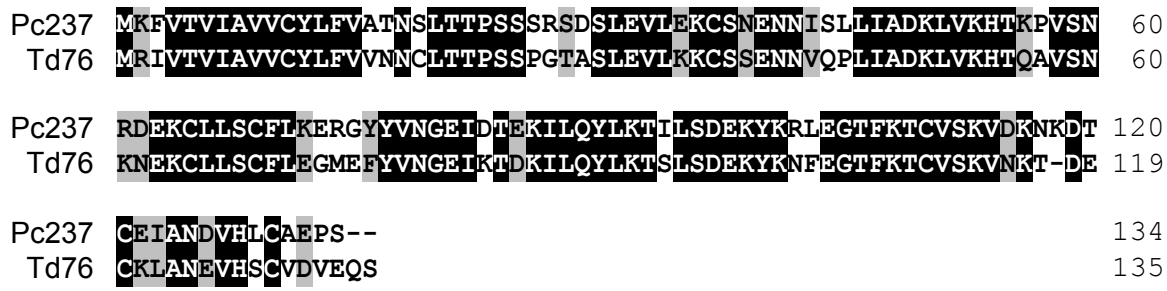

Pc80 (12)
Triatoma dimidiata: BAI50822
Triatoma infestans: ABR27897
Pc294 (1)
Rhodnius prolixus: AAQ20832
Apis mellifera: XP_001122516
Drosophila melanogaster: NP_650264
Aedes aegypti: EAT35709
Vespula vulgaris: Q05110
Solenopsis invicta: P35778
Anopheles sinensis: KFB42901
Phlebotomus argentipes: ABA12137
Phlebotomus duboscqi: ABI20191
Lutzomyia longipalpis: AAD32191
44
56
26
89
82
81
44
98
94
47
97
0.1

Fig. S4


Pc97 MLTVFLWRILAFVAAVYCQEELKDLLDFSNITSKISLYPHRDVEPTSVEASPEIDSSEHG 60
Ti trypsin MNYLYLLIGLVVVVEVP----------HAHTQGEGDDDEDSSEYG 35
Cd protease MMKWFI---LVAVVAL----------VQA----DSSEHG 22
Pc97 --VTPGKMETNCTCGRANR-GGARIIGGRQFQPFEYPFLALIS-LSTDPERPHCGSTIIS 116
Ti trypsin NRNVPGDKTTNCDCGWANK-EDKRIIGGEETNVNEYPMMAGLFYKPKE--LLFCGGSIIT 92
Cd protease --VSPGSKGTICACGWANRSGGSRIVGGTYYKANEYPFIVGIATVGARGYAPFCGGSIIT 80
Pc97 DRHLLTAAHCTS-KAGGNIGLLVTVAVHEIGN---SPKSYTVEVERLIQHENYNERNLLN 172
Ti trypsin QYHILTAAHCTQPFEEDVRDIQIVSGEHDQDKVDESSSTVYIDVLNFVPHEGYYLIGHRH 152
Cd protease ANHVITAAHCTDDIIKARTRTAVLLGSHDRSRP--SSTAVTINVERINQHEKYNANTIAN 138
Pc97 DISLLYLKNPLQLTEVVSPACMPLPGMSVIGKYVRVIGWGATEAYGPMTVLPQKVDLEVI 232
Ti trypsin DIAIILLKDKIVYTNIVGPACMPTEPIDMIGHKIKVLGWGKLSANGPSSKVLMKVYLNVV 212
Cd protease DISILTLASSINFNKLIGPVCLPLPGLDVSGQTVRVLGWGAERFQGAMTMRPKKLDTTAV 198
Pc97 STEKCHEYWQLQVATDPVTQICRMWENKSACHGDSGGPVVWLDPDTNRYTSVGIVSFGLP 292
Ti trypsin PLEECNNTHEYIGLVE-RRQICTYHPTKDSCQGDSGGPLLWLDREINRYVLAAVTSYGLS 271
Cd protease SPAQCAAIWRGLVSATNPTQVCTLSKKETACQGDSGGPVVWRDPQTNRYTLIGLVSFGAA 258
Pc97 CKSSVPNMDTSVVSYLPWIMKGIEATTPGRKLCTKIVN 330
Ti trypsin CATDVPGVNTNISYYMPWIQKVVAETRPEAPICTKQN- 308
Cd protease CTDEKPTVNTRVAAYLPWIKQQIAATKPAG-VCTKA-- 258

Fig. S5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Pc237 RDEKCLLSCFLKERGYYVNGEIDTEKILQYLKTILSDEKYKRLEGTFKTCVSKVDKNKDT 120
Td76 KNEKCLLSCFLEGMEFYVNGEIKTDKILQYLKTSLSDEKYKNFEGTFKTCVSKVNKT-DE 119
Pc237 CEIANDVHLCAEPS-- 134
Td76 CKLANEVHSCVDVEQS 135

Fig.S6