**Supplementary File S1. Alignment of all WIV domain homologs identified in this study**

They include viral sequences, metagenomics sequences, and sequences annotated as coming from arthropods.

>LakeSinai\_YP\_009333196.1\_/1-91

LATECLRAQLAMARQVADYL------CV-ERVCV--FDT-TGFF------DTA-SVHLT--------SSGLR

YRSRDG---------HVAVLS--LAAQAILPRAD-------PNVYQQIARC-----------RLI-----SS

--VHGLCL

>LakeSinai3\_AYP65074.1\_37-/1-91

LATECLRAQLALARQVADYL------CV-DHVYV--FDT-TGFF------DSA-SIHLT--------SSGLR

YRSRDG---------HVAVLS--LAAQSVLPMAD-------PNVYQQIARC-----------RLT-----NA

--AYGLCL

>LakeSinaiNE\_YP\_009388497./1-91

LATECLRAQLMLARQVADYL------CV-DHVYV--FDT-TGFF------DSA-SVHLT--------SSGLR

YRSREG---------HVAVLS--MAAQAILPMAD-------PNVYQQIARC-----------RLT-----NA

--AYGLCL

>LakeSinaiSA1\_YP\_009388489/1-91

LATECLRVQLELARRVADYL------SV-DHVYV--FDT-TGFF------DSA-SVHVT--------THGLR

YRTREG---------HVAVLS--QSAQAILPRAD-------PNVFQQIARC-----------RLV-----NA

--AYGLCL

>LakeSinaiSA2\_YP\_009388493/1-91

LATECLRVQLQLAKRVAEYL------GV-ECVYV--FDT-DGFF------DTA-SVHVT--------THGLR

YRTRDG---------IVAVLS--QSAQAILPRAD-------PNVFQQIARR-----------RLT-----PA

--EHGLCL

>HyperaSinaivirus\_QUS52856/1-91

LAHETIRLQVDIANKVADEL------EC-GFVYV--FDK-SNYF------LTG-TTKVT--------ARGYR

YTIRND---------NVAVLS--AAAQAVLPYDD-------TNVYTQLARR-----------HFE-----SD

--HIGLYI

>RiboviriaYbb117shi01|QJI53477\_/1-95 455-548

FVRESCNIQRDLGMKVMKEL------GI-NSIYT--FDS-IGFF------KQG-ESKLT--------DSGIR

YLHFDG---------KYAVLS--QSAQNVLPVSYDK---SSSNHFNQLAGY-----------QYT-----ID

--CIGCVL

>NasturtiumMaculaLike|QQG34660.1/1-88 ORF 3 [Nasturtium officinale macula-like virus 1]

LAKQSLLVQTNLARDVSKIT-------N-SRIYL--FDN-SNFF------DNA-DVVIY---------NSIR

TLTRSG---------KVAVLS--QACQSLVGD---------SSLYKSLIPPE----------HIS-----SD

--SIGVYL

>New|HeteropelmaAmictumTymo|ORF5/40-129 Heteropelma amictum tymo-like virus

VGRSHMLDQVSTALKVASLL-------R-ARVYV--FDS-SGFF------NCPNADVVT--------YDGVR

TLRVSG---------RTALLS--VSVQCSISE---------PLVYRSLVPPF----------RIS-----AD

--DIGVYV

>New\_BombyxMaculaLike\_YP\_0/1-90

IADNNLVTHKELALKVSSII-------G-TRVYV--FDP-SCYF------STPPFDTVL--------YDNIR

TVLKDN---------KTALLS--ASIQASLPS---------SEIYRQLVDSRH----------VS-----SD

--SFGVYV

>Bat\_tymo-like|NC\_030844\_ORF3\_5784-6356/99-188

LGLECLKVQLSLASTVANKL-------N-HRVYV--FCP-TNFF------STPPFDVVL--------YDGVR

TVLKDG---------KTALLS--ASAQSVITT---------NSSYRSFIPPT----------RIS-----ED

--ATGVYI

>New|XiphydriaTymo|ORF4/9-101 Xiphydria camelus tymo-like virus

IGTKCLLTQRDLALTVSATL-------K-QRVYI--FDK-SGVH--F---NTPPFDVVL--------VNNIR

THLKNG---------KYAVLS--VAAQDSIPCGD-------SAMYRSLLPPT----------YIS-----ED

--EIGVYI

>New|New|Diglyphus/17-109 isaea tymo-like virus |ORF8 6305-6640

IGKEALAVQYRMALTVSFRL-------R-QRVYL--FDK-SGKF--F---TPPEACVVL--------VDGIR

TYLRDG---------RTALIS--VSAQNIIPCGN-------TSLYRQLIPQT----------YVS-----ED

--EIGVYL

>TineaSemifulvella|ORF/9-102 694654-695526+ 268-585

IGRECLTIQLRLASIVAKSL-------N-HHVYV--FDP-SNSF--F---KEPDANILI--------IDNIR

TLHRDG---------QTAVLS--QAAQLVIPSLNG------NTVFRALIPSF----------NLD-----ED

--SLGVFL

>New|OrothripsTymo|ORF4/49-136 Orothrips kelloggi tymo-like virus

IADESIRIHRELAMKVAASL-------K-KKVYV--FDT-SSYF------ANA-DTIQV---------DNVR

TLTAHG---------NFAVLS--GSLSKCCKG---------ADDFRLLYPPE----------HLR-----TD

--SIGLFL

>HubeiVirga16\_YP\_009336680/1-89

FTRKSLSIQQNLASSLKTEL------SL-DRVYL--FDT-SDYF------SDA-EKRIS--------SKNLR

YLFKEN---------KVAFLS--ETAQAVFKN---------FNEYNQFCAV-----------PFL-----HD

--TIGVYM

>New|AcridaCinereaVirgaLike2|/101-188 Ne dmarre pas sur un M, 3 codons stops (espacs) avant, pb- Acrida cinerea virga-like virus 2

FTRESLRIQCNIAIKIAEAL------GA-PNIYV--YDS-SCYF------TNA-PVRVI---------GTYR

YKYRDG---------KFAALS--DTAQLVFQN---------WNEYTQFLQC-----------PWS-----HD

--DVGVFI

>New|CeracrisVirgaLike2|ORF10/10-97 Ceracris nigricornis virga-like virus 2

FTRESLRIQCNIALKVTEAL------GV-PSVYV--YDS-SCYF------TDA-AIRVI---------GNYR

YKYKSG---------KVAVLS--ETAQLVFKN---------WNEYTQFLQR-----------QWS-----SD

--DVGVFI

>ErysipheVirga1\_QKN22699.1\_/1-89 Erysiphe necator associated virga-like virus 1

FTRYCLKIQQDIAQRVAAAT------GH-DRVYV--YDT-AGYF------YDA-DNKTT--------ADCLR

YKEKCG---------RIAVLS--ESAQTVLKN---------PNEYQQFSSQ-----------RNP-----ID

--VVGVYL

>DougjudyVirga\_QIJ70140.1\_/1-89

FTRESITAQKRIANIIAKAM-------I-SDVYL--YDE-VKYF------DDA-ESRMF---------ETYR

YLFKDG---------KIAVLS--MAAQKAMHK---------SNEFVQFCTSTD---------DVG-----ID

--SIGVYY

>HangzhouMerodonVirga-like/1-89

FTRASITAQKRLAVKIAAHF-------V-TDVYL--FDE-SNYF------ANA-EDGVV---------DGLR

YKKKDG---------KYALLS--ISAQQAMRN---------RNEYLQFNTNTD---------DVA-----CD

--NIGVFL

>Bactrocera\_A0A034VNC8\_A0A/1-89

FTRASIKQQKQLAATLAQHF-------V-NDIYI--FDE-INYF------CDA-IDCSY---------NSIR

YKYKNG---------KFAVLS--FAAQKTMRD---------CNQFLQFNDNKE---------DVS-----MD

--KIGVFF

>Ceratitis|CAD6998875.1/1-86 unnamed protein product [Ceratitis capitata]

MTG---TQQRELAAKLAQHF-------V-NDIYI--FDE-KNFF------CDA-TDCTY---------NNTR

YKYQEE---------KLAMLS--VAAQQTMKE---------YNQYLPFNTNTE---------DVA-----TD

--GIGASL

>LygusHesperus|A0A0A9YLR6|A0A0A9YLR6\_LYGHE/25-113 DNA-directed RNA polymerase subunit beta OS=Lygus hesperus OX=30085 GN=rpoB\_7 PE=4 SV=1

FTRRSLTLQRAHDATVVATI-------A-KSVVI--FDS-TNFF------SDA-EQEII---------SGIC

VKKKNG---------KYAVLS--DTAQAVFTD---------KNQYVQFTTNQE---------HIK-----IT

--NEGVIL

>APOlygus|A0A6A4J3X7|A0A6A4J3X7\_APOLU/334-422 Uncharacterized protein OS=Apolygus lucorum OX=248454 GN=GE061\_06098 PE=4 SV=1

FVRESLTIQRGLAASVVVTV-------G-HGVYL--YDS-VKFF------DDA-ETDVV---------AGVR

VKKKDG---------KIAVLS--QAAQAVFEN---------SNQYIQFSDNVT---------HLD-----VL

--PDGVFM

>ApoLYGUS|A0A6A4JC69|A0A6A4JC69\_APOLU/12-100 Uncharacterized protein OS=Apolygus lucorum OX=248454 GN=GE061\_06133 PE=4 SV=1

FTRESLTIQRGLAASVVVTV-------G-HGVYV--YDS-VNFF------DDA-QVDTI---------AGIR

VKKKDG---------KIAVLS--QAAQAVFKD---------SNQYLQFSENVT---------HLE-----LL

--PDGVKM

>Apolygus|KAF6207353.1:1-150/1-72 hypothetical protein GE061\_018594 [Apolygus lucorum]

-----------------MAV-------Q-RGVYL--YDA-ANFF------SDA-ECETI---------AGVR

VKKKDG---------KYAVLS--QAAQAVFTD---------SNQYMQFSDNTT---------HLE-----VL

--PDGVKL

>New|SapyginaDecemguttataVirga|ORF4/20-107 Sapygina decemguttata virga-like virus ORF4

FVISSLNIQRSLAVEVAIAL-------K-SDVYL--FDA-VDYF------CDA-EDKII---------NNIR

YKTRES---------HHAVLS--QAAQQTLN----------RQQYLKYTEDKQ---------IIE-----TD

--LIGVKI

>New|SyrittaPipiens|ORF1/12-100 >LR994572.1:78307200-78307900 Syritta pipiens genome assembly, chromosome: 2

FLRKSYAIQWNLAKTLADIK-------S-SNIYI--YDA-CNFF------KNG-ETKIL---------NNIR

YKEKSS---------KYAVLS--MTAQDIMQN---------NYEYLAFNQYSH---------QTG-----SD

--EIGVYL

>LygusHesperus|A0A146LBM7|A0A146LBM7\_LYGHE/12-101 Uncharacterized protein OS=Lygus hesperus OX=30085 GN=g.89819 PE=4 SV=1

FVRYSLDIQRGLARKVSEAE------PG-SGVYV--FDT-TGYF------DGG-PTSLV---------AGVR

VQKVGG---------NYGVLS--SAAQNLFKS---------ANTYFQFTSVPS---------EVT-----AD

--SIGLKL

>AtratoVirga6\_QHA33765.1\_h/1-87

VARNLILLQRERALIIAQTF-------V-TDVYV--FDQ-SGYF------NVS-EQRRH---------DTIY

YLFKDG---------KFGVLE--PAVQASMKN---------SKQYLRFVSD-----------EVE-----SD

--GIGVYI

>HammarskogVirga\_QGA87340./1-87

IVANLLELQHQRALSIAAEF-------V-TDVYV--YDD-SAYF------TVA-EQRRF---------EVIY

YHFREG---------KYAVLE--PSVQNTLRD---------IQTYRRLAPQ-----------HIR-----AD

--RIGAYV

>HubeiVirga21\_YP\_009337662.1\_23/1-87 Hubei Virga-like virus 21

IVRELVRLQRERAITIARTV-------L-TDVYV--YDG-KAYF------RTA-EVRRH---------ENIY

YQYKDG---------KCAVLE--ESIQKVVRT---------CSAYSRFTSD-----------LIV-----ED

--DIGVLV

>New|ShanxiVirga-like1|strain\_SXRC2001/21-107 ORF13 12039-12464

IA--SVREQQRLAMRVGRNL-------L-NDVYV--YDA-AAFF------TTA-TQKMD---------GTIR

YLERDG---------RIAVLG--VASQRVCKS---------SAEYLQLSNENV---------ATE-----TD

--AIGVKI

>New|PsylliodesChrysocephala|CAH1114883.1/29-116 unnamed protein product [Psylliodes chrysocephala]

FTRESISIQIDLALRVADKL-------K-KNVYV--YDN-DEFF------ATGFEMEIV---------DNIR

VKTKKG---------SYAVLS--QAAQAVFAN---------DQHYRQYADK-----------PLC-----DN

--RTGLYV

>DiabroticaToursvirus3a|UOX61048.1\_ASCOVIRIDAE/5-94 hypothetical protein DiTV3a\_F4ORF11 [Diabrotica toursvirus 3a]

FVKESLNVQKMLALKVSSAL-------K-KDVFV--YDL-KNHF------DNC-DTKII---------DNIR

YQENNVSK-------NIAVLS--VSAQKSFKN---------SAEYLNFTDKV----------DYY-----LN

--DIGVFI

>HyperaAssociated1\_QUS52866/1-91

LAQTCLKIQKDLALKVMREA------SI-NKIYV--YDE-KDYF------KDA-TTSMC---------GNIR

YLEKDG---------EFALLS--GAAQQAIGGDER------ANTYCQILRD-----------RLK-----TD

--DIGVYL

>New|SolenopsisInvicta8|MH727525.2/7-93 ORF6

FVQASLTIQITLAMTVMRKL------NI-SKIYV--YDN-SHFF------DNA-TTHIT---------DNVR

YSKRQE---------NYAVLS--KAAQQTLT----------KENYRSHTNH-----------TLL-----SD

--HIGLYI

>New|PhyllotretaStriolata|CAG9854400.1/30-117 unnamed protein product [Phyllotreta striolata]

FVRRSLDIQYDLAAEVKRAV-------K-EPIYV--FDA-SGTF------KDA-RPIIV---------GHTR

VLKTDDG--------KFGVLS--ESAQFAFAG---------VKDYLQFTNR-----------TFD-----SD

--STGLYM

>New|LochmaeaCrataegi|ORF1/7-94 >OX387432.1:32142700-32143200 Lochmaea crataegi genome assembly, chromosome: 10

FIRKSFEIQLKLAAEVEGIV-------K-QRIYV--FDI-SRTF------SDA-EIVVI---------GNIR

VLLSNNK--------KYGVLS--QTAQFAFKS---------IDEYKRYTNV-----------DLH-----CD

--DVGLYI

>AnophelesIridovirus|YP\_009021198.1/1-90

FVRYSIRYQILLAQHVAKIC-------N-KNIYV--FNS-DGYF------KKDVFVETI---------DGVR

TLFKNG---------HRAVLS--IAVEESFGTD--------EHLFLQFVDKD----------IVQ-----KD

--ELGLYV

>InvertebrateIrido25|YP\_009010649.1/1-92

FVTYSLRYQLLLAQHVASIC-------N-CIIYI--FDK-NGYF------DSPDDTKVE-------VIDGVR

TVSKEG---------LRAVLS--VAVKESFGSN--------EDLFLKFIDDG----------VAQ-----KN

--DIGLYV

>WiseanaIrido|YP\_004732832.1/1-92

FVTYSLRYQLLLAQHVASIC-------N-CIIYI--FDK-NGFF------DNPEDTKVE-------VIDGVR

TVSKEG---------LRAVLS--VAVKESFGSN--------EDLFLKFIDHG----------VTQ-----KN

--DIGLYV

>Iridovirus22|YP\_008357405.1/1-92

FVTYSLRYQLLLAQHIASIC-------N-TKIYV--FDK-NGYF------DSKDDTKVE-------VIDGVR

TVSKNS---------LRAVLS--VAVKESFGSN--------EDLFLQYVDKG----------VVQ-----KD

--DTGLYV

>APOLYGUS|KAF6208318.1/264-363 hypothetical protein GE061\_016772 [Apolygus lucorum]

FVLTQFNAQVRLAQTVQAEV------SN-SSIYL--FDQ-IGYF------NNA-SQIVI---------ADVR

VVLKDD---------DYAVLS--VAAQGAFLT---------ANTYCQFTTDPSLAQVR-LAQTVQ-----AE

VSNSSIYL

>New|LasioglossumLativentre|ORF1/44-131 >OU744357.1:25872100-25872700 Lasioglossum lativentre genome assembly, chromosome: 3

FVEVTLKEQLRIARIICDHF-------G-SPVYI--FDK-KGVF------SDA-EVLLY---------GSYR

YLKSLS---------RYGVLS--SSAQSLFT----------THQYKMKIPNTE---------TLY-----ED

--ESNTNV

>New|SeladoniaTumulorum|ORF1/42-129 >OU565275.1:12277000-12277600 Seladonia tumulorum genome assembly, chromosome: 10

FVEASLREQLRIARIICNHF-------G-SPVYV--YDK-MEEF------SDV-EVLVY---------NNHR

YLKSLN---------RYGVLS--LSAQSTFT----------AQQYKGKAPNTE---------TLY-----ED

--EIGVYI

>NeteliaDilatata|OX328013.1/34-121 OX328013.1:15390700-15391250\_Netelia\_dilatata\_genome\_assembly,\_chromosome:\_3

FVRYSLKVQIEKARVICDHF-------G-SPVFI--FDA-VGMF------SGA-DTYVY---------EKIV

YCRARG---------SYAVLS--QAAQAVLV----------VANYLEYIPSDV---------SVS-----QS

--DNGIYI

>ChronicBeeARM39062.1\_9-95/1-87

FIYYSLAEQLRIAAIISSTF-------H-TPVVV--FSL-DPRW------NDA-DAQSH---------QGLR

YLRSGN---------EFAVLS--RAAQRTFIC---------PSQYIEYTTIP-----------LD-----CD

--ELNVRW

>FushunXinmovirus1\_UHM2767/1-90

FTVDVIARQRALAARVLAAL------KC-DKVYL--YDF-SGEF------NFA-TKRTV---------AGVT

YVESPTG--------KVGLLS--TSAQKLFQGN--------ANTYRNFSQV-----------PYP-----QD

--NIGVYM

>New\_Saiwaicho\_AWA82266.1\_/1-88

VVRSLIEEQQLQALELSKVS-------D-NSVYL--FDT-SDTF------VGA-SVKFH---------NNFV

YQQSTTG--------HLGIIL--TPLQKNFKS---------FNSYNQFSNI-----------ILL-----KD

--NIGLKI

>New|ND\_092901|Sinai-like\_ORF4/54-156 Organization similar Lake Sinai, with ChroparaMTase, Rdrp, Capsid noda-like, and ORF4

LARECLQTGIEMAWKAKKEL------SV-DRMYV--FDA-VDYF------DCNSNLITV---------GGIR

YKTKIPMVLGIMQSPSFAVLS--SAAQKTFRHVANS-----VDDYLKIAHMT----------ALT-----TD

--DIGVYI

>BeeMacula2\_AVH76851.1/1-90

LAQGLIEDHYSVARAASTAF-------D-RRVYV--FEK-EPFF------SRKTVLSFL--------YASHQ

FYYRND---------KIGLIY--DYVQDAFPS---------SSELIQLYPSS----------HVS-----ED

--EVGVYV

>ThripsPalmi\_XP\_034253369./1-97

FVKASIAYQKTLAEKVKALN-------G-RTVYL--FDA-TGFA------AGL-QDAVT--------AESLR

YKTGTLDG-----RQVDAVLS--VSAQTSLSGPAG------AQTYLRWAGQGQ---------DIH-----VD

--DHGVHI

>Frankliniella\_XP\_02628726/1-99

FVHASVGYQRELAEKIKQLN-------G-RRVYL--FDA-SGFS------AEF-ADELT--------PDNIR

YKTGVLAGG----LRVDAVLS--VSAHRALGDGPD-----AARTFLRWTGREQ---------DTL-----LD

--EHGVYV

>Megalurothrips|KAJ1532394.1/13-108 hypothetical protein ONE63\_000994 [Megalurothrips usitatus]

FARASLAVQTELAAKVCALN-------G-RRVYV--FDA-TGFS------AGW-RDART--------DDGVR

YKTGVLED-----RAADAVLS--ASAQRTLSGAPG------ARTFLSWTDKN----------GLT-----VD

--QHGVYF

>HangzhouFlavi1\_UHK03321.1/1-88

VGHTIVKMAVSMAKQLAVDV-------G-NDVCF--YDV-TGKF------KEATQLIIN--------SKRVL

YSNG-----------AYAVLS--GTLQKSVLSPAA------KQVLAEMDG-------------VR-----CD

--KGDLFI

>Brandeis\_AVZ66287.1\_32-11/1-88

FMRASVATQVDIAVRVRASQ-------N-RDYVL--FDP-DY--------HRV-NREMI---------NGYR

VEVDTYG--------RHAVLN--TASQKSLN----------FSQYFGLVSSLN--------KDIV-----SL

--DGKVYL

>MuthillVirus\_KU754517.2\_1/1-88

FMHVSVNTQIDIAIRVRQSQ-------N-RDYVL--YDA-DF--------HRS-NRVLV---------NGYR

VEVDALG--------RHAILN--TASQKSIS----------GLQYFGLVEKFS--------KDII-----FI

--DNKVFL

>HubeiVirga18akaBroomeVirga\_YP\_/1-89

FVVCSLKTQVDIAKRVRDIQ-------N-ADYIL--FDP-SF--------RRT-HRIRI---------GDYR

VEVDAMG--------RKAVTC--AAAKEVFD----------TDDYWQIVREFD-------CDDII-----LH

--HHCVAL

>MarsacVirus\_KU754518\_12-1/1-89

FVLCSLRTQVDIARRVRDIQ-------N-ADYIL--FDS-SF--------RRT-HRIRI---------GDYR

VEVDAMG--------RKAVTS--AAAKETFD----------ADVYWQIVSEFA-------YDDVV-----IC

--NNCVAL

>BofaVirus\_KU754515.1\_24-1/1-87

FVFATLQKQLEIARNVRDMQ-------N-SDYIL--FDP-NF--------VCN-TTKMV---------GKFR

VEVDKDG--------REAILS--YGAQKSFN----------VEKYMNFMVGQK---------DVT-----RS

--GSVVTL

>BeultVirus\_MF893262.1\_24-/1-87

FVFSTLQKQLEIARAVRDHQ-------N-LDRVL--FDP-SF--------VCV-NVRMV---------DKYR

VEIDAKG--------REAILS--YGAQQCFN----------VEKYMSFMVGQK---------DVS-----QN

--GSCVIL

>HubeiPicornaLike36|KX883970.1\_ORF2\_9360-9647/6-92 Identical to SichuanPicornaLike, which lacks 3' end

FVATTLSRQRDIALECRAIC-------N-KDRIL--YDR-SF--------HPA-RTIML---------GQYR

VEVDASG--------REAILS--AGAQKHFN----------VDQYWAYVHGWP---------NVV-----KS

--GSVVTM

>Mutum\_QSC42385.1\_5-91\_\_\_\_/1-87

FIRTTIRTQIDIAQSCRSIL-------N-SDYIL--FDL-SF--------IPA-SEEMV---------GRYR

VSRDSSG--------RRAILC--TGAHKHFT----------PDHYASFLPTTA---------FII-----RR

--GPIFYL

>AtractomorphaNegevLike1|Nege-like/9-95 OL672484.1 ORF5 11865-12161

FAKASVAKQLEICEEVRSLQ-------N-FDYVL--FDK-DF--------VVD-KFITV---------GHYR

VQIGRDG--------RRAVLS--YAAQETLV----------LGSYSPLIPKRV---------TVD-----VR

--GTSVIL

>ZeugodacusCucuNegev|UPT53700.1/11-103 MAG: hypothetical protein 5 [Zeugodacus cucurbitae negev-like virus]

FAIQSVRSQLSIAKNVRLVQ-------N-RPYVL--FDK-SF--------QRI-NTIRI---------KTYR

VQVDAHG--------RFGVLS--ESAQRCFE----------YQDFLEVFNAAND---IFEPSELS-----FD

--GNSVVL

>ZeugodacusTauNegev|UPT53683.1/12-97 MAG: hypothetical protein 5 [Zeugodacus tau negev-like virus]

FARGTLVKQLYIADAVRNIN-------N-KQRIL--FDP-NFIKD---------HRVRY---------ADYY

VDVNAQG--------EEAILS--AGAEAFG-----------VTNYLLYLPPST---------SII-----VD

--GNRVYY

>New|CeratitisNegevLike2|OL957307.1/9-94 10130-10423

FVRLTLGKQFDIALAVRDLN-------N-KRRIL--FDP-NFITV---------RRARY---------GDYY

VSVNEQG--------EEAILS--SGASAFD-----------ILTFLSFFPDSD---------SVL-----RD

--NSRVYL

>SichuanMosquitoTymoLike|UBJ25985.1/21-106 near-identical to Guadeloupe Culex tymo-like, Culex pseudovishnui tymo-like, Tymoviridae sp

FLVSMINFQVKIARSVRAID-------D-RDRVL--FDR-FF--------ITT-TGIHI---------GCHW

VAVNPEG--------QQALLL--PAQDALT-----------LEYYHRFVPSRD---------DIC-----VI

--GHQVLL

>GonipterusMaculaLike\_QWX9/1-87

FVEQSLKFQIDVAKAIRKVD-------N-RPRLI--YSS-TFVP--------VKTVFIE----------CTP

VLEDSQG--------VQAYFN--DAAQLTLS------------PEYYYDLINK-------DIEIV-----MQ

--HNNVVL

>HubeiVirga7\_YP\_009337770./1-90

FANDSIHKQIDIVKHVYTLQ-------T-RPYIL--WST-DVQW------NPKKFVTVD----------KYR

VSVTDAG--------LYGILN--EGAQKNFN------------SSDYLRFVKP------YGLKLD-----VT

--KSRITL

>LinepithemaC\_AXA52561.1\_2/1-89

FAIASIIQQLNVAQRVVDAK-------N-ESVIV--WTN-QTDW------QSWPSSILA--------GTTYR

YSVSPDG--------KPAVLS--HAAQAALQ----------PFDYPHLTSLP-----------LT-----LR

--GGDVYY

>HangzhouSolinvi1\_UHR49866/1-85 Identical to AcridaCinereaCalici-like 2101 2185 ie metagenomics I think

ILDLLAIAHLQFARKV-----------G-GKVCV--WVD-SNTA------PPL-KDHVR---------DGIR

YQTDEEG--------TVYVLG--VVMQQLMY----------SIVVGSLTQAGC---------TPA-----PD

--EHRIYY

>New\_Solenopsis7\_QBL75890./1-87

YLYQSIKRHLEFANEVARIK-------R-CPVTV--LSS-HPR-------GDG-DFNVE---------AGIR

YWRSKSG--------EIVVAS--ETSEHFG-----------WKRMRAIYLAQP---------GTT-----EQ

--GGKILV

>New|ElectricAnt1|OP518025/2119-2204 Electric ant virus 1

YMYECIKVHLECAGRLQQEF-------N-SPVVV--LAE-DAC-------GLG-PAEGE---------T-VR

YRRNDVG--------DLFVLS--ETANRLG-----------YEKMRSIYLAQP---------GTA-----EI

--GRKILV

>ApisPicorna5\_UCR92503/1-86

FLYKSIEVHLEGARGISAAL-------K-RPVCV--LSK-DHPN------GHD---DTM---------HGWR

FKRGSDG--------EIYVLS--STAQALG-----------YNKLHNIYHA-----------QPG-----TS

ERGCKIFV

>Apis5Like|MN034786\_ORF1\_Picornavirales\_sp/380-466 partial nucleotide seq only- Picornavirales sp. isolate H4\_Bulk\_46, similar Diabrotica undecimpunctata virus 1 QIT20099

FMYRSIQIHLGLAHTVSKAQ-------RNQKVCV--LSR-TMPN------GTD---ELI---------DNIR

CVRESDG--------TLFVPS--RTSQEMP-----------FLSMSVLYLT-----------QPG-----TT

QIGDRIYV

>Milolii|ARU76991.1/2334-2421 polyprotein [Milolii virus] \_R\_ ARU76991.1\_2332-2422.prf \_R\_ ARU76991.1\_2332-2422.prf \_R\_ Milolii\_ARU76991.1\_2332-2422.prf

FLYRSVMEHLKRATELATAL-------T-LPVIV--LHS-KSLTPVL-------RTEML---------SSTR

YQVDEMG--------NIYCLS--ATSQYFN-----------YKDMSAIYLMQP---------GTS-----DS

--SERILV

>Bundaberg8|AWK77859.1/1875-1962 polyprotein, partial [Bundaberg bee virus 8] \_R\_ AWK77859.1\_1873-1963.prf \_R\_ AWK77859.1\_1873-1963.prf \_R\_ Bundaberg8\_AWK77859.1\_1873-1963.prf

FLYRSVMEHLARATALAVEL-------A-SPIIV--LHS-KSQQPNL-------RTEVI---------SGTR

YEVDEEG--------NIYMLS--KTSQYFN-----------FKDMSSIYLMQP---------GTS-----EN

--SERILV

>Riboviria2\_HVAC-like\_/1-97

LMHSIVHEHLKCAKAISQEL-------K-IPVVV--LEL-ENTAA----NYDSKSLKVG--------DQVIN

YRVDDHG--------IPYVLA--ASIQRLNRIDRN------VMFEIYSAQPL---------THTD-----ER

--ECKILL

>HVAC\_AVD69112.1\_121-2/1-100

FMHASVSEQLFIASKISSKF-------K-RPVYV--YLL-DNPPK----NLVNRIVSID--------NEPFR

YAEDPGVP-----DGPFYVLS--RTSQKLYDYERV------AMYNYYLSFPN---------TYES-----SD

--RCKITL

>QKN88918.1\_160-261\_\_\_/1-102 YCA-associated putative Riboviria sp. 2, paper First Polycipivirus and Unmapped RNA Virus Diversity

YMFQSLSEQISLANKVSKSI-------N-RAVYV--YVL-NSTPE----NLVYRYIRVQ--------GDLIR

CQEDNSVS-----PGRLYVLS--RTSQSECWSVDQR----IAIMMTYLVFPG---------TYVS-----SD

--GCKITL

>LasiusPicorna9|UXD80004.1/117-218 putative structural polyprotein [Lasius neglectus picorna-like virus 9]

FMQKCIAEQLNIARAISTHY-------N-RAIGV--YMF-GRAPE----NLVLKVIRVK--------GETFR

YAEDDSIS-----PKGIYVLS--KTSELSTWSEDER----VAIRRVYLSFDD---------TYLS-----ED

--GCKVSL

>New|ND\_163732\_HVAC-like|ORF2/121-223

FVQASVAAQLRIAGTISSKL-------C-KPVVV--YMS-GRSPK----EAINRILISD--------GISYR

FKEVVDGP-----DEGLYVLS--EAAESLNPAYHV------AMASVYLEYPHT------YDKYLC-----ED

--GCKISL

>Acyrthosiphon\_QAA78863.1\_/1-86

AFSFYIENHINTAINNAD---------G-KKYII--IIG-KRLA--------DDAVEQI---------DGFY

KFHRGG---------NCYILS--PIIEKLGR-KTA------AECYRYYPGV-----------SFD-----SS

--TNEVTL

>Sitobion1\_QCI31816.1\_2236/1-86

AFSFYIENHINTAINNAD---------G-KKYII--IIG-KRLA--------DDSVEQI---------DGFY

KFHRGG---------NCYILS--PIIEKLGR-KTA------AACYRYYPGV-----------SFD-----SS

--TNEVTL

>RosyAppleAphid\_QVW10091.1/1-86

AFSFYIEDHINAAIRNAD---------G-KKYII--IIG-KRLA--------DDIVEQV---------DGFC

KFHRGG---------NCYFLS--PIIEKLGR-KTA------AQCYGYYPGV-----------SFD-----SS

--TNEVTL

>ABB89048.1\_2243-2328\_\_\_\_p/1-86

AFSFYIEDHINAAIRNAG---------G-KKYII--VIG-KRLA--------DDTVEQV---------DGFY

KFHRNG---------NCYFLS--SIIEKLGR-KTA------AQCYSYYPGV-----------SFD-----SS

--TNEVTL

>QKN88913.1\_481-566\_\_\_\_hyp/1-86

AFCFYMEAHLEAAKRLAD---------G-KKYII--IIG-ERYS--------SDNVEEI---------DGFH

RFYRDG---------NCYLLS--PIIAKVGR-KNA------AACYARYPGI-----------KYD-----QT

--TKEVTF

>QJI53497.1\_2204-2289\_\_\_\_h/1-86

AFCFYMEAHLEAAKRLAD---------G-KKYII--IIG-ERYS--------SDNVEEI---------DGFH

RFYRDG---------NCYLLS--PIIAKVGR-KNA------AACYARYPGI-----------RYD-----QT

--TKEVTF

>QJI53508.1\_1088-1173\_\_\_\_h/1-86

AFCFTMEAHLKAAKSLSD---------G-KKYVI--IVA-SRLG--------INNVEEI---------GGYI

RFYRNG---------NCYVLS--PIIERLGR-KTA------AACYARYPGV-----------TYD-----TK

--TKEVTY

>HubeiPicorna55\_QQP18685.1/1-86

AFCYTMEAHLEAAKSLSN---------G-KKYVI--IVA-SRLG--------ANNMEEI---------GGYI

RFYRNG---------NCYVLS--PIIERLGR-KTA------AACYARYPGV-----------TYD-----TK

--TKEVTY

>QJI53506.1\_2249-2334\_\_\_\_h/1-86

AFCLLMEEHLKAASHLSG---------G-KRYVI--IIG-ERHV--------EDIVEQV---------DGYI

RFYRNG---------NCYILS--PIVCKLGR-KKA------AACYARYPGI-----------SPL-----NE

--LKEVTY

>AphisCitricidusPicornaLike/1-86 Near identical to Holothuria scabra associated picornavirus 1

FFSFYMEEHLKTAARYAE---------G-KKFVI--IIG-KRPT--------GVVVEQI---------EGFI

RFYHHG---------NCYILS--PIVERLGR-KTA------ATCYARYPGI-----------IYK-----PE

--TNEVTY

>GrapevineRNAassociated1\_Q/1-86

AFSLYIEKHIKTAKKCSD---------G-KRYVK--LLS-SGYT--------RRHLENH---------DGFD

CFYNDG---------HRYVLS--DIISKLNK-EDT------AACYMRYPGI-----------TWN-----DV

--TREITL

>HangzhouSolinvi2\_UHK03205/1-86

VTSLYIESHIKTAAENSD---------G-KRFVK--LNS-KNVF--------KGSVENI---------NGFH

VYYRDG---------SRYVVS--PILSEVSS-AAT------KTCYLRYPGI-----------RYD-----SI

--TEEIVL

>HubeiPicorna56\_YP\_0093365/1-85

ATALLIEHHISQAKANSM---------G-RPSVI--LVS-KRSY--------NGDISKI---------DGFD

RFLLDG---------HCYFLS--PIIQELGR-TQA------ASCYLRYPGI-----------TMN-----SD

---KEIIM

>LasiusPicorna5|UXD80100.1/910-994 putative polyprotein, partial [Lasius neglectus picorna-like virus 5]

GFSFLIEHHISTASANSL---------G-RPVIV--LVS-KRSP--------CGDVEEI---------HGYM

RFFYDG---------VCYFLS--PVIQQLGR-AQA------GPCYQRYSGV-----------TIN-----DL

---KEVVY

>VespaAcypi\_QGL51724.1\_219/1-86 Near identical to Guiyang Solinvi-like virus 2

FVRHYVARHIEAAEINAAKR-------G-RGLAI--VAV-RNAN--------HDIFEVV---------DHFH

SYIDEE---------KYYFVS--PLFGHTAW-KDI------TKIYAGFPGV-----------TYD-----E-

---NEVMV

>DarwinBee7\_AWK77849.1\_956/1-86

FVRHYVARHIEAAEINAAKK-------G-RGSAV--VAV-RNAN--------HDVFEVV---------DHYH

SYIDEE---------KYYFVS--PLFGHTSW-KDI------TKIYAGFPGV-----------TYD-----E-

---KEVMV

>rfb198shi5\_AcypiOutgroup|QJI53504.1/1-86

FLLHYITTQVEEAKKSGTNL------GY-ASAIL--AVR-NNPE-----------VEFS-------TNDHFL

VLEYQN---------SYYFVS--PLLGHTPW-SAK------KKLYAHFPG-------------VI-----IN

--DDAITV

>PNGbee9\_QKW94212.1\_832-91/1-81

LLKQLVTAHIEVATRTG----------F-PEIIV--WAP-AWPC--------TPTLMQN----------SIR

YHLLDD---------KPAVLG--KALVAYKM------------SDVVGEFEQQ---------GCV-----VQ

--GNYILL

>TomatoSpottedWilt\_9632389/1-95

VPMLWLETHTSLHKFFATNL-------Q-EDVII--YTL-NNLE------LTPGKLDLG--------ERTLN

YSEDAYK--------RKYFLS--KTLECLPSN---------TQTMSYLDSIQI------PSWKID-----FA

--RGEIKI

>CAZ63989.1\_338-432\_\_\_\_\_no/1-95

IVHSLLEIHTELAQTICDSV-------Q-QDIIV--FTI-NEPD------LKPKKFELG--------KKTLN

YSEDGYG--------RKYFLS--QTLKSLPRN---------SQTMSYLDSIQM------PDWKFD-----YA

--AGEIKI

>YP\_009346013.1\_336-430\_\_\_/1-95

IVHSLLEVHTSLAKKLSDFL-------R-EEVII--YTL-NLPE------TEVKKLDLA--------GRTLN

YNESPSG--------KKYFLS--QTLNCLPKN---------SQSLAYLNSFQF------CSLHVD-----YI

--RGEICV

>MulberryVein\_A0A0C5GTS4\_A/1-95

IAKELIAVHTSFALKLSEIL-------K-KPVIV--FKM-YDKE------LEYDSANLM--------ERVLS

YQKDAEG--------NIYFLS--KTLDILPKS---------PSTLIYLNSIVP------NYWKES-----AE

--GQHYTV

>AIZ47385.1\_343-437\_\_\_\_\_NS/1-95

IAREMIIVHTNFALKLSEAL-------K-KPVIT--FKM-YEKE------LEYESYDLS--------GRMIS

YQKDSTG--------NIYFLS--RTLEILPKS---------LSILTYLKNISP------ACWKES-----IS

--MQHFYV

>gi\_422035861\_gb\_AFX74693./1-95

IAHELLSVHTNFALKISKVL-------Q-KPVIV--YKV-YEKE------LLPKRVEID--------GRTFN

YQEDIDG--------NVYFLS--TTLAILPLS---------LSVLSYLDSASP------PCWKES-----KG

--LGHFTV

>QVY47389.1\_345-439\_\_\_\_\_no/1-95

IAQELLSVHTMLALKISDAL-------K-KPVIV--YKL-YDRE------LKNEVIKIG--------DRVYN

YNSDGNG--------DIYFLS--ATLSILPKT---------ISVMKYLSSVAP------SCWDES-----ES

--FGHFSV

>gi\_556795639\_gb\_AGZ80148./1-95

IARSLIKTHTLFALEISKYL-------E-KKVII--FML-YEKQ------LTKKTMPYP--------VRDLS

YLEDSDG--------NVYFTS--ETLKLLPKS---------LSTITYLKGIAP------SCWKES-----IE

--NQHFYV

>ACY38609.1\_341-435\_\_\_\_\_NS/1-95

IARSLVNMHTLFALELSKHL-------R-KKVIV--FTL-YEKQ------LTKKTMPSP--------TRDLS

YLEDSDG--------NVYFTS--ETLKTLPKS---------ISAIIYLKGVAP------CCWRES-----IE

--DQHFYV

>gi\_4958986\_gb\_AAD34200.1\_/1-95

IASDFLRLQTVLSFRVSKHF-------K-KPVIV--YKL-YDKE------TELKKVKID--------GKFVS

YNEDSEG--------NVYVLN--KTLDLFPKS---------NSSFMYLSKTMS------PFWKEF-----PF

--EQHLVV

>BeanNecrotic\_YP\_006468899/1-97

IVQSLIKIHNEFASKISEKL-------N-KSVIV--YTL-RSVD-----SFKKEITEID--------SRAMN

YLISPEG--------EVFFLS--RTFQESLPTN--------MSSLTYFFDLQT------FGWSAN-----YL

--SGDLVV

>QQP18714.1\_361-457\_\_\_\_\_no/1-97

IVQSLMRIHNEFALSLSKFL-------K-KKVIV--YTL-RDSL-----SFTKKVAEID--------SRFLN

YLEDSDG--------NIYLLS--RTFQESLPLN--------RDSLSYFFDLQT------FGWAAN-----HA

--AGDLAT

>GroundnutYellowSpot\_34003/1-96

ICKNLVAVHLELAQDISKKL-------N-KPINV--FTI-KDTS-----NMTGDTVDVN--------GKKFR

ILKDSSG--------DCYFTS--ATFEKTFIGVYKS----CQTFIDYCDNK-----------KLS-----IN

--GDNVFI

>PeanutChlorotic\_AAC99404./1-96

ICKNLVSVHLGLATDLAKKL-------N-KPINV--FTI-KDTS-----SMTTDMVEVD--------GKKYR

VLKDSNG--------DYYFTS--ATFEKTLIGAYKS----CQTFVDYCDNK-----------KLS-----IN

--GDNVFI

>BarleriaSevere\_QVY47427.1/1-94

VFNNIVETHSDRCEYFLRSI-------D-SRMVV--VFT-INKP--------INLKEKV--------GPMGT

YLVDDYG--------VAYVLS--SNLQDSLPKS--------DSALKYVYESLP------REWKVD-----YS

--RGHIYY

>LisanthusNecrotic\_5431728/1-90

IVGALMEIHLGLAGKLRESI-------K-KDIVV--YTK-QEEP---------LDVILD-------PQTNLR

YYVKGE---------NAYFLS--KTFQNALPVD---------HALNYFISKAA--------KAIV-----IK

--GGDIFL

>PterostylisBlotch\_ULN9919/1-95

IVKKAIQNHTLHSKEFKNYT-------T-KIIVV--FTI-RNEL------LLDAFFTGK-------NKEIIP

YKTNN-----------KHIISYSELLQELPCL---------IDSLYYLEFIQE------SDWKFD-----YE

--NGIAYI

>ND\_241453\_SINHALI-LIKE|ORF4/1-79

VTRTLFDKHISLAKQLCDELHL-------SAIVI--WHLHDDFWD---------EKRIS--------KGGIR

YSIDGDG--------RCCLVS--ATFQTVLDM---------HNYLSFFSEID--------------------

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>InvertebrateIridescent6\_Q/1-108

IVNSLVKAHLKFASKALGD--------D-EKIVV--FVP-PEIW------NTVKKLPVIPQEGNSEEKGKWR

VRKDEE---------NTYFLS--ESLQSSSLD---------SEAFQLFKSVANDDDIQIPDLEKK-----LV

-EENGFVI

>ArmadillidiumIridovirus\_Y/1-107

IVKSLVKAHLTFANKALEDDAF--TAVK-AKIVV--FVT-PEAW------KKVRDLPIEN------TASNWR

VRKDKK---------YTYFLS--ESLQSSSLN---------LEALQLFKSVAEDD-IQIPNLSEK-----LV

-EENEFIV

>New|ND\_146872\_PicornaLike|Polyprotein/1960-2043

IGHNVVNNHLGFATKIGNVI-------G-KNIYVEVFEP-ENFN----------NDIII---------DNFR

LKKDDEG--------NLLFSS--ASIVRGHPK-----V-----------------------WKESGFPIIVD

--EKGYLL

>106967\_INVICTO-LIKE-DIVERGENTORF1\_ND\_106967.3/276-364

VTKALFLAHLNFASKVVSTL-------Q-DDVYV--YTT----------EPPAGTEEMA---------DRFR

VLRARYG----------VVFS-SATFEGLRSDHH-------SSIMSYLQQNHP---------ELM-----KD

--RHGFFI

>New|ND\_10713\_9PICORNA-LIKE|ORF1/649-734

IVQDLVNNHVALASKVARLT-------Q-ASLCY--VQV-REAW------KEGWLPKTV---------DRFR

YEESASF------RGTIKFES--LTIRDEFL------------------------------WDLSETPVFQN

--PVGFFI

>Feksystermes\_QRW42904.1\_2/1-102 HHblits finds distant Iridovirus Liz-CrIV

LVRELFSTHLALAGKVSVVL-------Q-ERIGV--FVR-PEFYNRVRFDSEEKNVCVE--------GKTIR

VSEYPGSEQ---IPAGYYMLS--MSVQASIAEVPV------AFPIVIIQRA-------------S-----DV

--GCPIIY

>AphisCitricidusMesoni|YP\_010800406/1-91 Aphis citricidus meson-like virus

FLHLYTDSHNNIGLNLSKSL-------N-KTIYI--YST-SPI---------WKVNTTSD-----YNCYKIT

YTYFNSS-------VYYGYFD--YLLQSVI-----------YSYTQYNQYST---------YKFQ-----NE

--DLGFAY

>XianghanSinhali\_UDL13955./1-97 HHblits finds distant Virga16

IMSLPSSAHQALASHLESVVAFGFFFPG-QRIYF--YDA-AGTF------ARS-PPIPT--------ALGVP

FQMVSS---------DVAILS--AVVQTLFGPDS-------CDEVAAASSL-----------PCE-----VD

--SVGVFW

>PicornaSinaiLike\_QKE55054/1-104

FARRVVSVYVQGAIQASHRL------NI-DEFVM--FAP-DKEV-------KAGTTKTT--------QDGWR

YIVLSDG--------SIYIGS--IAIQQMAVSLGMGTPKASKTFLPWLCNMVN------PRLKPK-----LD

--GSRIVG

>ND\_045051\_PICORNA\_CHROPARA\_MTASE/1-99

FAKRVIDVYIEGAIKLADEL------GI-DSFCV--VAP-GRD-------LNNATDYVA-------SRTKWR

YKKLVDG--------TTYIAS--LAMQEVVVSEGL------YWSLPWVQSVLN------PRLKAS-----IV

--NGRIVA

>RiboviriaSinaiLike\_UGO576/1-97

FARRTLQVFIDHAVRTCDEL------GI-QEFIM--VPT-SKDL-------RVADTRLA---------SGVR

YMVLPGG--------DFIIHS--AAMQQLVVSHGM------TNALPWVQNMVN------PRLKCS-----IV

--NGRILA

>HainanSedimentToti9Coat|UHS72513.1:1-134/23-113 putative coat protein [Totiviridae sp.], in fact Hainan sediment toti-like virus 9 HHblits finds no hit

VVKQLCIEQSKIAQVVGQLD------QQ-DEIAL--FTT-NRGW------LET-PITIL---------DNYR

TQIHPTK--------GILVKS--ATFQALLTL---------EEALEDYQSAGL---------SVT-----AD

--TDTIYL