Supplementary Figure S1.A. Amino acid alignment of *vic2a*

```
CnYM2      1 MGLFSKKKK--DTDVNPYAQAD----------------------------TAPAPAVSNT
CnES19     1 MGLFSKKKK--DADVNPYAQAD----------------------------TAPAPAVSNT
CnIF3      1 MGLFSKKKK--DADVNPYAQAD----------------------------TAPAPAVSNT
CnIF6      1 MGLFSKKKK--DADVNPYAQAD----------------------------TAPAPAVSNT
CpEP146    1 MGLFSKKKK--DAEANPYAQAG----------------------------TAPAPAVSNT
CpBRU17    1 MGLFSKKKK--DAEANPYAQAG----------------------------TAPAPAVSNT
Cp09503    1 MGLFSKKKK--DAEANPYAQAG----------------------------TAPAPAVSNT
CpJA78     1 MGLFSKKKK--DAEANPYAQAG----------------------------TAPAPAVSNT
CpYS522    1 MGLFSKKKK--DAEANPYAQAG----------------------------TAPAPAVSNT
CrM2269    1 MGFFSKKKKDADADANPYAQAG----------------------------TAPAPAVSNT
CrM270     1 MGFFSKKKKDADADANPYAQAG----------------------------TAPAPAVSNT
CnOB1_6    1 MGLFSKKKK--DADVNPYSQAD----------------------------TAPAPAVSNT
CnYM5      1 MGLFSKKKK--DADVNPYSQAD----------------------------TAPAPAVSNT
CpDU74     1 MGFFSKKKK--DGNANPYAQDGAQVPFSNPLTPYQQARNDLAQGRPAGLSSSTAPTASNT
Cp09515    1 MGFFSKKKK--DGNANPYAQDGAQVPFSNPLTPYQQARNDLAQGRPAGLSSSTAPTASNT
CpEP155    1 MGFFSKKKK--DGNANPYAQDGAQVPFSNPLTPYQQARNDLAQGRPAGLSSSTAPTASNT
CpR112     1 MGFFSKKKK--DGNANPYAQDGAQVPFSNPLTPYQQARNDLAQGRPAGLSSSTAPTASNT
CpJA69     1 MGFFSKKKK--DGNANPYAQDGAQVPFSNPLTPYQQARNDLAQGRPAGLSSSTAPTASNT
Cr09491    1 MGFFSKKKK--DANANPYAQDGAQVPFSNPLTPYQQARNDMAQGRPVGLSTGTAPAASNT
CrGM8A     1 MGFFSKKKK--DANANPYAQDGAQVPFSNPLTPYQQARNDMAQGRPVGLSTGTAPAASNT

CnYM2     31 PPPPYHNPSIASSGYSDAKYGAQNGYGADRY---GQGSAPAGYGGFNS-AGNNRSQASPA
CnES19    31 PPPSYHAPSIASSGYGDAKYGAQNGYGADRY---GQGPAPGGYGGFSS-AGNNRGQVSTA
CnIF3     31 PPPSYHAPSIASSGYGDAKYGAQNGYGADRY---GQGPAPGGYGGFSS-AGNNRGQVSTA
CnIF6     31 PPPSYHAPSIASSGYGDAKYGAQNGYGADRY---GQGPAPGGYGGFSS-AGKNRGQVSTA
CpEP146   31 PPPSYHSPSIASSRYGDEKLGTQNGYGADRY---GSGPAPGGYGGFNP-AGNNRSQASTA
CpBRU17   31 PPPSYHSPSIASSRYGDEKLGTQNGYGADRY---GSGPAPGGYGGFNP-AGNNRSQASTA
Cp09503   31 PPPSYHSPSIASSRYGDEKLGTQNGYGADRY---GSGPAPGGYGGFNP-AGNNRSQASTA
CpJA78    31 PPPSYHSPSIASSRYGDEKLGTQNGYGADRY---GSGPAPGGYGGFNP-AGNNRSQASTA
CpYS522   31 PPPSYHSPSIASSRYGDEKLGTQNGYGADRY---GSGPAPGGYGGFNP-AGNNRSQASTA
CrM2269   33 PPPSYHSPSIASSRYGDEKYGTQNGYGAGRY---GLGPAPGGYGSFNP-AGNNRSQASTA
CrM270    33 PPPSYHSPSIASSRYGDEKYGTQNGYGAGRY---GLGPAPGGYGSFNP-AGNNRSQASTA
CnOB1_6   31 PPPSYHAPSIASSRYGDEKYGAQSGYGADRY---GQGPAPAGYGGFSS-AGNNRSQASTA
CnYM5     31 PPPSYHAPSIASSRYGDEKYGAQSGYGADRY---GQGPAPAGYGGFSS-AGNNRSQASTA
CpDU74    59 PPPSYHSPSIASSRYGDEKYGNQKGYGTDRYGSTGSGPAPGGYGGFNSDAGNNRSQASAA
Cp09515   59 PPPSYHSPSIASSRYGDEKYGNQKGYGTDRYGSTGSGPAPGGYGGFNSDAGNNRSQASAA
CpEP155   59 PPPSYHSPSIASSRYGDEKYGNQKGYGTDRYGSTGSGPAPGGYGGFNSDAGNNRSQASAA
CpR112    59 PPPSYHSPSIASSRYGDEKYGNQKGYGTDRYGSTGSGPAPGGYGGFNSDAGNNRSQASAA
CpJA69    59 PPPSYHSPSIASSRYGDEKYGNQKGYGTDRYGSTGSGPAPGGYGGFNSDAGNNRSQASAA
Cr09491   59 PPPSYHSPSIASSRYGDEKYGNQKGYGADRYGNTGSSPAPGGYGGFSS-AGNNRSQASTA
CrGM8A    59 PPPSYHSPSIASSRYGDEKYGNQKGYGADRYGNTGSSPAPGGYGGFSS-AGNNRSQASTA

CnYM2     87 TPAGGGGNPALFGNAEARYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEERAEAETQAI
CnES19    87 TPAGGNGNAALFGNAEARYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEAETQAI
CnIF3     87 TPAGGNGNAALFGNAEARYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEAETQAI
CnIF6     87 TPAGGNGNAALFGNAEARYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEERAEAETQAV
CpEP146   87 TPAAGDGNPALFGNAKDRYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEADTQAL
CpBRU17   87 TPAAGDGNPALFGNAKDRYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEADTQAL
Cp09503   87 TPAAGDGNPALFGNAKDRYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEADTQAL
CpJA78    87 TPAAGDGNPALFGNAKDRYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEADTQAL
CpYS522   87 TPAAGDGNPALFGNAKDRYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEADTQAL
CrM2269   89 PPAGGDRNPALFGNAQERYNPYGGSKPLAQSGPEGDEYGGYGAPRELTEEEKAEAETQAY
CrM270    89 PPAGGDRNPALFGNAQERYNPYGGSKPLAQSGPEGDEYGGYGAPRELTEEEKAEAETQAY
CnOB1_6   87 PPTGAGGNAALFGNAQDRYNPYGGSTPQAQSGTQGDEYGGYGAPRELTEE---EAKTQAL
CnYM5     87 PPTGAGGNAALFGNAQDRYNPYGGSTPQAQSGTQGDEYGGYGAPRELTEE---EAKTQAL
CpDU74   119 QPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPQGDEYGGYGAQRELTEEEQAEAQAQAH
Cp09515  119 QPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPQGDEYGGYGAQRELTEEEQAEAQAQAH
CpEP155  119 QPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPQGDEYGGYGAQRELTEEEQAEAQAQAH
CpR112   119 QPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPQGDEYGGYGAQRELTEEEQAEAQAQAH
CpJA69   119 QPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPQGDEYGGYGAQRELTEEEQAEAQAQAH
Cr09491  118 PPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPEGDDYGGYGAPRELTEEEKAEAQTQAY
CrGM8A   118 PPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPEGDDYGGYGAPRELTEEEKAEAQTQAY
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```
CnYM2     147  VNETNAVRGESNASINRSIGGLEQGLAVLQASRMRVAQQDSRIINAEKNLDQSLMHAKDG
CnES19    147  VDKTNAVRDESNASINRSINGLESGLAQIQASRMRVAQQDSRLINADKNLNQSLIHARDG
CnIF3     147  VDKTNAVRDESNASINRSINGLESGLAQIQASRMRVAQQDSRLINADKNLNQSLIHARDG
CnIF6     147  VDETNAVRDESNASLNRTIGGLEHSIGVIKSSRMKIAQQDSMLINTDKNLNQSLVHARDG
CpEP146   147  VDQTNAVRDESWASIQRTIGGIEGGLAQVQASRMRVAQQDSRLNNAERNLDQSLSHARDG
CpBRU17   147  VDQTNAVRDESWASIQRTIGGIEGGLAQVQASRMRVAQQDSRLNNAERNLDQSLSHARDG
Cp09503   147  VDQTNAVRDESWASIQRTIGGIEGGLAQVQASRMRVAQQDSRLNNAERNLDQSLSHARDG
CpJA78    147  VDQTNAVRDESWASIQRTIGGIEGGLAQVQASRMRVAQQDSRLNNAERNLDQSLSHARDG
CpYS522   147  VDQTNAVRDESWASIQRTIGGIEGGLAQVQASRMRVAQQDSRLNNAERNLDQSLSHARDG
CrM2269   149  VDQTNAVRDESLASVQRTAAGLESGLAQLQSSRMRVAEQDSRLNNAERNLDSSLSHARDG
CrM270    149  VDQTNAVRDESLASVQRTAAGLESGLAQLQSSRMRVAEQDSRLNNAERNLDSSLSHARDG
CnOB1_6   144  KDEANGLRDEGIASLQRTLAMGNQAFEQVTGTMVRIDQQDEMMFNANKNLDSSLAHARDG
CnYM5     144  KDEANGLRDEGIASLQRTLAMGNQAFEQVTGTMVRIDQQDEMMFNANKNLDSSLAHARDG
CpDU74    179  VDEAHGVRNESIAALQRTLAMGNQAFEQATGTLVRIDQQDEMMFNANKNLDSSLAHARDG
Cp09515   179  VDEAHGVRNESIAALQRTLAMGNQAFEQATGTLVRIDQQDEMMFNANKNLDSSLAHARDG
CpEP155   179  VDEAHGVRNESIAALQRTLAMGNQAFEQATGTLVRIDQQDEMMFNANKNLDSSLAHARDG
CpR112    179  VDEAHGVRNESIAALQRTLAMGNQAFEQATGTLVRIDQQDEMMFNANKNLDSSLAHARDG
CpJA69    179  VDEAHGVRNESIAALQRTLAMGNQAFEQAIGTLVRIDQQDEMMFNANKNLDSSLAHARDG
Cr09491   178  VDEANGVRDESIAALQRTLAMGNQALDQACGTLVRIDQQDEMMFNANKNLDSSLAHARDG
CrGM8A    178  VDEANGVRDESIAALQRTLAMGNQALDQACGTLVRVDQQDEMMFNANKNLDSSLAHARDG

CnYM2     207  AQKTKTLHTLNKKPFFVPVGGTSSKAVQREVDRDTENYRSDRAKKEDTRQADWANRQRTR
CnES19    207  AQKTKTLDKLNRTPFILPVGGSSSKAVERDVAQKTQEYQSDKAKQEDTRQEDWRLRQRTR
CnIF3     207  AQKTKTLDKLNRTPFILPVGGSSSKAVERDVAQKTQEYQSDKAKQEDTRQEDWRLRQRTR
CnIF6     207  AQKTKTLDTLNRKPFFMPVGGTSVKAVERDVAQKTQDYQSDKATQENTRQANWKLGQRTR
CpEP146   207  AQKTKTLDTLNRKPFFMPVGGTSVKAVERQVAQETEEHSGDKAKAEVTRQARWEIEKRLK
CpBRU17   207  AQKTKTLDTLNRKPFFMPVGGTSVKAVERQVAQETEEHSGDKAKAEVTRQARWEIEKRLK
Cp09503   207  AQKTKTLDTLNRKPFFMPVGGTSVKAVERQVAQETEEHSGDKAKAEVTRQARWEIEKRLK
CpJA78    207  AQKTKTLDTLNRKPFFMPVGGTSVKAVERQVAQETEEHSGDKAKAEVTRQARWEIEKRLK
CpYS522   207  AQKTKTLDTLNRKPFFMPVGGTSVKAVERQVAQETEEHSGDKAKAEVTRQARWEIEKRLK
CrM2269   209  AQKTKTLDTLNRKPFFMPVGGTSARAVERKADQDLKEYRGDKSVKEGTRETAWKTQQRLR
CrM270    209  AQKTKTLDTLNRKPFFMPVGGTSARAVERKADQDLKEYRGDKSVKEGTRETAWKTQQRLR
CnOB1_6   204  QAKTKTLQKYNNTAFFIPV-EPGKKAQAKLRELAVMNGAQDREQRGQTQHARYTDQQQTE
CnYM5     204  QAKTKTLQKYNNTAFFIPV-EPGKKAQAKLRELAVMNGAQDREQRGQTQHARYTDQQQTE
CpDU74    239  QAKTKTLRKLNDTPFFIPV-EPGRKAQDKLAEMAVLNNRQDREQREQTLQAGYTDRQKME
Cp09515   239  QAKTKTLRKLNDTPFFIPV-EPGRKAQDKLAEMAVLNNRQDREQREQTLQAGYTDRQKME
CpEP155   239  QAKTKTLRKLNDTPFFIPV-EPGRKAQDKLAEMAVLNNRQDREQREQTLQAGYTDRQKME
CpR112    239  QAKTKTLRKLNDTPFFIPV-EPGRKAQDKLAEMAVLNNRQDREQREQTLQAGYTDRQKME
CpJA69    239  QAKTKTLRKLNDTPFFIPV-EPGRKAQDKLAEMAVLNNRQDREQREQTLQAGYTDRQKME
Cr09491   238  QSKTKTLRKLNDTPFFIPV-EPGKKAQDKLAEMAVMNNRQDREQREQTLRAGYTDRQKME
CrGM8A    238  QSKTKTLRKLNDTPFFIPV-EPGKKAQDKLAEMAVMNNRQDREQREQTLRAGYTDRQKME

CnYM2     267  EIEKS---GPSAPGLLGSKKPVNSKWVFEDDEEGAAMEEDIQAGIDKLGFLSGELNQQAS
CnES19    267  EIEKS---GPSAPGLLGSKKPVKSKWVFEDDEEGAAKEEEIQAGIEKLGFLSGELNEQAS
CnIF3     267  EIEKS---GPSAPGLLGSKKPVKSKWVFEDDEEGAAKEEEIQAGIEKLGFLSGELNEQAS
CnIF6     267  EIEKS---NQSSPGLLGSKKPVNSKWVFEDDEEGAAKEEEIQAGIQKLGFLSGELNEQAS
CpEP146   267  AAEKN---GPTAPGLLGSKKPVDSKWVFEDDEEGAAKEENIQAGIETLGYLSGQLNSQAS
CpBRU17   267  AAEKN---GPTAPGLLGSKKPVDSKWVFEDDEEGAAKEENIQAGIETLGYLSGQLNSQAS
Cp09503   267  AAEKN---GPTAPGLLGSKKPVDSKWVFEDDEEGAAKEENIQAGIETLGYLSGQLNSQAS
CpJA78    267  AAEKN---GPTAPGLLGSKKPVDSKWVFEDDEEGAAKEENIQAGIETLGYLSGQLNSQAS
CpYS522   267  AAEKN---GPTAPGLLGSKKPVDSKWVFEDDEEGAAKEENIQAGIETLGYLSGQLNSQAS
CrM2269   269  ETGKS---GPSAPGLLASKKPVNSKWVFEDDEEGAAKEEEIQAGIETLGYLSTELNHQAT
CrM270    269  ETGKS---GPSAPGLLASKKPVNSKWVFEDDEEGAAKEEEIQAGIETLGYLSTELNHQAT
CnOB1_6   263  QDMQQLTRGSPGPRLLAAGRGAS-KFALEDDEEGQAKEENIGNLLVDVLGVSQKLNEASK
CnYM5     263  QDMQQLTRGSPGPRLLAAGRGAS-KFALEDDEEGQAKEENIGNLLVDVLGVSQKLNEASK
CpDU74    298  QDMQQLARASSGPRLLGAGKPAN-KFALEDDEEGQAQEEQIGGLMDDVLVVSKNLNMASS
Cp09515   298  QDMQQLARASSGPRLLGAGKPAN-KFALEDDEEGQAQEEQIGGLMDDVLVVSKNLNMASS
CpEP155   298  QDMQQLARASSGPRLLGAGKPAN-KFALEDDEEGQAQEEQIGGLMDDVLVVSKNLNMASS
CpR112    298  QDMQQLARASSGPRLLGAGKPAN-KFALEDDEEGQAQEEQIGGLMDDVLVVSKNLNMASS
CpJA69    298  QDMQQLARASSGPRLLGAGKPAN-KFALEDDEEGQAQEEQIGGLMDDVLVVSKNLNMASS
Cr09491   297  QDMQQLSRGPSGPRLLGAGKPAN-KFALEDDEEGQAKEEQIGGMMDDVLVVSQKLNMASN
CrGM8A    297  QDMQQLSRGPSGPRLLGAGKPAN-KFALEDDEEGQAKEEQIGGMMDDVLVVSQKLNMASN
```

```
CnYM2     324 AFGDEIQESNNGINRVRDKVWSPFPHRLLINLLTFDAGX---------------------
CnES19    324 GLGDEIQQSNKMINGIEDKVWSPFRHRLKINLLTFDAGX---------------------
CnIF3     324 GLGDEIQQSNKMINGIEDKVWSPFRHRLKINLLTFDAGX---------------------
CnIF6     324 GLGDDIQRSNKMINGIEDKVWSPFRHRLQINLLTFDAGX---------------------
CpEP146   324 ALGDDLQQSIKVINRVVDKVWSPFPRWLQTNLLTFDAGX---------------------
CpBRU17   324 ALGDDLQQSIKVINRVVDKVWSPFPRWLQTNLLTFDAGX---------------------
Cp09503   324 ALGDDLQQSIKVINRVVDKVWSPFPRWLQTNLLTFDAGX---------------------
CpJA78    324 ALGDDLQQSIKVINRVVDKVWSPFPRWLQTNLLTFDAGX---------------------
CpYS522   324 ALGDDLQQSIKVINRVVDKVWSPFPRWLQTNLLTFDAGX---------------------
CrM2269   326 ALGGDLQESIKVINRVVDKVWSLFVHRQQMNLLTFDAGX---------------------
CrM270    326 ALGGDLQESIKVINRVVDKVWSLFVHRQQMNLLTFDAGX---------------------
CnOB1_6   322 ATTSKLQRSNAQIDAVHGKVCSHFCTLLQSHSLTFGVGRFGGRQGKSALNPYLEVPIWSX
CnYM5     322 ATTSKLQRSNAQIDAVHGKVCSHFCTLLQSHSLTFGVGRFGGRQGKSALNPYLEVPIWSX
CpDU74    357 AMTGKLERSIAQINDVSGKVCSPFRTLLQSRSLTSGAGX---------------------
Cp09515   357 AMTGKLERSIAQINDVSGKVCSPFRTLLQSRSLTSGAGX---------------------
CpEP155   357 AMTGKLERSIAQINDVSGKVCSPFRTLLQSRSLTSGAGX---------------------
CpR112    357 AMTGKLERSIAQINDVSGKVCSPFRTLLQSRSLTSGAGX---------------------
CpJA69    357 AMTGKLERSIAQINDVSGKVCSPFRTLLQSRSLTSGAGX---------------------
Cr09491   356 AMTGKLERSIAQINDVSGKVCSPLVHCYSR------IHX---------------------
CrGM8A    356 AMTGKLERSIAQINDVSGKVCSPLVHCYSR------IHX---------------------
```

Supplementary Figure S1.B. Amino acid alignment of helicase-like gene

```
CpEP155    1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CpDU74     1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
Cp09515    1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CpJA69     1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CpR112     1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CnIF6      1  YGRVLLAAGDSKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQQSRKELYRREGDLL
CpEP146    1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFYQLRSEEEIEEIRESRKELYRREGDLL
CpBRU17    1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFYQLRSEEEIEEIRESRKELYRREGDLL
Cp09503    1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFYQLRSEEEIEEIRESRKELYRREGDLL
CpJA78     1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFYQLRSEEEIEEIRESRKELYRREGDLL
CpYS522    1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFYQLRSEEEIEEIRESRKELYRREGDLL
Cr09491    1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFHQLRSEEEIEEIQESRKELYRREGDLL
CrM2269    1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFHQLRSEEEIEEIQESRKELYRREGDLL
CrM270     1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFHQLRSEEEIEEIQESRKELYRREGDLL
CrGM8A     1  YGRVLLAAGDPKNDCLLEVIDIIACLTAGDDIFHQLRSEEEIEEIQESRKELYRREGDLL
CnYM2      1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CnOB1_6    1  YGRVLLAAGDPKNDCLLETIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CnYM5      1  YGRVLLAAGDPKNDCLLETIDIIACLTAGDDIFYQLRSEEEIEEIQESRKELYRREGDLL
CnES19     1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEVQESRKELYRREGDLL
CnIF3      1  YGRVLLAAGDPKNDCLLEAIDIIACLTAGDDIFYQLRSEEEIEEVQESRKELYRREGDLL

CpEP155   61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CpDU74    61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
Cp09515   61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CpJA69    61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CpR112    61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CnIF6     61  TYLTTVQQYTAEHADRVEWCKRRKVNARVMKQALNIRKQLRGLCLKEKLLDDAPPQDPQP
CpEP146   61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CpBRU17   61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
Cp09503   61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CpJA78    61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CpYS522   61  TYLTTVQQYTAEHSDRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
Cr09491   61  TYLTTVQQYTAEHADRIEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CrM2269   61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CrM270    61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CrGM8A    61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLADAPPQDPQP
CnYM2     61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLDDAPPQDPKP
CnOB1_6   61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLDDAPPQDPQP
CnYM5     61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLDDAPPQDPQP
CnES19    61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLDDVPPQDPQP
CnIF3     61  TYLTTVQQYTAEHADRVEWCKRRKVNTRVMKQALNIRKQLRGLCLKEKMLDDVPPQDPQP

CpEP155  121  FTPTSPERAEIILKCFLTGFAMKTALLAPDASYMTTFGKHVVAIHPASVMHGQKREAIM
CpDU74   121  FTPTSPERAEIILKCFLTGFAMKTALLAPDASYMTTFGKHVVAIHPASVMHGQKREAIM
Cp09515  121  FTPTSPERAEIILKCFLTGFAMKTALLAPDASYMTTFGKHVVAIHPASVMHGQKREAIM
CpJA69   121  FTPTSPERAEIILKCFLTGFAMKTALLAPDASYMTTFGKHVVAIHPASVMHGQKREAIM
CpR112   121  FTPTSPERAEIILKCFLTGFAMKTALLAPDASYMTTFGKHVVAIHPASVMHGQKREAIM
CnIF6    121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTTFGKHVVAIHPASVMHGQKREAIM
CpEP146  121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTSFGKHVVAIHPASVMHGQKREAIM
CpBRU17  121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTSFGKHVVAIHPASVMHGQKREAIM
Cp09503  121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTSFGKHVVAIHPASVMHGQKREAIM
CpJA78   121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTSFGKHVVAIHPASVMHGQKREAIM
CpYS522  121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTSFGKHVVAIHPASVMHGQKREAIM
Cr09491  121  FTPTSPERAEVILKCFLAGFAMKTALLAPDASYVTTFGKHVIAIHPASVMHGQKREAIM
CrM2269  121  FTPTSPERAEVILKCFLAGFAMKTALLAPDASYVTTFGKHVVAVHPASVMHGQKREAIM
CrM270   121  FTPTSPERAEVILKCFLAGFAMKTALLAPDASYVTTFGKHVVAVHPASVMHGQKREAIM
CrGM8A   121  FTPTSPERAEVILKCFLAGFAMKTALLAPDASYVTTFGKHVVAIHPASVMHGQKREAIM
CnYM2    121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTTFGKHVVAIHPASVMHGQKREAIM
CnOB1_6  121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTTFGKHVVAIHPASVMHGQKREAIM
CnYM5    121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTTFGKHVVAIHPASVMHGQKREAIM
CnES19   121  FTPTSPERAEVILKCFLTGFAMKTALLAPDASYVTTFGKHVVAIHPASVMHGQKREAIM
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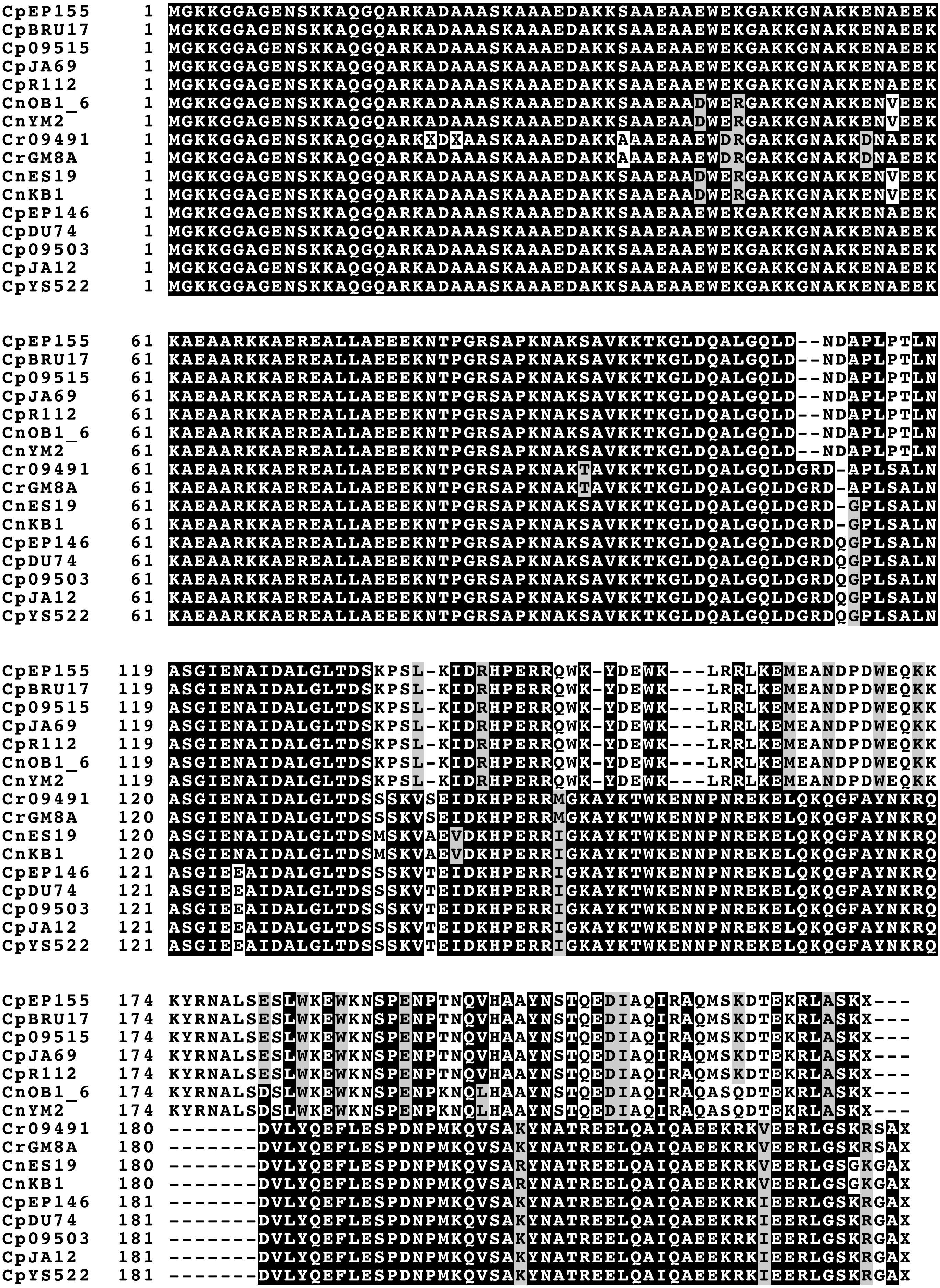
Supplementary Figure S1.C. Amino acid alignment of *pix6*



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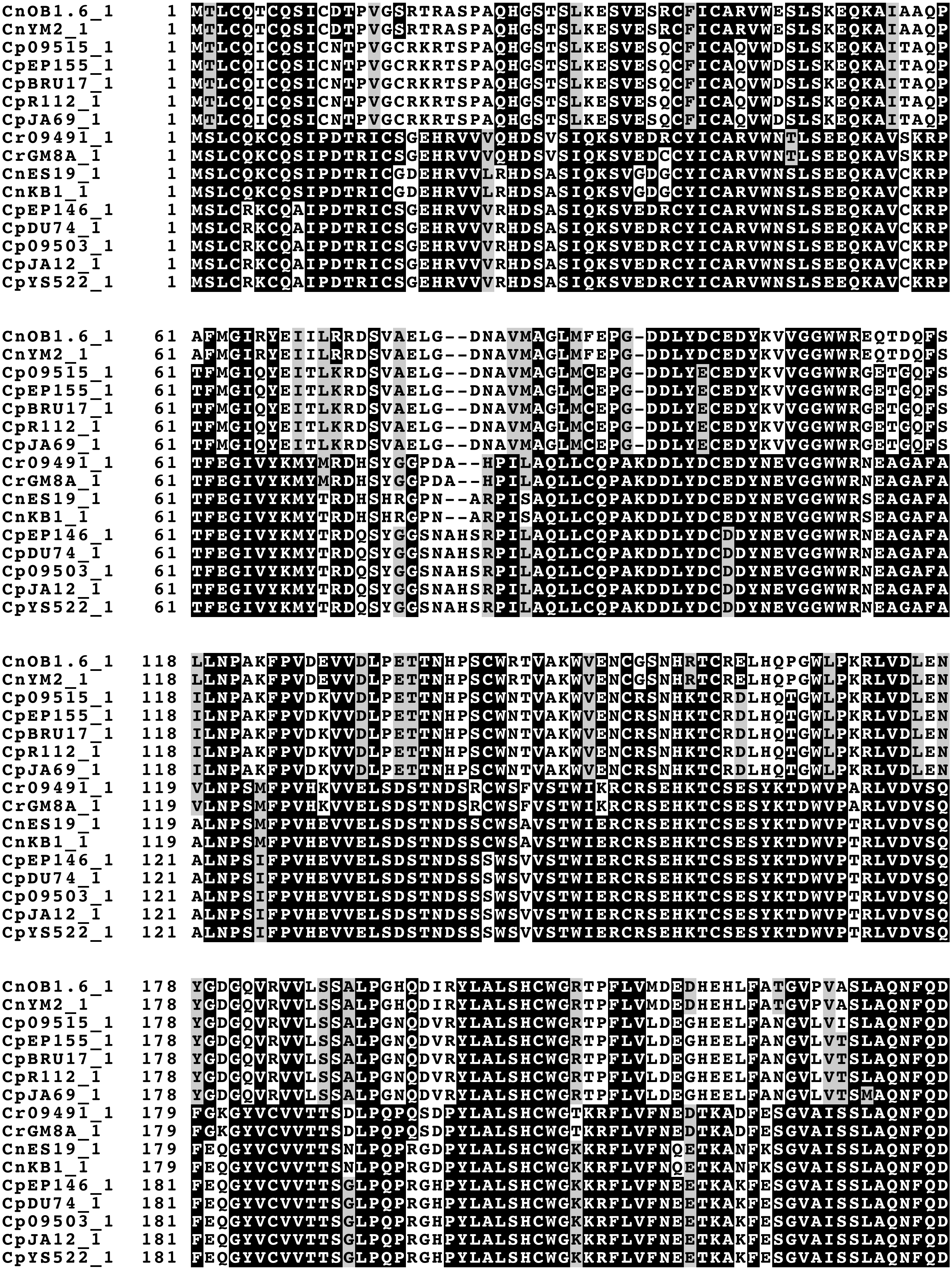
Supplementary Figure S1.D. Amino acid alignment of *vic6*



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CnOB1.6_1   418 AD-PALDNMRWYDSPYQVWDEILQLYASCALTRGDDKLVAISGIAKDLAAYLDDEYLAGL
CnYM2_1     418 AD-PALDNMRWYDSPYQVWDEILQLYASCALTRGDDKLVAISGIAKDLAAYLDDEYLAGL
Cp09515_1   418 AD-PELDTMRWYDSPYQVWDEILQLYSSCALTQGGDKLVAISWIAKDLAVYLDDEYLAGL
CpEP155_1   418 AD-PELDTMRWYDSPYQVWDEILQLYSSCALTQGGDKLVAISGIAKDLAVYLDDEYLAGL
CpBRU17_1   418 AD-PELDTMRWYDSPYQVWDEILQLYSSCALTQGGDKLVAISGIAKDLAVYLDDEYLAGL
CpR112_1    418 AD-PELDTMRWYDSPYQVWDEILQLYSSCALTQGGDKLVAISGIAKDLAVYLDDEYLAGL
CpJA69_1    418 AD-PELDTMRWYDSPYQVWDEILQLYSSCALTQGGDKLVAISGIAKDLAVYLDDEYLAGL
Cr09491_1   418 EEIHETDVERFYESPYQVWNEILHTYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
CrGM8A_1    418 EEIHETDVERFYESPYQVWNEILHTYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
CnES19_1    418 AEIRETDVERFYESPYQVWNEILHLYVRCGLTKPEDKFVAISGVVKDFAEAVGDEYLAGL
CnKB1_1     418 AEIRETDVERFYESPYQVWNEILHLYVRCGLTKPEDKFVAISGVVKDFAEAVGDEYLAGL
CpEP146_1   421 AKLHETDLDRFYESPYQVWNEILHSYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
CpDU74_1    421 AKLHETDLDRFYESPYQVWNEILHSYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
Cp09503_1   421 AKLHETDLDRFYESPYQVWNEILHSYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
CpJA12_1    421 AKLHETDLDRFYESPYQVWNEILHSYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
CpYS522_1   421 AKLHETDLDRFYESPYQVWNEILHSYVRCGLTKPEDKFVAISGVVKDFADVVGDEYLAGL
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CnOB1.6_1   477 WRAKLVDGLLWRVERDEMTGAYIPASRPKRYRAPTWSWAAVDTIRIRARTSV-FGEVHDG
CnYM2_1     477 WRAKLVDGLLWRVERDEMTGAYIPASRPKRYRAPTWSWAAVDTIRIRARTSV-FGEVHDG
Cp09515_1   477 WRAKLVDGLLWRVERDEMTGAYIPAKRPQRYRAPTWSWASVDAIRTRAHTAV-FGEVHDG
CpEP155_1   477 WRAKLVDGLLWRVERDEMTGAYIPAKRPQRYRAPTWSWASVDAIRTRAHTAV-FGEVHDG
CpBRU17_1   477 WRAKLVDGLLWRVERDEMTGAYIPAKRPQRYRAPTWSWASVDAIRTRAHTAV-FGEVHDG
CpR112_1    477 WRAKLVDGLLWRVERDEMTGAYIPAKRPQRYRAPTWSWASVDAIRTRAHTAV-FGEVHDG
CpJA69_1    477 WRAKLVDGLLWRVERDEMTGAYIPAKRPQRYRAPTWSWASVDAIRTRAHTAV-FGEVHDG
Cr09491_1   478 WRKNLIDGLLWHIQEEELTGLYTPATRVEPYRAPSWSWASVDSPHVRVQSPAHLTYDDSG
CrGM8A_1    478 WRKNLIDGLLWHIQEEELTGLYTPATRVEPYRAPSWSWASVDSPHVRVQSPAHLTYDDSG
CnES19_1    478 WRKNLIDGLLWHVQEEELTGLWVPATRVEPYRAPSWSWASVDSPHVRVQSLAHLTYDSSG
CnKB1_1     478 WRKNLIDGLLWHVQEEELTGLWVPATRVEPYRAPSWSWASVDSPHVRVQSLAHLTYDSSG
CpEP146_1   481 WRKNLIDGLLWHVQEEELTGLYVPATRVEPYRAPSWSWASVDSPHVRVQSRAHLTYDDSG
CpDU74_1    481 WRKNLIDGLLWHVQEEELTGLYVPATRVEPYRAPSWSWASVDSPHVRVQSRAHLTYDDSG
Cp09503_1   481 WRKNLIDGLLWHVQEEELTGLYVPATRVEPYRAPSWSWASVDSPHVRVQSRAHLTYDDSG
CpJA12_1    481 WRKNLIDGLLWHVQEEELTGLYVPATRVEPYRAPSWSWASVDSPHVRVQSRAHLTYDDSG
CpYS522_1   481 WRKNLIDGLLWHVQEEELTGLYVPATRVEPYRAPSWSWASVDSPHVRVQSRAHLTYDDSG

CnOB1.6_1   536 YTEFVDVNVVPKGS----------------DPTGELDHACLHARGHLVRTRRKPVGPRIA
CnYM2_1     536 YTEFVDVNVVPKGS----------------DPTGELDHACLHARGHLVRTRRKPVGPRIA
Cp09515_1   536 YTELVDVHVVPKGS----------------DPTGELDHACLLARGHLVRTRRKPVDPRTA
CpEP155_1   536 YTELVDVHVVPKGS----------------DPTGELDHACLLARGHLVRTRRKPVDPRTA
CpBRU17_1   536 YTELVDVHVVPKGS----------------DPTGELDHACLLARGHLVRTRRKPVDPRTA
CpR112_1    536 YTELVDVHVVPKGS----------------DPTGELDHACLLARGHLVRTRRKPVDPRTA
CpJA69_1    536 YTELVDVHVVPKGS----------------DPTGELDHACLLARGHLVRTRRKPVDPRTA
Cr09491_1   538 YAAIDEVNLVPREE------DQEGGSGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA
CrGM8A_1    538 YAAIDEVNLVPREE------DQEGGSGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA
CnES19_1    538 YAAIDEVTLVPRDE-----EEDGGGGGAPGPLAGELSHACLRARGHLIRTRRPPVRDRNA
CnKB1_1     538 YAAIDEVTLVPRDE-----EEDGGGGGAPGPLAGELSHACLRARGHLIRTRRPPVRDRNA
CpEP146_1   541 YAAIDEVNLVPRNEEEKEEEEGGGGGGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA
CpDU74_1    541 YAAIDEVNLVPRNEEEKEEEEGGGGGGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA
Cp09503_1   541 YAAIDEVNLVPRNEEEKEEEEGGGGGGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA
CpJA12_1    541 YAAIDEVNLVPRNEEEKEEEEGGGGGGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA
CpYS522_1   541 YAAIDEVNLVPRNEEEKEEEEVVGGGGAPGPPAGELSHACLRARGYLIRTRRPPVRDRNA

CnOB1.6_1   580 HPGLFGTFYPDNYDEVTGDEFYCLPLREDLGVNV---PSLTGLVLVPFREGTVTGGAA--
CnYM2_1     580 HPGLFGTFYPDNYDEVTGDEFYCLPLREDLGVNV---PSLTGLVLVPFREGTVTGGAA--
Cp09515_1   580 RHDLFGTFYPDSYDEVTGDEFYCLPLREDLCAKL---PSLTGLVLMPFRDSTVTGEAA--
CpEP155_1   580 RHDLFGTFYPDSYDEVTGDEFYCLPLREDLCAKL---PSLTGLVLMPFRDSTVTGEAA--
CpBRU17_1   580 RHDLFGTFYPDSYDEVTGDEFYCLPLREDLCAKL---PSLTGLVLMPFRDSTVTGEAA--
CpR112_1    580 RHDLFGTFYPDSYDEVTGDEFYCLPLREDLCAKL---PSLTGLVLMPFRDSTVTGEAA--
CpJA69_1    580 RHDLFGTFYPDSYDEVTGDEFYCLPLREDLCAKL---PSLTGLVLMPFRDSTVTGEAA--
Cr09491_1   592 -LGSFGQFYPDT-EGLEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHQEAAGKEATADE
CrGM8A_1    592 -LGSFGQFYPDT-EGLEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHQEAAGKEATADE
CnES19_1    593 -LGSFGQFYPDT-EALEGNAFFCWPLRERINDGDVSGNFLMGLVLGTYHEAAGEDEAAEK
CnKB1_1     593 -LGSFGQFYPDT-EALEGNAFFCWPLRERINDGDVSGNFLMGLVLGTYHEAAGEDEAAEK
CpEP146_1   601 -LGSFGQFYPDT-EALEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHPEAAGEEEE---
CpDU74_1    601 -LGSFGQFYPDT-EALEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHPEAAGEEEE---
Cp09503_1   601 -LGSFGQFYPDT-EALEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHPEAAGEEEE---
CpJA12_1    601 -LGSFGQFYPDT-EALEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHPEAAGEEEE---
CpYS522_1   601 -LGSFGQFYPDT-EALEGDVFFCWPLRERINDGDVSGNYLMGLVLGTHPEAAGEEEE---

CnOB1.6_1   635 ------AHGAATSSCCSRCAGKMLLVRIGTFDIAKGDPLQALGLVQPDNWAEWGPEGVHL
CnYM2_1     635 ------AHGAATSSCCSRCAGKMLLVRIGTFDIAKGDPLQALGLVQPDNWAEWGPEGVHL
Cp09515_1   635 ------AQGAATS-SCSRCAGKMLLVRIGTFEIAKGDPLQALGLVKPDNWAECGPEGVHL
CpEP155_1   635 ------AQGAATS-SCSRCAGKMLLVRIGTFEIAKGDPLQALGLVKPDNWAECGPEGVHL
CpBRU17_1   635 ------AQGAATS-SCSRCAGKMLLVRIGTFEIAKGDPLQALGLVKPDNWAECGPEGVHL
CpR112_1    635 ------AQGAATS-SCSRCAGKMLLVRIGTFEIAKGDPLQALGLVKPDNWAECGPEGVHL
CpJA69_1    635 ------AQGAATS-SCSRCAGKMLLVRIGTFEIAKGDPLQALGLVKPDNWAECGPEGVHL
Cr09491_1   650 DE-KGDGRARRKRTSCDMCAGRRVFTRVGTFEIDHGDPLQYLSMKKPGDWADWGEEKDHL
CrGM8A_1    650 DE-KGDGRARRKRTSCDMCAGRRVFTRVGTFEIDHGDPLQYLSMKKPGDWADWGEEKDHL
CnES19_1    651 GEEDDGGAAKRKWTSCDRCSGRRVFFRVGTFEMDHGDPVQYLSMKKPDDWADWGEEKDHL
CnKB1_1     651 GEEDDGGAAKRKWTSCDRCSGRRVFFRVGTFEMDHGDPVQYLSMKKPDDWADWGEEKDHL
CpEP146_1   656 GEQDADAATNRKRTSCDRCSGQRVFTRVGTFEIDHGDPLQYLSMKKPGNWADWGEEKDHL
CpDU74_1    656 GEQDADAATNRKRTSCDRCSGQRVFTRVGTFEIDHGDPLQYLSMKKPGNWADWGEEKDHL
Cp09503_1   656 GEQDADAATNRKRTSCDRCSGQRVFTRVGTFEIDHGDPLQYLSMKKPGNWADWGEEKDHL
CpJA12_1    656 GEQDADAATNRKRTSCDRCSGQRVFTRVGTFEIDHGDPLQYLSMKKPGNWADWGEEKDHL
CpYS522_1   656 GEQDADAATNRKRTSCDRCSGQRVFTRVGTFEIDHGDPLQYLSMKKPGNWADWGEEKDHL
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CnOB1.6_1  689 WFLPDHPVSEFVIL*
CnYM2_1    689 WFLPDHPVSEFVIL*
Cp09515_1  688 WFLPDHPVSEFVIL*
CpEP155_1  688 WFLPDHPVSEFVIL*
CpBRU17_1  688 WFLPDHPVSEFVIL*
CpR112_1   688 WFLPDHPVSEFVIL*
CpJA69_1   688 WFLPDHPVSEFVIL*
Cr09491_1  709 WFPEDAQPYEFFVV*
CrGM8A_1   709 WFPEDAQPYEFFVV*
CnES19_1   711 WFPEDAQPYEFLVV*
CnKB1_1    711 WFPEDAQPYEFLVV*
CpEP146_1  716 WFPEDAQPYEFIVV*
CpDU74_1   716 WFPEDAQPYEFIVV*
Cp09503_1  716 WFPEDAQPYEFIVV*
CpJA12_1   716 WFPEDAQPYEFIVV*
CpYS522_1  716 WFPEDAQPYEFIVV*
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