A P-Glycoprotein Is Linked to Resistance to the *Bacillus thuringiensis* Cry3Aa Toxin in a Leaf Beetle

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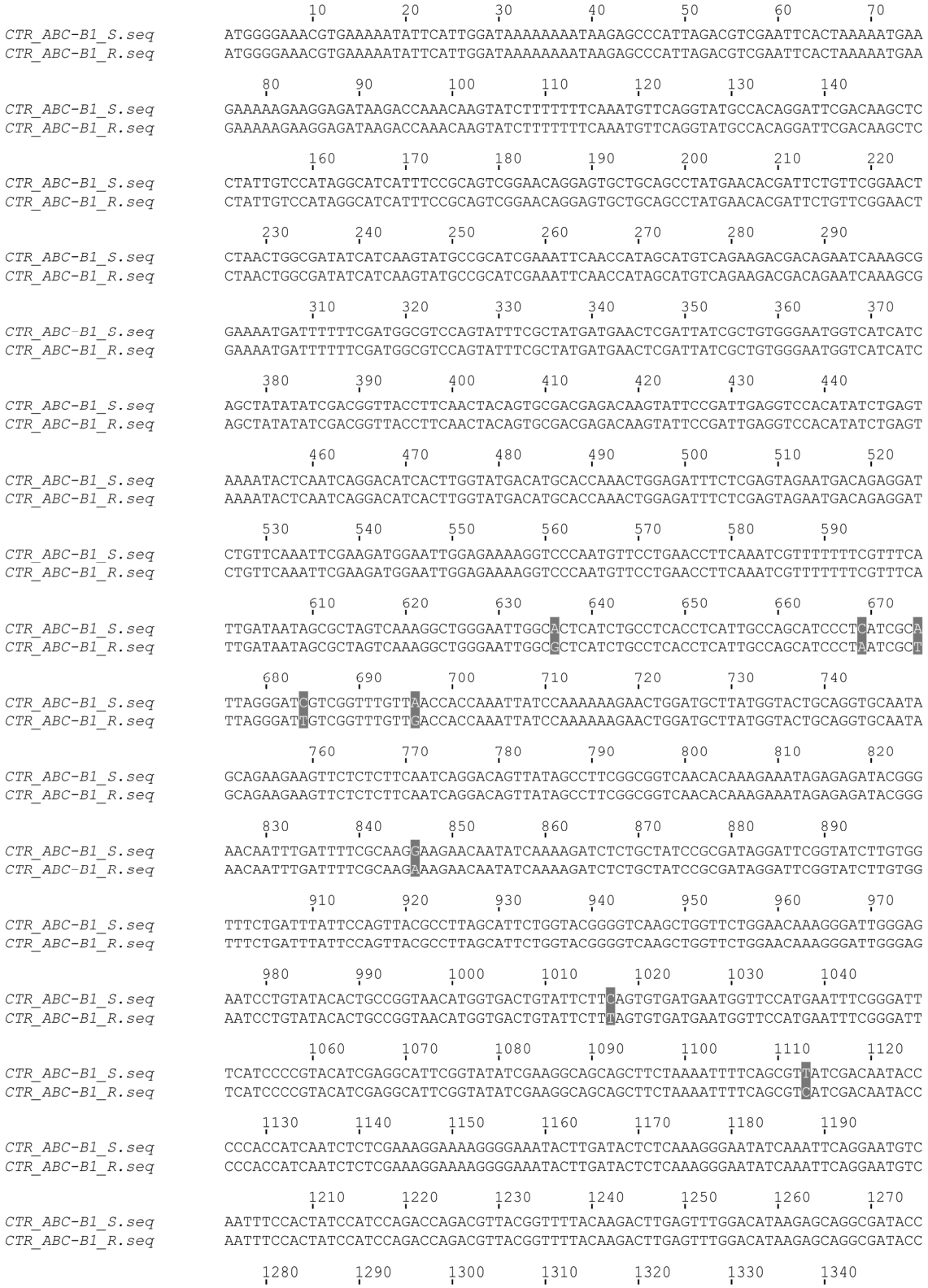
Table S1. Primers used in this study and their function.

Primer Name	Sequence (5′–3′)	Function
CTR_ABCB1_del_F	TGTAAAACGACGGCCAGTAAAGACCTCGACCTCACCTG	Genotyping
CTR_ABCB1_del_R	CAGGAAACAGCTATGACCGAAGTGGCTTCGTCCAAGAG	Genotyping
M13_F	TGTAAAACGACGGCCAGT	Genotyping/ sequencing
M13_R	CAGGAAACAGCTATGACC	Genotyping/ sequencing
CTR_ABCB1_F	***ACC***ATG***G***GGAAACGTGAAAAATATTC	Cloning pIB/ V5-His TOPO/TA
CTR_ABCB1_R	AGTTGTCTGTCTTTGCAACTTAT	Cloning pIB/ V5-His TOPO/TA

The M13 "tails" of the primers used for the genotyping are underlined. The Kozak sequence introduced on the forward primer used to amplify *CtABCB1* for cloning in the expression vector is indicated in bold/italic.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CTR_ABC-B1_R.seq GAAAAAGAAGGAGATAAGACCAAACAAGTATCTTTTTTTCAAATGTTCAGGTATGCCACAGGATTCGACAAGCTC
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CTR_ABC-B1_R.seq CTATTGTCCATAGGCATCATTTCCGCAGTCGGAACAGGAGTGCTGCAGCCTATGAACACGATTCTGTTCGGAACT
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CTR_ABC-B1_R.seq CTAACTGGCGATATCATCAAGTATGCCGCATCGAAATTCAACCATAGCATGTCAGAAGACGACAGAATCAAAGCG
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CTR_ABC-B1_R.seq GAAAATGATTTTTTCGATGGCGTCCAGTATTTCGCTATGATGAACTCGATTATCGCTGTGGGAATGGTCATCATC
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CTR_ABC-B1_R.seq AAAATACTCAATCAGGACATCACTTGGTATGACATGCACCAAACTGGAGATTTCTCGAGTAGAATGACAGAGGAT
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CTR_ABC-B1_R.seq CTGTTCAAATTCGAAGATGGAATTGGAGAAAAGGTCCCAATGTTCCTGAACCTTCAAATCGTTTTTTTCGTTTCA
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CTR_ABC-B1_R.seq GCAGAAGAAGTTCTCTCTTCAATCAGGACAGTTATAGCCTTCGGCGGTCAACACAAAGAAATAGAGAGATACGGG
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CTR_ABC-B1_R.seq AATTTCCACTATCCATCCAGACCAGACGTTACGGTTTTACAAGACTTGAGTTTGGACATAAGAGCAGGCGATACC
1280 1290 1300 1310 1320 1330 1340

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                                1510      1520      1530      1540      1550      1560      1570
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                            1580      1590      1600      1610      1620      1630      1640
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                            1730      1740      1750      1760      1770      1780      1790
CTR_ABC-B1_S.seq        CTAGACTCGGCTAGTGTGGATTGCACGACAGTCATTGTCGCTCATCGGTTGTCCACCATACAAGGAGCTAACAAG
CTR_ABC-B1_R.seq        CTAGACTCGGCTAGTGTGGATTGCACGACAGTCATTGTCGCTCATCGGTTGTCCACCATACAAGGAGCTAACAAG

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CTR_ABC-B1_R.seq        TATAATCTAGTAACGACACAAGTCAAGAGTAAAGAAACGGTGACACAATATAGTAAGAGTTATAAGACTCAAGAA

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CTR_ABC-B1_R.seq        AAACTTTCTAGCGATGCTGCAAGCGTTCAGGGAGCAACAGGGCAAAGAGTTGGCGTAGTTTTGCAGTCGATGGCC

                            2480      2490      2500      2510      2520      2530      2540
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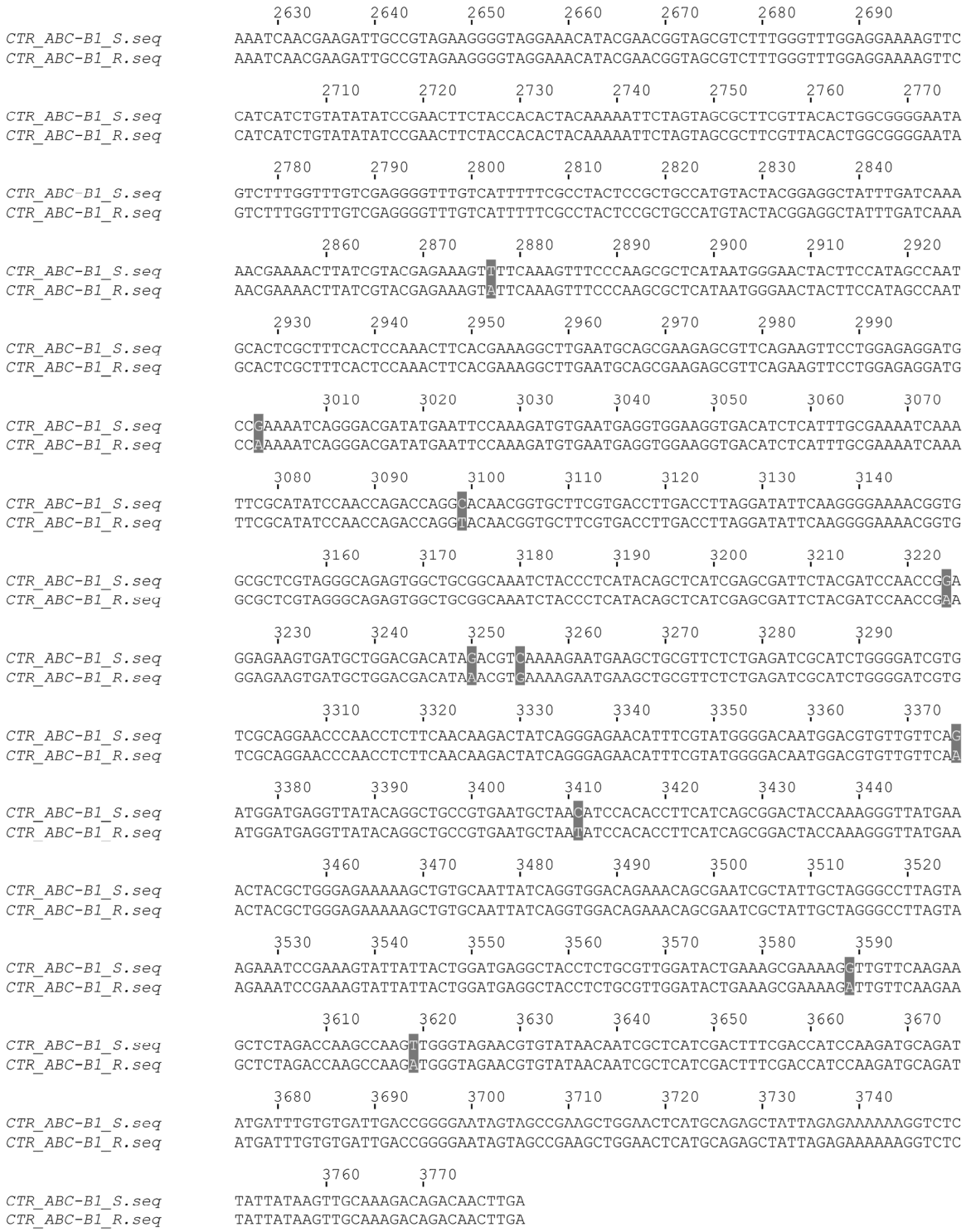

Figure S1. Comparison between CtABCB1 cDNA sequences derived from either the susceptible or the resistant populations. Nucleotide sequences corresponding to the cDNAs (open reading frames) of CtABCB1 cloned from the *C. tremula* susceptible (S) and the resistant (R) populations were aligned using CLUSTAL W (version 2.0.12). The 23 single nucleotide polymorphisms (SNPs) are shaded in grey. Only 5 SNPs are non-synonymous. The four-base pair deletion present in *abc-b*1 is located at position 1561.

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CTR_ABC-B1    MGKREKYSLDKKNKSPLDVEFTKNEEKEGDKTKQVSFFQMFRYATGFDKLLLSIGIISAVGTGVLQPM  68
                                    Y
CTR_ABC-B1    NTILFGTLTGDIIKYAASKFNHSMSEDDRIKAENDFFDGVQYFAMMNSIIAVGMVIISYISTVTFNYS 136
CTR_ABC-B1    ATRQVFRLRSTYLSKILNQDITWYDMHQTGDFSSRMTEDLFKFEDGIGEKVPMFLNLQIVFFVSLIIA 204
CTR_ABC-B1    LVKGWELALICLTSLPASLIALGIVGLLTTKLSKKELDAYGTAGAIAEEVLSSIRTVIAFGGQHKEIE 272
CTR_ABC-B1    RYGNNLIFARKNNIKRSLLSAIGFGILWFLIYSSYALAFWYGVKLVLEQRDWENPVYTAGNMVTVFFS 340
CTR_ABC-B1    VMNGSMNFGISSPYIEAFGISKAAASKIFSVIDNTPTINLSKGKGEILDTLKGNIKFRNVNFHYPSRP 408
CTR_ABC-B1    DVTVLQDLSLDIRAGDTVALVGSSGCGKSTVIQLIQRFYDPVAGEVSIDGKNIKDLDLTWMRTNIGVV 476
                                                    4 bp deletion
CTR_ABC-B1    GQEPVLFGTTIMENIKYGNADATEDDVVVAAKKANAHTFIKSLPNGYNTLVGERGAQLSGGQKQRIAI 544
CTR_ABC-B1    ARALVRKPSILLLDEATSALDNNSEAKVQAALDSASVDCTTVIVAHRLSTIQGANKIMVFSKGAVVEQ 612
CTR_ABC-B1    GTHDELMALKNEYYNLVTTQVKSKETVTQYSKSDKTQEYDDDIDEVVPVEASFAAEDDEDDFVSDRNM 680
CTR_ABC-B1    RLIDVIKMNAPEWPQIVVASIGSTVIGCAMPIFSVLFGSIIGTLANSDTEYVRTETNKYVVYFVIAGA 748
CTR_ABC-B1    VAMVSVFLQMYMFGIAGEKMTERIRGKMFSAMLNQEIGFFDKKTNGVGALCAKLSSDAASVQGATGQR 816
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              Y
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CTR_ABC-B1    AVQLSGGQKQRIAIARALVRNPKVLLLDEATSALDTESEKVVQEALDQAKLGRTCITIAHRLSTIQDA 1224
CTR_ABC-B1    DMICVIDRGIVAEAGTHAELLEKKGLYYKLQRQTT                                  1259
```

Figure S2. Predicted protein sequence of CtABCB1. Feature predictions include 12 transmembrane helices (pink), two ATP-binding domains (green), two transporter motifs (blue), and predicted glycosylation sites on the outside loops (underlined in blue, and indicated by 'Y'). The position of the four-base-pair deletion is indicated by a red arrow.

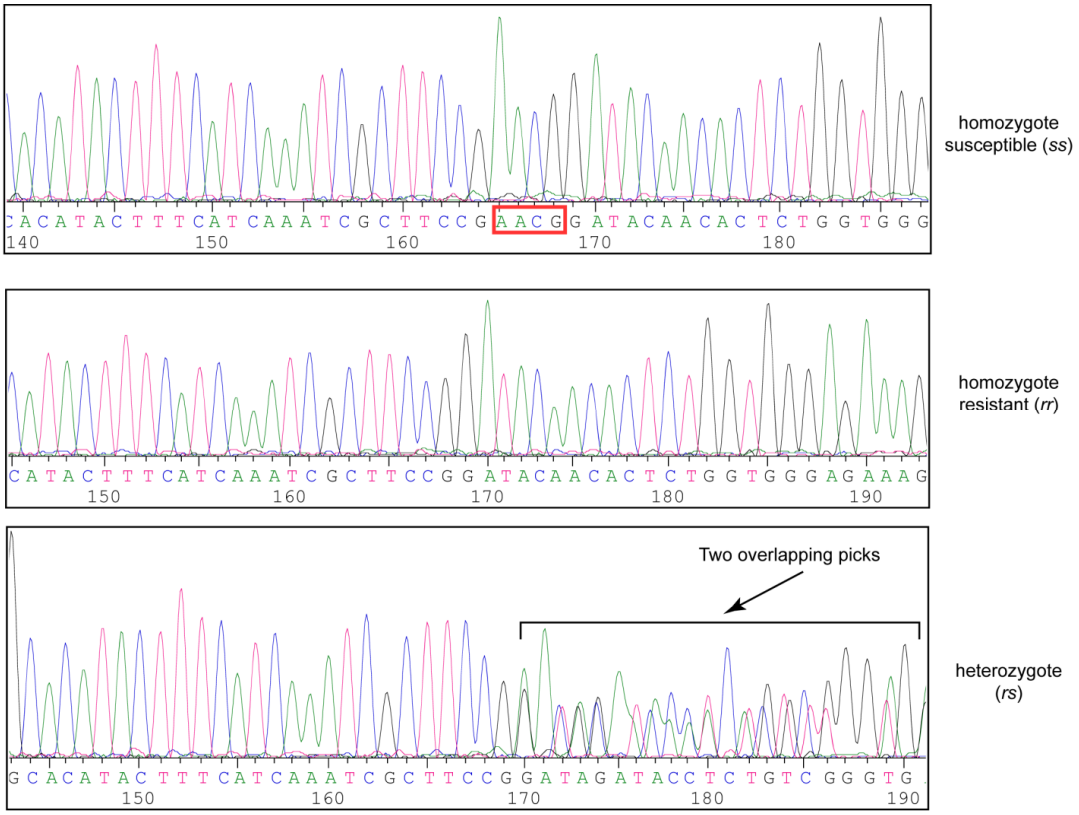

Figure S3. Determination of the genotype for the backcrosses between susceptible and resistant *C. tremula*. Genomic DNA was prepared from the grandparents, parents and offspring of each backcross. A primer pair was designed to amplify by PCR the region where the deletion is located in CtABCB1. PCR products were then processed by Sanger sequencing. The four nucleotides present in the "normal" version of *abc-b*1 but absent in resistant individuals is boxed in red.

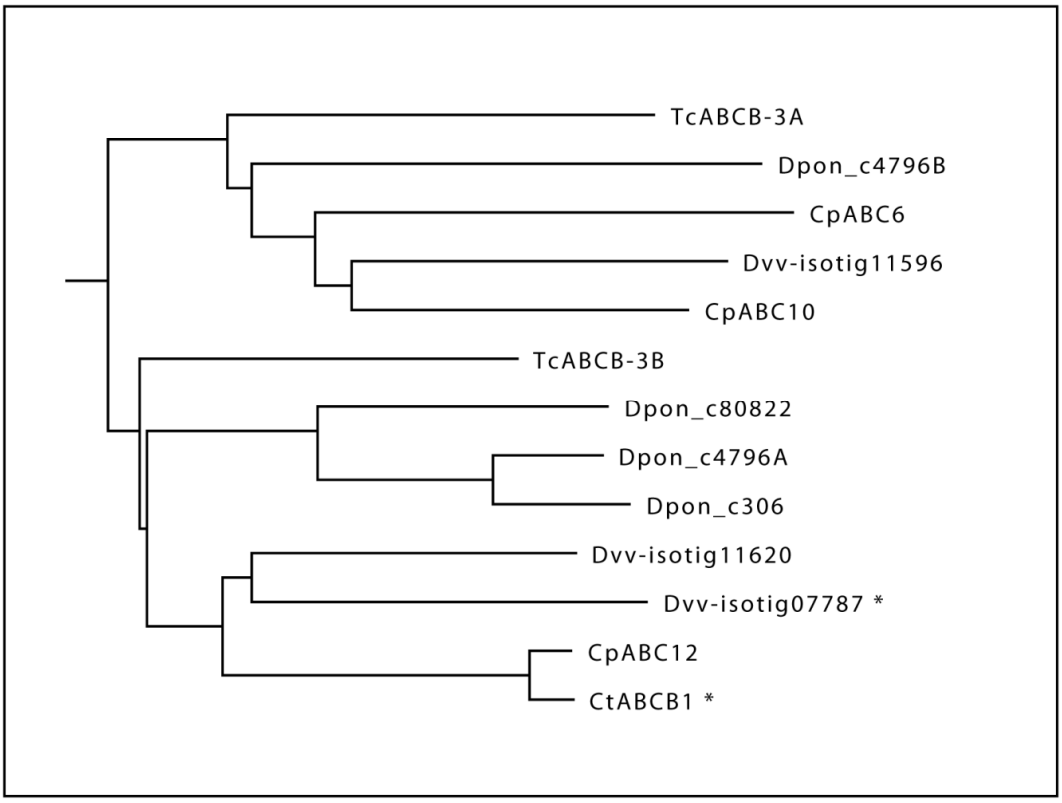

Figure S4. Neighbor-joining tree of full-transporter ABCB protein sequences from Coleoptera. Tc: *Tribolium castaneum*, Dpon: *Dendroctonus ponderosae*, Cp: *Chrysomela populi*, Dvv: *Diabrotica virgifera virgifera*, Ct: *Chrysomela tremula*. * The asterisks denote proteins genetically linked to Cry3 toxin resistance.

```
TcABCB-3A           1 MAKDDFQENGLEETVPLNTEYVKNKLKIKKTKDGKKEDKKEEK-------   43
Dpon_c4796B         1                            MEIKKNHSSDQQEPPERQ-------   18
CpABC6              1                            MCQVSYRQPESLARSLKC-------   18
Dvv-isotig11596     1                            MGNKKNENDLKCEKNKTN-------   18
CpABC10             1                            MGERKLYSVDKSEKKDKSKKVPNDS   25
TcABCB-3B           1                MGKKAYDLESSEKNGKKDALTPEFVQEPSEK-----L   32
Dpon_c80822         1                MSDEK---HDQKNGVDKPSPLEAKFQPPPDP-----D   29
Dpon_c4796A         1                MAAKKTDGDQDGKAADKKQALDVKFQSIDDPADP--D   35
Dpon_c306           1                MTER-----HDGTATDKERASDVNVPPIDDP------   26
Dvv-isotig11620     1                MTEEK----KHSIKDKEKIGIDAQFVNSEEPK-----   28
Dvv-isotig07787     1                MG-TK----KDDIKEKKTNALDAKFVKKKENE-----   27
CpABC12             1                MGKRE----KYSLDKKNKSPLDVEFTKNEEKEG----   29
Ct-ABCB1            1                MGKRE----KYSLDKKNKSPLDVEFTKNEEKEG----   29

TcABCB-3A          44 ----KISYFQLFRYTTLQDKLCIALGTLCAVICGCIQPYVMILFGDVTEV   89
Dpon_c4796B        19 ---PDVPYHQLFQFATLLDKLLIAVGIIASIICGVFQPYLMVLFGDVSGV   65
CpABC6             19 ----IYFYFKCFRYATALDKICLLVASSCTICCGILMPFAMLFFGDVTGS   64
Dvv-isotig11596    19 ----EISYLRLFQYCTTLDIIFMSIGAICAALSGIVQPYSMTLFGDVTGA   64
CpABC10            26 KEKQTIPYYRLFQYSTNLDKICLLLASACTILCGALQPFMMTIFGEITGS   75
TcABCB-3B          33 EKAPPVGFFKLFRYATKWDTFLMIIAVFASIGTGILQPLNTLLFGDLTGT   82
Dpon_c80822        30 EDISPPSFLQLYRYATGWEKFLLFIGVISALASGAIQPLNNLLFGQLIQT   79
Dpon_c4796A        36 EAVDASSFTGLYRFATQPQKYVIVIGAIIALISGALQPLNNLLFGDLTQT   85
Dpon_c306          27 ESTDASSFTGLYRFATRPQKCVIIIGAIIALICGALQPLNHLLFGDLTQI   76
Dvv-isotig11620    29 EKIKNVSFPQMFRYASTYDKFLMVVGLISATGTGVLQPLNTILFGSLTGD   78
Dvv-isotig07787    28 TKIKPISFFGMFKYASKGDKLLMFIGTLSAVITGCLPPINTILFGELAGN   77
CpABC12            30 DQTKQVSFFQMFRYATGLDKVLLSIGIISAFGTGVLQPMNTILFGTLTGD   79
Ct-ABCB1           30 DKTKQVSFFQMFRYATGFDKLLLSIGIISAVGTGVLQPMNTILFGTLTGD   79
                             .   .....      . .    .  .*   *     ** .

TcABCB-3A          90 IIQFAETLKSN-NSEINRTQAVDDLFRGVTDFAIYSSSSGIVMIITTYLA  138
Dpon_c4796B        66 LLDFTTAMNAN-LTFEEEKLATEKLYDGTEYFAIMTSVSALIILVCTYIS  114
CpABC6             65 IIDYAAAIKES-PPEDEKEKLIETLRHEIGLFAAQAAIIIIAVIALLYLS  113
Dvv-isotig11596    65 IVTYASNYNES-LSEPEKTLLADELINAVWLFGMKSVGVGIGVILTTYIS  113
CpABC10            76 IVDYATAFNDS-ITEEQKAVLVEQLWSDMKIFVIYSCIIGIVTILATYIS  124
TcABCB-3B          83 IVDYVFTINSNETSEEQKQNATDVFIDGITDFAVYNTLIGVGMLVLSYIS  132
Dpon_c80822        80 IVDYAQICYDD-PSSDQCVSAGDGLIDGVTHYAIWNSAIGVGIFVTSYVS  128
Dpon_c4796A        86 IIEYSQACFI--PSSTECGAAGDNLLAGIKHFALWNSLNGVAIMITAYLA  133
Dpon_c306          77 IIEYSEACLN--PNSTNCSVAGDNLSAGIKHFGIWSSINGVAIMITGYLA  124
Dvv-isotig11620    79 IIAYATS-IQINLPADQKKIAEDNFFDGIRYFALMNSLIGIGMFVFSYLA  127
Dvv-isotig07787    78 AVQYAETLYNATLSQNEQAEAQEKFFDGIKFFALANSMVGVAMLCFSYLS  127
CpABC12            80 IIKYAASKFNDSMSEDDRIKAENDFFDGVQYFALMNSIIAVGMVIISYIS  129
Ct-ABCB1           80 IIKYAASKFNHSMSEDDRIKAENDFFDGVQYFAMMNSIIAVGMVIISYIS  129
                        . .                              .       .     *..

TcABCB-3A         139 GILFSSSALRQIFHIRKLILQKTLNMDISWYDLNKTGDFATTFTENLSKL  188
Dpon_c4796B       115 VVFFTQSSLRQTCKMRKLFMEKTINQDIGWYDQNQTGDFASIITDNIPKI  164
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Dvv-isotig11596   114 TVLFIYSASRQIFKIRKAFLEKTLNQDIAWFDQNRTGDFASTFTQNISKL  163
CpABC10           125 VVLYSFSANRQIFKMRKMFLEKTLHQDIGWFDINQTGDFATTFTQNISKI  174
TcABCB-3B         133 TEFFNYTALKQVFKVRTLYLEKVFNQDISWYDVNNTGDFSSRMSDDLSKF  182
Dpon_c80822       129 TEAFSYTAIKQVFRVRSKYLQALLNKDVPWFDVHNSGDFASRMTDDLQRY  178
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Dpon_c306         125 TEAFSYNAIKQVFRVRSLYLQKLLNKDISWFDVHNSGDFSSRMADDLSKF  174
Dvv-isotig11620   128 TVTFNYSAMRQIFKIRSAYLKSILNQDVGWYDINQTGDFASRMSDDLFKF  177
Dvv-isotig07787   128 TITFNYSSTKQIFQIRSDYLKSILNQDISWYDQNQTGDFASRMSDDLSKF  177
CpABC12           130 TVTFNYSATRQVFRLRSIYLSKILNQDITWYDMHQTGDFSSRMTEDLFKF  179
Ct-ABCB1          130 TVTFNYSATRQVFRLRSTYLSKILNQDITWYDMHQTGDFSSRMTEDLFKF  179
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TcABCB-3A          189 EEGIGEKVGIFLYFETIFVTGIVMGLVLGWELALICLISLPVSFAVAFLI  238
Dpon_c4796B        165 EDGIGEKVGVVVFLGTTCVSGMIWALIKGWQLALVCLASLPLQTLVMGAI  214
CpABC6             164 EDGIGEKIGLFLYSIAWFLTGIIISLYEGWKLALVAMVSLPLSTILILII  213
Dvv-isotig11596    164 EEGIGEKIGTFLFFESTFVAGCVLGLVKGWKLALVCMVSLPLSTTIMTII  213
CpABC10            175 EEGIGEKIGVFLFFESTFVAGIIIALIKGWKLALVCVVSLPLSTIIMALI  224
TcABCB-3B          183 EDGIGEKVPMFVHFQATFLASLIMALVKGWQLALICLVSLPLSMIAIGII  232
Dpon_c80822        179 EDGIGEKMPLFLMLQGTFISAITLAMVKGWQLALICLISLPVSLLALGII  228
Dpon_c4796A        184 EDGIGEKVPLFLTLQGSFISAITLALVKGWELALICLISLPVSLIAVGLI  233
Dpon_c306          175 EDGIGEKVPLFLTLQGSFISAITLALVKGWELALICLISLPVSFIAVGLI  224
Dvv-isotig11620    178 EDGIGEKVPVFWSFQVVFLTSLIIALVKGWELALICLTSLPATLITIGIV  227
Dvv-isotig07787    178 EDGIGEKVPMFIHFQVLFVAAVGTALAKGWELALISLVAIPASLVSFGVI  227
CpABC12            180 EDGIGEKVPMFLNLQIVFFVSLIIALVKGWELALICLTSLPASLIALGIV  229
Ct-ABCB1           180 EDGIGEKVPMFLNLQIVFFVSLIIALVKGWELALICLTSLPASLIALGIV  229
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TcABCB-3A          239 SWLSTKFSKQELEAYANAGAIAEEVLSSVRTVVAFDGQGKEFERYEKHLQ  288
Dpon_c4796B        215 AWFSAKYCKQEMAAYSAAGAIAEEVLSSIKTVVAFDGQEKEEKRYEKFVK  264
CpABC6             214 TKIAAKFSKGEMEAYQDAGAIAQEVFGSIKTVVAFNGQDKECKIYEDHLV  263
Dvv-isotig11596    214 SWISTKFSAQEMESYGEAGTIAEEVFTAIKTVVAFDGQDKEIERYNKHLV  263
CpABC10            225 TTISTKFSQQELEAYGLAGSVAQEVLGSIRTVVAFEGQQKESSRYHQHLV  274
TcABCB-3B          233 AVLTSKLAKKEQDAYGSAGSIAEEVLTSIRTVIAFGGQHKEITRYDEELE  282
Dpon_c80822        229 AFLTTKFTSKELDAYGTAGSLAEEVFTFIRTVVAFGGEKQEKERYDESLV  278
Dpon_c4796A        234 AFLTTKFSKKELDAYAEAGSIAEEVLTSIRTVIGFGGEKLETQRYDKSLI  283
Dpon_c306          225 AYLTTQFSKKELDAYAEAGSIAEEVITSIRTVIGFGGEKLETQRYEKNLI  274
Dvv-isotig11620    228 GLLTTKLAKNELEAYGAAGSIAEEALSLIRTITAFGGQKKEVDRYNKNLV  277
Dvv-isotig07787    228 NLLTTKLAKNEMEAYAASGSIAEEVFSLIRTVTAFGGQQKEIDRYKEHLV  277
CpABC12            230 GLLTTKLSKKELDAYGTAGAIAEEVLSSIRTVIAFGGQHKEIERYGNNLI  279
Ct-ABCB1           230 GLLTTKLSKKELDAYGTAGAIAEEVLSSIRTVIAFGGQHKEIERYGNNLI  279
                          ... .  *  .*  .*..*.*    ..*.  * *.  *   *   .

TcABCB-3A          289 AAKKNNIRKNLFTGVSNAVMWFFVFASYALSFWYGVGLILKEKELPYEER  338
Dpon_c4796B        265 IAQNNNVKRCLFNSINQGFLWFLAYGCYALAFWYGVGLVIEERNLPEADR  314
CpABC6             264 HAERNNVLRCIFNSTNNFFLWFSMFACYSLTYWCGIHLIIGDRDLPSEER  313
Dvv-isotig11596    264 DAKKNNLKRSFFTAVSNGCLWFFVYACYALSFWYGVTLILNDRHLPEHEQ  313
CpABC10            275 HAQNNNIKRGLFNALSNGCLWFFVYACYALSFWYGVGLILEERQLPEAER  324
TcABCB-3B          283 FAKKNNIKRQSMTAIGFGLLWFFIYGSYALAFWYGVKLVLEDRNKPAKDK  332
Dpon_c80822        279 FARNNNIRRHFFEGIGYGTLWFCVFSSYALAFWYGVKLMLDG------NP  322
Dpon_c4796A        284 FARNNNIRRHFFEGIGYGLLWLCIFSSYGLAFWYGVKLMLDG------NP  327
Dpon_c306          275 FAKDNNIRRHFFEGIGYGMLWLCIFSSYGLAFWYGIKLMLDG------NP  318
Dvv-isotig11620    278 EAKNNNIRRSMFSALGFGLLWFMIYASYALAFWYGVKLVLRDRT--ATNQ  325
Dvv-isotig07787    278 SARKNNIKRTMIVGIGFGLVYLLLYSSYALSLWYGVKLVLKDRF--NPNA  325
CpABC12            280 FARKNNIKRSLLSAIGFGILWFLIYSSYALAFWYGVKLVLEQRD--WDNP  327
Ct-ABCB1           280 FARKNNIKRSLLSAIGFGILWFLIYSSYALAFWYGVKLVLEQRD--WENP  327
                        *  **. .          .    . .* *. * *. *..

TcABCB-3A          339 VYTPGNMVSVFFCTLMASWNFGTGAPYFEIFGTACGAAAKVFEILDTKPD  388
Dpon_c4796B        315 VYTPGNMMGVFFATLIASWNCGTISPYLEVFGMARGAAFKVFQVLESRPE  364
CpABC6             314 VYTPSSLVTIFFATLGATWYFGLAAPLLEVFATARTAAQKVFFILDSKPK  363
Dvv-isotig11596    314 VYTPANMVSVFFSTLIATWNFGLGAPLLETFGTAKGAAQKIFFVLDSKPV  363
CpABC10            325 VYTAGNMVSVFFCTLVATWNFGMGAPILEIFGAAKGAAQKIFAVLDSEPK  374
TcABCB-3B          333 VYDPGTMVTVFFSVMTGSMNFGISSPYIEAFGVARAAASKVYQIIDNIPK  382
Dpon_c80822        323 VYTPGNMITVFFSVMAGSVGFGMASPFIEAFSTAKAAGGKIFHIIETSPT  372
Dpon_c4796A        328 VYTPGNMITVFFSVMTGSMNFGVASPFIEAFATAKAAGGKIFHIIDTSPT  377
Dpon_c306          319 VYTPGNMLTV---VMAGSMSFGSASPFIEAFATAKAAGRKIFHMIKTSPI  365
Dvv-isotig11620    326 IYTPSNMVTVFFSVMTGSMNFGIASPYIEAFGISKAAASKIFSVIDHKPT  375
Dvv-isotig07787    326 SYTPANMVTIFFAVLSASLNFGAASTYLEMFAISKAAAAKIFNVIESKPD  375
CpABC12            328 VYTAGNMVTVFFSVMNGSMNFGISSPYIEAFGISKAAASKIFSVIDNTPT  377
Ct-ABCB1           328 VYTAGNMVTVFFSVMNGSMNFGISSPYIEAFGISKAAASKIFSVIDNTPT  377
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TcABCB-3A         389 INLSKTKGLKPKNLKGDIVFKDVSFHYPSRPDVKILQNFSIEIKAGQTVA  438
Dpon_c4796B       365 MYKQYDVGKRP-DFMSNIAFKNVKFSYPSRANVQVLKNINLEIRFGETVA  413
CpABC6            364 INTIKEKGRKLYRFQNCIRFDEVYFSYPTRSELKVLWGFDLQINIGETVA  413
Dvv-isotig11596   364 IRKFANSGIVINDAALEVTFEDVHFSYPSRSDVKILRGINLTISKGETVA  413
CpABC10           375 INQSKSVGKKLDDFKSNIRFENVFFSYPARPDVKILQGLNLQINFGETIA  424
TcABCB-3B         383 INLSKGNGDKIDNLKGDIKFRNVRFVYPSRQDVPILLGLDLDIKAGQTVA  432
Dpon_c80822       373 INLSKNNGKKPEEVKGNISFKNVHFYYPSRKEVEVLQGLTLDIAAGDTVA  422
Dpon_c4796A       378 INQSKNSGAKLDQVRGNIKLQNVKFQYPSRKDVPILQGIDLEIQAGDTVA  427
Dpon_c306         366 INQSKNNGAKLAQVRGNIKLQNVKFQYPSRKDVPVLQGIDLEIQAGDTVA  415
Dvv-isotig11620   376 INLSKGNGKTLNVLIGNIQFKDVAFRYPSRKDVPILKGLSLNIKSGDTVA  425
Dvv-isotig07787   376 INLSKSNGAKLDHLKGNIQFKNVKFHYPSRPDIPVLQGLDIEINPGETVA  425
CpABC12           378 INLSKGKGQQLDALKGNIKFRNVNFHYPSRPDVTVLQDLSLDIKAGDTVA  427
Ct-ABCB1          378 INLSKGKGEILDTLKGNIKFRNVNFHYPSRPDVTVLQDLSLDIRAGDTVA  427
                      .      *          .    * * **.*  . .*    . *  * *.*

TcABCB-3A         439 LVGSSGCGKSTCIQLIQRFYDAVTGTVKIDDNNIKDLNLTWLRSKIGVVG  488
Dpon_c4796B       414 LVGPSGSGKSTIVQLMQRFYDPNSGMISIDDVNLKDVNLSYLRQNVGVVS  463
CpABC6            414 LVGSSGCGKSTCIQLLQRFYDPTLGRITIDDVDIKDMSLKWLREKIAVVS  463
Dvv-isotig11596   414 LVGKSGCGKSTCIQLLQRFYDPDMGQIKINGIDIKQLNLDWLKQKISVVS  463
CpABC10           425 LVGSSGCGKSTCIQLLQRFYDPVVGNVLIDGVNLRDLNLTWLRQKIAVVS  474
TcABCB-3B         433 LVGSSGCGKSTCIQLIQRFYDPLEGEVSLDGKNLKDFDLTWLRNNIGVVG  482
Dpon_c80822       423 LVGSSGCGKSTVLQLVQRFYDALEGRVTIDGQDVKELDLTSYRQNIGVVS  472
Dpon_c4796A       428 LVGSSGCGKSTVLQLVQRFYDPLQGQVFIDGKDVKDLDLSWYRQSIGVVS  477
Dpon_c306         416 LVGRSGCGKSTLLQLVQRFYDPLQGQVFIDEKDVKELDLSWYRQYIGVVS  465
Dvv-isotig11620   426 LVGSSGCGKSTVIQLLQRLYDADSGEVTIDGKNIKEYDLTWLRSQIGVVG  475
Dvv-isotig07787   426 LVGSSGCGKSTVVQLIQRFYNAVSGEILVDGTNIQNLDLTWYRNNIGVVG  475
CpABC12           428 LVGSSGCGKSTVIQLIQRFYDPSAGEVSIDGKNIRDLDLTWMRTNIGVVG  477
Ct-ABCB1          428 LVGSSGCGKSTVIQLIQRFYDPVAGEVSIDGKNIKDLDLTWMRTNIGVVG  477
                      *** **.**** .**.** *    * . .    ..   *   .  . **

TcABCB-3A         489 QEPALFGATIAENIKFGNVTATQSDVERAAKKANAHNFIQKLPRGYNTVV  538
Dpon_c4796B       464 QEPSLFATTIAENIRYGKLSATMEEIIAAAKKANAHRFVTNLPFGYQTVI  513
CpABC6            464 QEPALFTTTVAENIRFGKEGAPQEEIETAARKARVHEFILTLPNGYETVI  513
Dvv-isotig11596   464 QEPDLFSTTIAENIRYGKLNATQQEIENAAKKADIHTFIQTLPRGYQTVL  513
CpABC10           475 QEPALFATTIAENIRLGKLDAKQAEIEEAAKKANVHKFILTLPHGYDTVI  524
TcABCB-3B         483 QEPVLFATTIAENIRYGNSKATDEEIKNAAIKANAHEFIKKLPSGYDTLV  532
Dpon_c80822       473 QEPVLFGTTIYENIRYGNKDATEEDITRAAKMANAHQFIKGLPHGYYTLV  522
Dpon_c4796A       478 QEPVLFGTTIAENIRYGNKEATEQDIVQAAKRANAHRFIKGLPEGYHTLV  527
Dpon_c306         466 QEPVLFGTTIAENIKYGNRDATELDIVQAAKMANAHQFIKGLPGGYHTLV  515
Dvv-isotig11620   476 QEPILFGTSILENIRYGKDGVTEEDVIQAAKKANAHNFIKALPNGYNTLV  525
Dvv-isotig07787   476 QEPVLFGTTILENIRYGKEEATEEEIIEAAKKANAHAFIKLLPKGYNTLV  525
CRW424                                                  FIKLLPKGYNTLV
CpABC12           478 QEPVLFGTTIMENIKYGNAEANEDDVIAAAKKANAHTFIKSLPNGYNTLV  527
Ct-ABCB1          478 QEPVLFGTTIMENIKYGNADATEDDVVVAAKKANAHTFIKSLPNGYNTLV  527
                      *** ** ... ***. *       ..  **  *  * *.  ** ** *..

TcABCB-3A         539 GERGAQLSGGQKQRIAIARALIREPKILLLDEATSALDTTSEAEVQAALD  588
Dpon_c4796B       514 GERGSQLSGGQKQRIAIARALIKAPNLLILDEATSALDTASEVEVQQALD  563
CpABC6            514 GERGGQLSGGQKQKLAIARALIRRPQILLLDEATSALDTSSESEVQAALD  563
Dvv-isotig11596   514 GERGTQLSGGQKQKIAIARALVRTPEFLLLDEATSALDTTSEAEIQEALD  563
CpABC10           525 GERGAQLSGGQKQRIAIARALVRKPEILLLDEATSALDTTSEAEVQAALD  574
TcABCB-3B         533 GERGAQLSGGQKQRIAIARALVRNPAILLLDEATSALDTNSEAKVQAALD  582
Dpon_c80822       523 GERGAQLSGGQKQRIAIARALVRNPAILLLDEATSALDTNSEAKVQAALD  572
Dpon_c4796A       528 GERGAQLSGGQKQRIAIARALVRNPAILLLDEATSALDTNSEAKVQAALD  577
Dpon_c306         516 GERGAQLSGGQKQRIAIARALVRNPAILLLDEATSALDTNSEAKVQAALD  565
Dvv-isotig11620   526 GEKGAQLSGGQKQRIAIARALVRNPTLLLLDEATSALDNTSEAKVQAALD  575
Dvv-isotig07787   526 GERGTQLSGGQKQRIAIARALVRKPTLLLLDEATSALDNASEAKVQEALD  575
CRW424                GERGTQLSGGQKQRIAIARALVRKPTLLLLD
CpABC12           528 GERGAQLSGGQKQRIAIARALVRKPTILLLDEATSALDNNSEAKVQAALD  577
Ct-ABCB1          528 GERGAQLSGGQKQRIAIARALVRKPSILLLDEATSALDNNSEAKVQAALD  577
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TcABCB-3A          589 AVSGECTTIIVAHRLSTIRNANRIVVVSHGSVIEEGTHSELMAKKGAYFD  638
Dpon_c4796B        564 AISGECTKLVVAHRLSTIRNATRIIVFDQGEVVEHGSHAQLMAAKGVYYN  613
CpABC6             564 SISGECTTIIVAHRLSTIRNAKKIVYISEGRVSEIGSHAELMAKKGAYFK  613
Dvv-isotig11596    564 SIRGTCTIIIVAHRLSTIRQASKIVVINEGKVLEMGTHTELMDMKGAYHN  613
CpABC10            575 SVSGECTTIIVAHRLSTIRNANRIVVISAGKVQEIGSHAELMAKEGGYYN  624
TcABCB-3B          583 KASKGCTTVIVAHRLSTIRNANKIVVISKGKVVEQGTHNELMELKSEYYN  632
Dpon_c80822        573 KASQNRTTIIVAHRLTTIRGANKIVVISEGKVVEEGTHHELMKLQREYYT  622
Dpon_c4796A        578 RASENRTTIIVAHRLSTIRGANKIVVISDGKVVEQGTHEDLMELKKEYYT  627
Dpon_c306          566 RASEHRTTIIVAHRLSTIRGANKIVVISDGKVVEQGTHEDLMELKNEYYA  615
Dvv-isotig11620    576 AASVECTTIIVAHRLSTIRGANKIIVLSQGVVVEEGTHEELMELKQEYYR  625
Dvv-isotig07787    576 LASAECTTIIVAHRLSTIRGANKIIVLLEGTVVEQGTHDELMSLKGEYFK  625
CpABC12            578 SASVDCTTVIVAHRLSTIQGANKIMVFSKGAVVEQGTHDELMALKKEYYN  627
Ct-ABCB1           578 SASVDCTTVIVAHRLSTIQGANKIMVFSKGAVVEQGTHDELMALKNEYYN  627
                           * ..*****.**. * .*.    * * * *.*  **     *

TcABCB-3A          639 LVQSQGLVETEETT--TEEKQKQNGVVDTKPNQTEVTEIISTENLNDAQA  686
Dpon_c4796B        614 MITSQGYTDLKSENDKDNDKALQKSKSFSNHSRESAEDDQQVTEEEYFPQ  663
CpABC6             614 LVNSQGLMDTKPFS---QIQKIMRQVSSPMHQFVTDREDENVDEKSNDTQ  660
Dvv-isotig11596    614 LVISQGLTETLEEK---GNRRRSRKFSEANKS-INEKEDEELEDTQINQP  659
CpABC10            625 LVKSQGFTETQETT---GDRRLSRSFSLSNKSCIVEDEEEKIEDETAEES  671
TcABCB-3B          633 LVMTQVSAVEKFDGDQEGESRKLVELER-QVSLLDDEKHDDAEEEVQEA-  680
Dpon_c80822        623 LVTTQVQSGSQFESSTNEESKTEVAAAEDDEDEALSDKVEDEEAETDNY-  671
Dpon_c4796A        628 LVTTQVQGSEKFENIGETKEKKILDYAEDDDEDFAPKKEIDEEAEVDNY-  676
Dpon_c306          616 LVTTQVHSSEQFENIGEASEKKIFDSVEDDDEDFAPKRETDEESEVDNY-  664
Dvv-isotig11620    626 LVTAQVKSSEQFEVAEKKKVVRAISLAESSTGSD-HNIEATKEDNEDDFN  674
Dvv-isotig07787    626 LVTAQVASSNQIELSNDETETKGNNEAYEEYNDDDDDISDDEKNEIDDFK  675
CpABC12            628 LVTTQVKSKETVTQYTKSDKTQEHEDVIDEVVP--VEAAFAAEDDEDDFV  675
Ct-ABCB1           628 LVTTQVKSKETVTQYSKSDKTQEYDDDIDEVVP--VEASFAAEDDEDDFV  675
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TcABCB-3A          687 ENKGSPILQILKMNKPEWFHIFTGCVTAVINGSAFPIYGLVFGDIIGVLA  736
Dpon_c4796B        664 EGSSRTILKILRMNSSEWLSMIIGTLASFMNGASLPLYGLIFGDILGALS  713
CpABC6             661 VDKI--FIKVMKMCKPEWYLIAIGCVSSVIKGVAYPINGWIFGSIIGILF  708
Dvv-isotig11596    660 VAKN-ILWKVLKLNASEWFYILIGCLSSLITGASLPIYGLVFGGIMGIFA  708
CpABC10            672 VESKGVVLKVIKMNKPEWFYNFIGCLCSGLTGASLPVYGLVFGGIVGVLA  721
TcABCB-3B          681 -ERSVSLMSILRMNKPEWVSISIGCIASIVMGCSMPAFAVIFGDIMGVLA  729
Dpon_c80822        672 -VKKASIWSISKLNAPEWYLIVLGCVGAAAMGTSMPFFAVLFGNILTVLQ  720
Dpon_c4796A        677 -VKTASLWSIVKLNSPEWLSLVLGCIGAGAMGTAFPIFAILFGNILQVLQ  725
Dpon_c306          665 -VKTASLWSIVKLNSPEWLSLFLGCFGAAVMGTVLPIFAVLLGSILQVLQ  713
Dvv-isotig11620    675 ENKDVSVFEILKMNAPEWPYILFAGLGSIVVGCGMPVFAVLFGSILGTLA  724
Dvv-isotig07787    676 NGKKITLFSIMKLNAPEWPYILIAGVGSIVVGWGWPIFAVFFGSVLGTLA  725
CpABC12            676 SDRNMRLIDVIKMNAPEWPQIVVASIGSTVIGCAMPIFSVLFGSIIGTLA  725
Ct-ABCB1           676 SDRNMRLIDVIKMNAPEWPQIVVASIGSTVIGCAMPIFSVLFGSIIGTLA  725
                             . ..   **         .   *   *      * ..

TcABCB-3A          737 DPRDS--YVREQSNIFSLYFVIIGIVTAVATFLQIYYFAVAGEKLTKRLR  784
Dpon_c4796B        714 IIDNT--VLRREANFYCLYFLYLGIASGIAMFFQIYGFGYAGEKLTYRLR  761
CpABC6             709 LEEDD--ELLSENNTLCLYFICLAFIIGGSTFFQLLTFGIAGEKLTLRVR  756
Dvv-isotig11596    709 NDNDG--EVRSESNMYCLYFLILGVVTGVAMFWQTTSFSVAGEHLTLKIR  756
CpABC10            722 LTDDE--SVRRESNLYCLYFLILGIVTGIAMFFQMFSFGIAGEKLTRRIR  769
TcABCB-3B          730 EKNED--EVISETNRFCIYFVIAGVVSGIATFLQIFMFSVAGEKLTMRLR  777
Dpon_c80822        721 STDEE--YVRTQTNKYCLYFVYAGLMSMVATFMQMYMFGRAGQKLTYRIR  768
Dpon_c4796A        726 DIDSNPDYVRQETNKYCLYFVLAGVLSMCATFLQMYMFGRAGQKLTLRIR  775
Dpon_c306          714 DSDKN--YVRQETNKYILYFVLAGVLAMFATFLQLYMFGRAGENLTLRMR  761
Dvv-isotig11620    725 NGDPD--FVRSETNKYCLYFVLGGLITMVSVFTQMYLLGIAGEKMTERVR  772
Dvv-isotig07787    726 KYDTE--YIETETTRYCIFFVIAGVICMISVFLQNYLLGIAGEKMTERIR  773
CpABC12            726 DSKTE--YVRSETNKYVVYFVIAGAVAMVSVFLQMYMFGIAGEKMTERIR  773
Ct-ABCB1           726 NSDTE--YVRTETNKYVVYFVIAGAVAMVSVFLQMYMFGIAGEKMTERIR  773
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TcABCB-3A         785 AKMFRAMLNQEMAWFDRKENGVGALCAKLSGEAASVQGAGGIRIGTVLNS  834
Dpon_c4796B       762 NKMFGCMLRQEMGWFDRKENGVGALCAQLSGDAASVQGAGGSRIGLILNS  811
CpABC6            757 LNTFRAILRQEMGWFDRKENGVGAICARLASDANNIQGLAGLHIGTVLNT  806
Dvv-isotig11596   757 SKTFEAMLRQEIGWYDQKSNGVGALCARLAGDAVAVQGAAGPQIGTTINF  806
CpABC10           770 HKTFEAMMNQEMGWFDKKENGVGALCAQLAGDAAAIQGVAGVQIGTVLNF  819
TcABCB-3B         778 SMTFIAMLKQEMGWYDRKDNGVGALCARLSGEAAHVQGATGQRVGTILQS  827
Dpon_c80822       769 SRMFEALLKQEMAYYDRKSNGVGSLCAKLSDEAASVQGATGQRIGSIMSS  818
Dpon_c4796A       776 SRMFDALLKQEMGYFDRKENGVGSLCAKLSNEAAQVQGATGQRIGTIVNS  825
Dpon_c306         762 SRMFDALLKQEMGYFDRNENGVGSLCAKLSNEASQVQGATGQRIGAIVNS  811
Dvv-isotig11620   773 SRLFKAMIYQEIGFFDKKTNGVGALCAKLSSDASNIQGATGIRVGTILQS  822
Dvv-isotig07787   774 TQMFTAIISQEMGFFDKKSNGVGALCAKLAGDSSSIQGATGQRVGAILQS  823
CpABC12           774 GKMFSAMLNQEIGFFDKKSNGVGALCAKLSSDAASVQGATGQRIGVVLQS  823
Ct-ABCB1          774 GKMFSAMLNQEIGFFDKKTNGVGALCAKLSSDAASVQGATGQRVGVVLQS  823
                        * ... **.  .*.  ****..**.*. ..  .**  * ..*  .

TcABCB-3A         835 LATFIISNIIALYFEWRLALVLISFSPIILLSVFFEQKFTQGDSQVNQKY  884
Dpon_c4796B       812 VSTFILAACIGFYLEWRLTLVAGVFFPLMFFSISYERKSVQQETQAAQKL  861
CpABC6            807 LTTFTVTLVFCFYYEWKLTLVLIAIFPLIFLSVYLEQKFLQDDIIKNQLM  856
Dvv-isotig11596   807 ISTFILTCTFSFYFEWRTSFVLFSLCPVIFFSVYFEQKVLQEDATKNQKM  856
CpABC10           820 LCTFILTCAFSFYYEWKLTLVLLSFCPLIFFSVYFEQKSMQNDAIKNQKM  869
TcABCB-3B         828 IATIGLSVGLSMYYQWKLGLVALAFTPFILLAVFFQHRLMNVENEAHHKS  877
Dpon_c80822       819 LSTLAFALFLALFYQWRLGLVALSFFPLILISTFFQRRQMSQESDEYRAS  868
Dpon_c4796A       826 LATLSLSVFLAVYYEWRLGLVAMVFVPLIIVATFLQRRQMSQESDDYKES  875
Dpon_c306         812 LATLILSVFFAVYYEWRLGLVAMVFVPLIIAATFIQKKQMSQESDDYKES  861
Dvv-isotig11620   823 IATFCLAIGLSMYYEWKLGLVTAAFTPVILIAMFFERRNTRGGNDSRDSA  872
Dvv-isotig07787   824 LSTFGIAIALSMYYQWKLGLLMASFTPLMLVAIFIEKRNTTGLSEAREKS  873
CpABC12           824 MATFCLAVGLAMYYEYRLGLVTVAFMPFLLIAFFFERRNSSGQNDTRDKA  873
Ct-ABCB1          824 MATFCLAVGLAMYYEYRLGLVTVAFMPFLLIAFFFERRNSSGQNDTRDQS  873
                      ..*   .     . . .   .     * .  .   ...

TcABCB-3A         885 LENSAKIAVEAIGNIRTIASLGCEEVFHGYYVKELTPYVANV-KKQMHFR  933
Dpon_c4796B       862 LEKSAKIAIEAIDNIKTVKALGCERVFCDTYEKELDLCRQAG-FKRSHIK  910
CpABC6            857 LEKSSKLAIEAIGNIRTVVSLGCEQVFLDLFVKELLPYRAMA-NRKSHMR  905
Dvv-isotig11596   857 LEASAKLAVEAIGNIRTVVSLGCEKVFMEQYIKELLPYQKMA-RKKSHYR  905
CpABC10           870 VERSSKLAVEAIGNIRTVVSLGCERVFHDMYVKELSPYQALA-RRKSHFR  918
TcABCB-3B         878 LQKSNKLAVEAVGNVRTVVSLGLEETFHKLYISYLMEHHKRT-LRNTHFR  926
Dpon_c80822       869 LQKSTKIAVEAVGSIRTVVSLGCEDIFYNLYISELMPHIKTC-LRNSHGR  917
Dpon_c4796A       876 LQKSTKIAVEAVGSIRTVVSLGCEETFLNLYINELTPHIKKC-LRNTHAR  924
Dpon_c306         862 LEKSTKIAVEAVGSIRTVVSLGCEKTFFKLYISELMPHIKKC-LRNTHAR  910
Dvv-isotig11620   873 LQKSTRTAVEAVGNIRTVASLGLEEKFQQLYESELMPHYKSS-LKTVHWR  921
Dvv-isotig07787   874 LQKSTKIAVEAVGNIRTVAGLVAEDKFQKSYITELKPHYKAA-LAAVHWR  922
CpABC12           874 LQKSTKIAVEGVGNIRTVASLGLEEKFHHLYISELMPHYKNSNRASLHWR  923
Ct-ABCB1          874 LQKSTKIAVEGVGNIRTVASLGLEEKFHHLYISELLPHYKNSSSASLHWR  923
                      .. * . *.* .  ..*.  *  *  *   .   *           * .

TcABCB-3A         934 SAVLGVARSVMLFAYAVGMGYGAKLMVDSDVDYGTVFIVSETVIVGSWSI  983
Dpon_c4796B       911 AGLIGMARCIQFLAYAGGMTYGAQLLEQNEVDSATLFKVLEVIVTSSWSI  960
CpABC6            906 GLILGMARALMIASYLAGIMYGGKIIIDGEAEYGTVFKVCEIMTMGSWAI  955
Dvv-isotig11596   906 GIIVGLARSLMLFAYVAGIRYGINLIISGDCPYGTIFIVCEVMIVGTWSV  955
CpABC10           919 GTVLGMARSLIVFAYAAGMGYGIKLIIDGAVEYGIVIKVCEVMIVGSWSI  968
TcABCB-3B         927 AVVLGLARSIMFFAYSACMYYGGHLIRDEGLLYQDVFKVSQSLIMGTVSI  976
Dpon_c80822       918 ALVLAFSRAILLFAISACLYYGGHLIRDGQVEFGDVFKVTQGLVMGTTSI  967
Dpon_c4796A       925 AFILGFSRAIMIFAFSACLVYGGYLIKNDNVQYGDVFKVAQALIMGTVSI  974
Dpon_c306         911 AFILGFSRAIMIFAFSACLVYGGYLIKHENVQYGVVFKVAQALIMGTVSI  960
Dvv-isotig11620   922 AIVFGLSRSLLFFAYATAMYYGGFLIR-DGLPYDRVFKVSQAQIMGTVSI  970
Dvv-isotig07787   923 GLVFGLSRSLGYFAYAAAMYYGGFLIR-DGLYYDKVFKVAQAQLMGTISI  971
CpABC12           924 GIVFGLSRGLSFFAYSAAMYYGGYLIKNDNLSYEKVFKVSQALIMGTTSI  973
Ct-ABCB1          924 GIVFGLSRGLSFFAYSAAMYYGGYLIKNENLSYEKVFKVSQALIMGTTSI  973
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TcABCB-3A          984 GNAFSFSPNFQKGLSAADRIFSLLKRVPEVKNSLEPVYLNDVRGNIEYSN 1033
Dpon_c4796B        961 GNALSFSSNMQKGITAAAKIFRLLNREPAIKNSPNGIVRYLEKADVEYSK 1010
CpABC6             956 GNALALPPNFQQALNAAARTISLLERKPSVKTTGNP----WRDGNVEYND 1001
Dvv-isotig11596    956 GNALSLSPNFQKGLVAASRIITLLERQPVVQNMPDALNFLWEDENVEYSE 1005
CpABC10            969 GNAMSMTPNFQKGLIAARRIISLLDRTPLVKNIANPSKKLWENENIEFSQ 1018
TcABCB-3B          977 ANALAFTPNLQKGLVAAARIIRLLRRQPLIRDEPGAKDKEWENGAIQYDT 1026
Dpon_c80822        968 ANSLAFTPNLEKGLIAAKSVMNTINRITQIRNLPDAKNKTQAEGDLGYSD 1017
Dpon_c4796A        975 ANSLAFTPNLEKGLVAARTVMNMINRIPKVSNSQNALIKKTADGNVDYSQ 1024
Dpon_c306          961 ANSLAFTPNFEKGLVAARTVMNMINRIPKVSNSQNALIKNTADGNVNYSQ 1010
Dvv-isotig11620    971 ANSLAFSPNFAKGVAAAKKVKSFLSRIPLIRDLPSSRQMVKASGNFSFSE 1020
Dvv-isotig07787    972 ANSLAFTPNLNRGISAAKRIKSFLSRIPLIRDGPSSKPMNQVDGNIGYSN 1021
CpABC12            974 ANALAFTPNFTKGLSAAKSVQKFLERVPKIRDDMNSKDVNEVEGDISFSK 1023
Ct-ABCB1           974 ANALAFTPNFTKGLNAAKSVQKFLERMPKIRDDMNSKDVNEVEGDISFAK 1023
                         *. .   *  . . **      . *   .                .

TcABCB-3A         1034 IYFSYPTRSSVSVLNGLNLNVLQGKTVALVGASGCGKSTIIQLLERFYDP 1083
Dpon_c4796B       1011 IYFSYPTRPAIPILNGLDLSILNGKTVALVGGSGCGKSTLIQLLIRFYDP 1060
CpABC6            1002 IFFSYPTRPSISVLNGLDLRVMQGKTVALVGSSGCGKSTVVQLLERFYDP 1051
Dvv-isotig11596   1006 VYFSYPTRPSIPILKALNLLIPKGKTVALVGSSGCGKSTIIQLLERFYDP 1055
CpABC10           1019 IYFSYPTRPSISILNSLNLSILKGKTVALVGSSGCGKSTIIQLLERFYDP 1068
TcABCB-3B         1027 IYFSYPTRPNIMVLKGLNLSVLQGKTVALVGPSGCGKSTIIQLIERFYDP 1076
Dpon_c80822       1018 VHFSYPTRVKIPVLRGLDLSVLRGKTVALVGPSGCGKSTIVQLLERFYDP 1067
Dpon_c4796A       1025 IRFAYPTRDSIQVLKGLDLSVLQGKTVALVGPSGCGKSTIIQLLERFYDP 1074
Dpon_c306         1011 IHFSYPTRDSIEVLKGLDLSVLQGKTVALVGPSGCGKSTIIHLLERFYDP 1060
Dvv-isotig11620   1021 IEFTYPTRPNVLILKGLNLDILNGKTVALVGESGCGKSTIIQLIERFYDP 1070
Dvv-isotig07787   1022 VEFFYPTRKNIQVLRGLTINIPKGSTVALVGESGCGKSTIIQLIERFYDP 1071
CpABC12           1024 IKFAYPTRPGTMVLRDLDLKIFKGKTVALVGQSGCGKSTLIQLIERFYDP 1073
Ct-ABCB1          1024 IKFAYPTRPGTTVLRDLDLRIFKGKTVALVGQSGCGKSTLIQLIERFYDP 1073
                       . * ****    .*  * . .  * ****** *******...*. *****

TcABCB-3A         1084 VSGEVSLDGESVKTVDIQNLRSHLGIVSQEPNLFDRTIAENIAYGAND-R 1132
Dpon_c4796B       1061 GYGEVAIGGDDVRALSLKHLRSHLGIVSQEPNLFDLTIAENISYGIHD-R 1109
CpABC6            1052 AGGAITVDGVDTRSMRLGQLRSQLGIVSQEPNLFDRTVAANISYGAVEEK 1101
Dvv-isotig11596   1056 SYGKVEISDKNIRYVDLKSLRSQLGIVSQEPNLFDKTIAENIAYGANY-K 1104
CpABC10           1069 DYGQITVDGEDTTKTDMATMRSQLGIVSQEPNLFDRTIAENISYGANQ-K 1117
TcABCB-3B         1077 LEGTLTVDNEDIRNIRLGSHRSHLGIVSQEPNLFDRTIGDNIAYGDNS-R 1125
Dpon_c80822       1068 LSGSVTLDRGDLKSLTLSSLRSHLGIVSQEPNLFSRTIAENIAYGDNA-R 1116
Dpon_c4796A       1075 ASGTVSLDKDDIKSITLDSLRSHLGIVSQEPNLFSRSIAENIAYGDNS-R 1123
Dpon_c306         1061 ASGTVSLDEDDIKSITLASLRSHLGIVSQEPNLFSRSIAENIAYGDNS-R 1109
Dvv-isotig11620   1071 RSGEVKMDGVDLKDISLDSLRSHMGIVSQEPNLFNKSIAENIAYGDNS-R 1119
Dvv-isotig07787   1072 SSGDINLDEQNIKHITLSSLRSHLGIVPQEPNLFNKSIAENIAYGDNS-R 1120
CpABC12           1074 SEGEVMLDEINVKRMRLSSLRSHLGIVSQEPNLFNKTIRENISYGDNG-R 1122
Ct-ABCB1          1074 TGGEVMLDDIDVKRMKLRSLRSHLGIVSQEPNLFNKTIRENISYGDNG-R 1122
                         * . .         .   **..*** ******  ..  **.**    .

TcABCB-3A         1133 TVGMNEIVEAAKSANIHTFISSLPGGYETSLGSKGAQLSGGQKQRVAIAR 1182
Dpon_c4796B       1110 KVDLKEIMEAAKSANVHSFVTSLPLGYETRLGSKGKQLSGGQKQRIAIAR 1159
CpABC6            1102 DARIDRIMEAAKSANIHTFISSLPMGYDTRVGTNGTQLSGGQKQRIAIAR 1151
Dvv-isotig11596   1105 QVEMDAIIDAAKSANIHEFILNLPKGYETKVGSKGTQLSGGQKQRIAIAR 1154
CpABC10           1118 EVDMEKVMESAKSANIHNFITALPMGYETRIGSNGTQLSGGQKQRIAIAR 1167
TcABCB-3B         1126 EVTQEEIIEAAKNANIHNFIASLPLGYETRLGEKGTQLSGGQKQRVAIAR 1175
Dpon_c80822       1117 TVPMAEIIEAATKANIHTFITGLPKGYDTKLGDKGTQLSGGQKQRIAIAR 1166
Dpon_c4796A       1124 QATEVEIIEAARKANIHNFIAHLPKGYKTKLGEKGTQLSGGQKQRIAIAR 1173
Dpon_c306         1110 HSTDSEIIEAARKANIHNFITQLPEGYNTKLGEKGTQLSGGQKQRIAIAR 1159
Dvv-isotig11620   1120 EVSMDEIIKAAKNANIHNFITGLPKGYETKLGEKAVQLSGGQKQRIAIAR 1169
Dvv-isotig07787   1121 NVPIDEIIQAAKNANIHNFIVGLPNGYDTELGEKATQLSGGQKQRIAIAR 1170
CpABC12           1123 VVQMDEVIQAAVNANIHNFISGLPKGYETSLGEKAVQLSGGQKQRIAIAR 1172
Ct-ABCB1          1123 VVQMDEVIQAAVNANIHTFISGLPKGYETTLGEKAVQLSGGQKQRIAIAR 1172
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TcABCB-3A        1183 ALIRNPKILLLDEATSALDNESEKVVQEALDNAKKNRTCITIAHRLTTIQ 1232
Dpon_c4796B      1160 ALLRDPKILLLDEATSALDNESEKIVQEALDNARKGRTCITIAHRLTTIQ 1209
CpABC6           1152 ALMRNPKILLLDEATSALDNESKKIVQQALEVARKGRTCITIAHRLTTIQ 1201
Dvv-isotig11596  1155 ALLRNPKILLLDEATSALDNESEKIVQEALDNARKSRTCITIAHRLTTIQ 1204
CpABC10          1168 ALMRNPKILLLDEATSALDNESEKIVQEALDNARQGRTCITIAHRLTTIQ 1217
TcABCB-3B        1176 ALVRNPKLLLLDEATSALDSESEKVVQEALDNAKKGRTCITIAHRLTTIQ 1225
Dpon_c80822      1167 ALVRNPKVLLLDEATSALDAESEKVVQEALDNAKQGRTCLTIAHRLTTIQ 1216
Dpon_c4796A      1174 ALIRQPKVLLLDEATSALDAESEKVVQEALDNAKQGRTCLTIAHRLTTIQ 1223
Dpon_c306        1160 ALIRHPKVLLLDEATSALDAESEKVVQDALDNAKQGRTCLTIAHRLTTIQ 1209
Dvv-isotig11620  1170 ALVRNPKVLLLDEATSALDTESEKVVQEALDQAKKGRTCVTIAHRLTTIQ 1219
Dvv-isotig07787  1171 ALVQNPKILLLDEATSALDTESEKVVQAALDEAKKGRTCITIAHRLTTIQ 1220
CpABC12          1173 ALVRNPKVLLLDEATSALDTESEKIVQEALDQAKMGRTCITIAHRLSTIQ 1222
Ct-ABCB1         1173 ALVRNPKVLLLDEATSALDTESEKVVQEALDQAKLGRTCITIAHRLSTIQ 1222
                      **.. **.*********** ** *.** **. *.  ***.******.***

TcABCB-3A        1233 DADLICVLNEGVVAEMGKHNELLDKKGLYYDFYKLQTGQK   1272
Dpon_c4796B      1210 DADVICVVKEGQIAEMGTHGELLKLKGHYYDYYKMQSGQN   1249
CpABC6           1202 DADLICVLEKGMVAEMGDHQTLLQRRGLYYEFYKLQTCQ    1240
Dvv-isotig11596  1205 DADVICVLKEGNVVEMGTHKELLEKQGLYYKFYKLQSVESIS 1246
CpABC10          1218 DADVICVLKEGFIAEMGTHTELLIKRGMYYKFYKLQAGQT   1257
TcABCB-3B        1226 DADVICVIDKGVVAEIGTHSELLSQKGLYYKLHSLQNK     1263
Dpon_c80822      1217 DADVICVVNEGVIAEQGTHSELIEKKGLYYKLHALQH      1253
Dpon_c4796A      1224 DADLICVVNDGVIVEQGNHTDLIERKGLYYRLHAHQH      1260
Dpon_c306        1210 DADLICVVNNGVIVEQGAHTDLIERNGLYYRLYARQHYFL   1249
Dvv-isotig11620  1220 DADLICVVANGVIAESGSHQELLQKEGLYYKLYTQKT      1256
Dvv-isotig07787  1221 DADIIYVIDKGIVVESGTHRELLNKNGFYYKLYTQKH      1257
CpABC12          1223 DADMICVIDRGIVAEAGTHAELLEKKGLYYKLQRQAT      1259
Ct-ABCB1         1223 DADMICVIDRGIVAEAGTHAELLEKKGLYYKLQRQTT      125
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Figure S5. CLUSTAL Alignment of ABCB protein sequences from Coleoptera. CRW424: Chromosome 8 marker linked to Cry3Bb resistance in *Diabrotica virgifera virgifera* (Ref. [17]). Other abbreviations as in Figure S4. * The asterisks denote identical amino acids and the dots denote conserved amino acids.