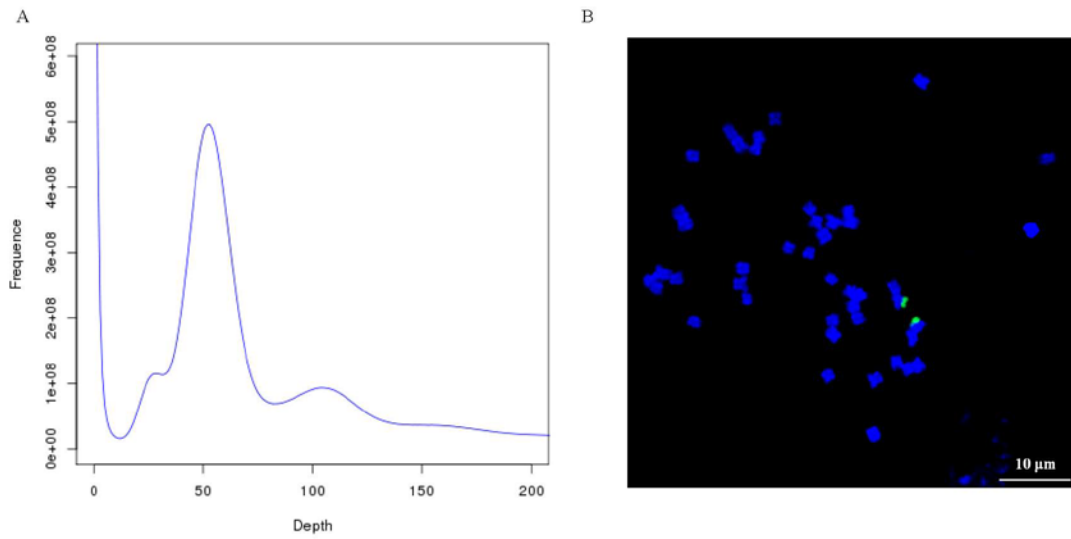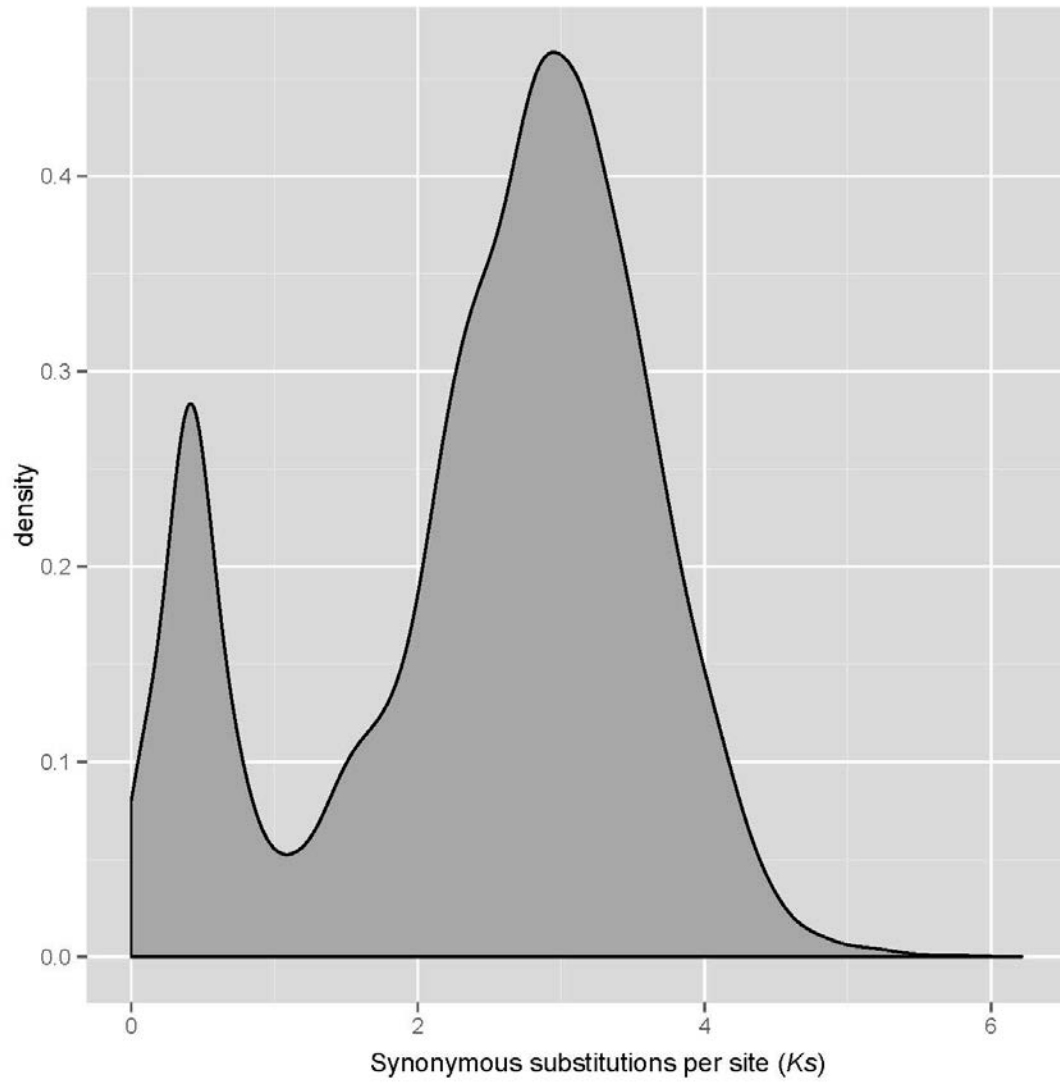## Supplementary Figures

Figure S1. A. 17 K-mer analysis for estimating the genome size of *Neolamarckia cadamba* B. Cytological analysis of *Neolamarckia cadamba* metaphase chromosomes by FISH using 45s rDNA as probe. 45S rDNA was labeled with Chroma Tide Alexa Fluor 488 (green signal), and the chromosomes were counterstained with DAPI (blue). Bars = 10 μm

**Figure S2. Estimation of synonymous substitutions per site (*Ks*) in *N. cadamba* genome**
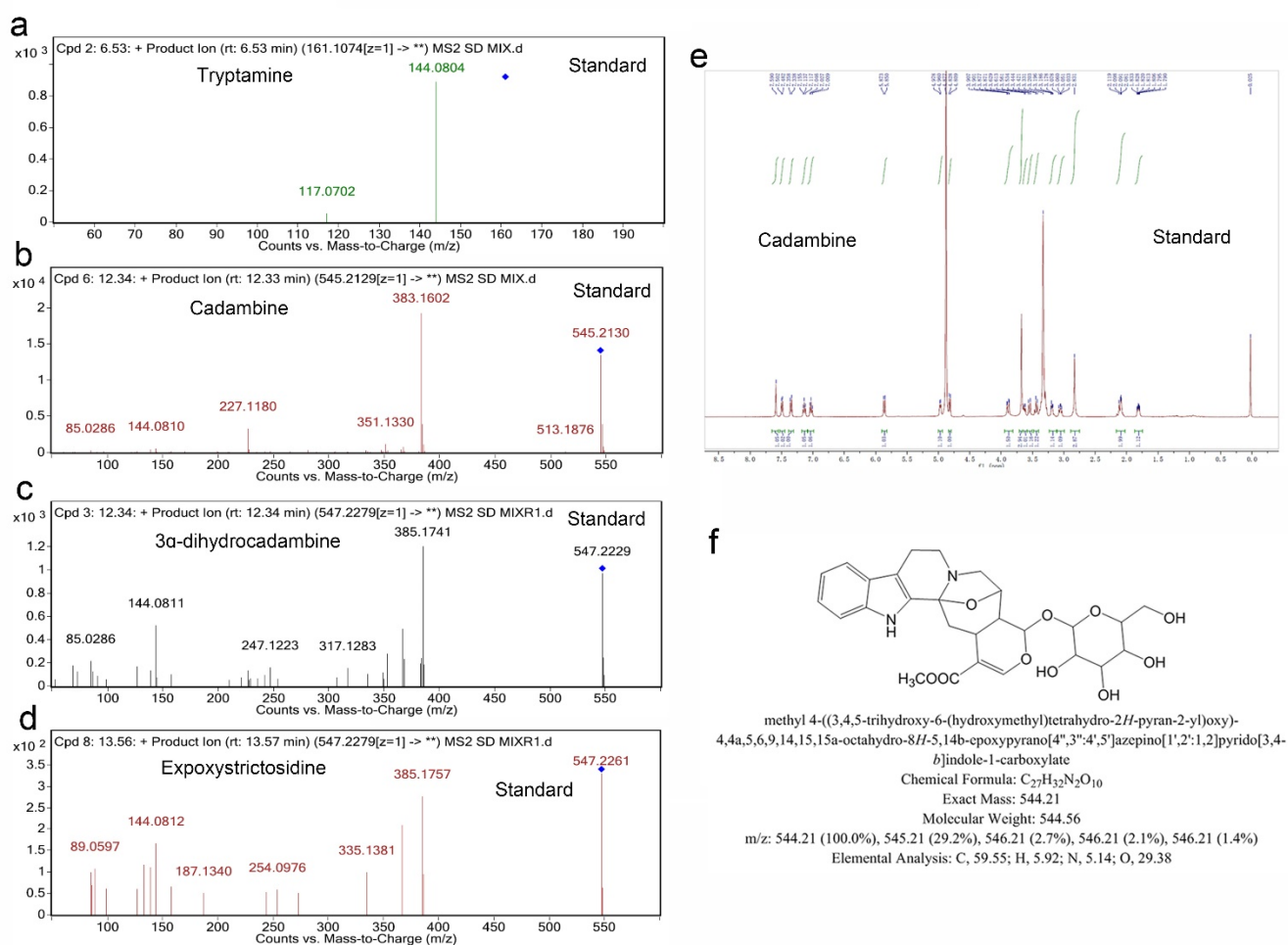
Figure S3 Characterization of standard compounds by Q-TOF LC-MS/MS and NMR. Tryptamine, expoxystrictosidine, 3α-dihydrocadambine and cadambine used as standards (see "Methods") were analyzed by Q-TOF LC-MS/MS. Cadambine was further tested by NMR to verify its structural formula. NMR spectra were carried out on a Bruker AV 400 spectrometer in CD$_3$OD using tetramethylsilane (TMS, δ = 0) as internal reference. ^{1}H NMR(CD3OD, 400MHz)δ = 7.59 (1H，s), δ = 7.48 (1H，d), δ = 7.34 (1H，d), δ = 7.12 (1H，t), δ = 7.01 (1H，t), δ = 5.85 (1H, d), δ = 4.96 (1H，d), δ = 4.81 (1H，d), δ = 3.90 (1H，m), δ = 3.53 (1H，m), δ = 3.63 (3H， s), δ = 3.56 (1H，m), δ = 3.42 (1H，m), δ = 3.18 (1H，m), δ = 3.03 (1H，m), δ = 2.08 (2H，m), δ = 1.79 (1H，m). In accordance with the results of Handa *et al.* (1983) and Xu *et al.* (2011), this compound is characterized as cadambine. **a-d** MS/MS spectrum of tryptamine (a), cadambine (b), 3α-dihydrocadambine (c) and expoxystrictosidine (d). **e** NMR spectrum of cadambine. **f** The structural formula of cadambine.
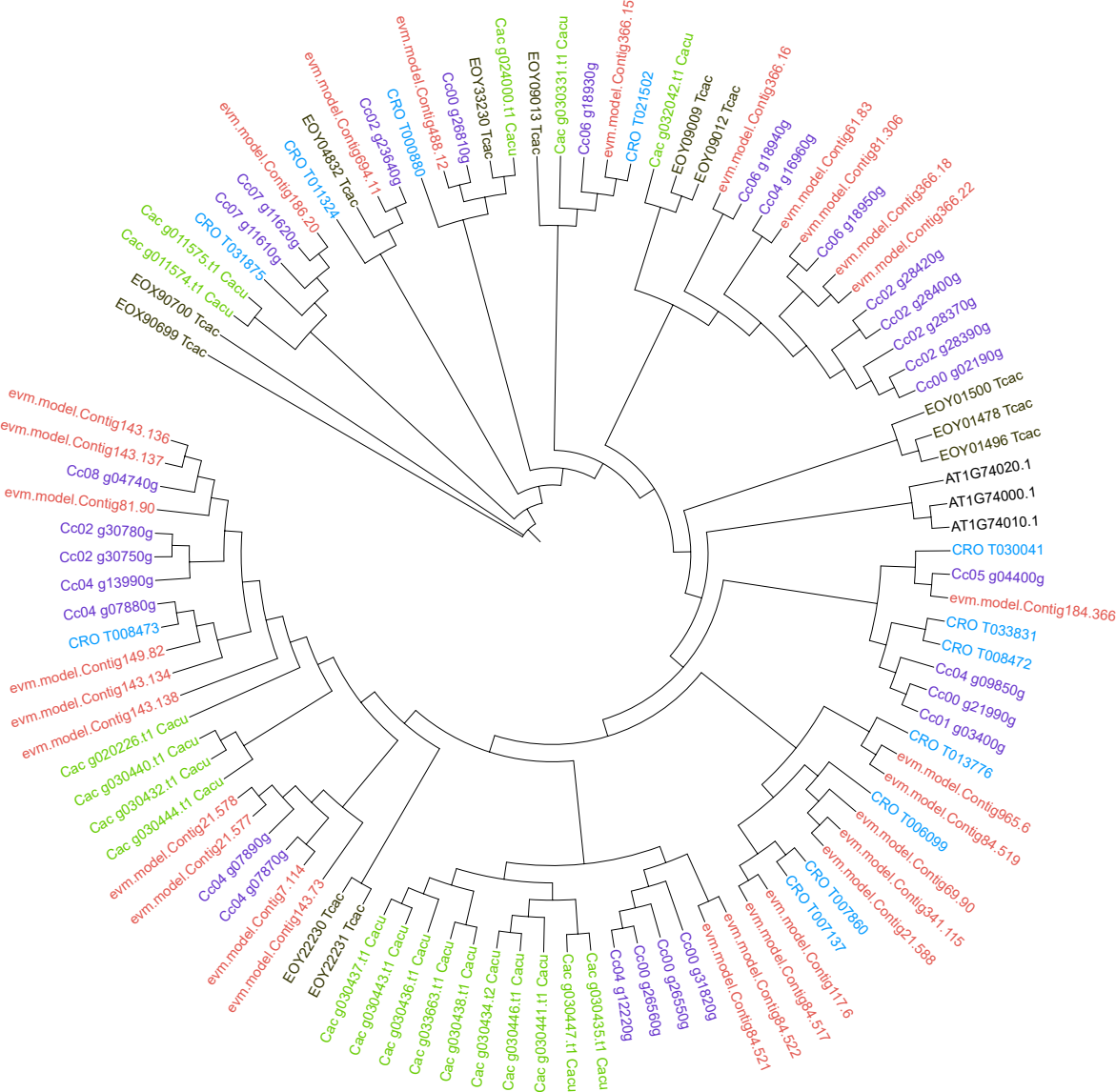
Figure S4. Phylogenetic tree of STR genes from six plant species. The genes from *Arabidopsis thaliana* (AT) , *Catharanthus roseus* (CRO), *Coffea canephora* (Cc), Camptotheca acuminate (Cac), *N. cadamba* (evm.model) and *Theobroma cacao* (EOY).
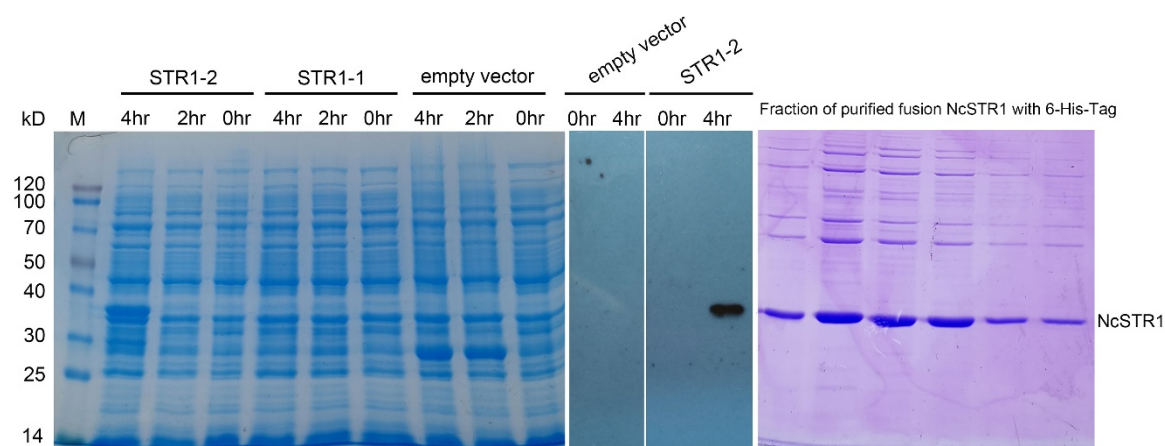
Figure S5. *In vitro* **expressed fusion NcSTR1. Left,** SDS-PAGE of NcSTR1 expressed in *E. coli* and the strain STR1-2 successfully expressed His-tagged NcSTR1; **Middle,** *in vitro* expressed fusion NcSTR1 validated by immunoblotting; **Right**, SDS-PAGE of purified fusion NcSTR1 by His-trap.
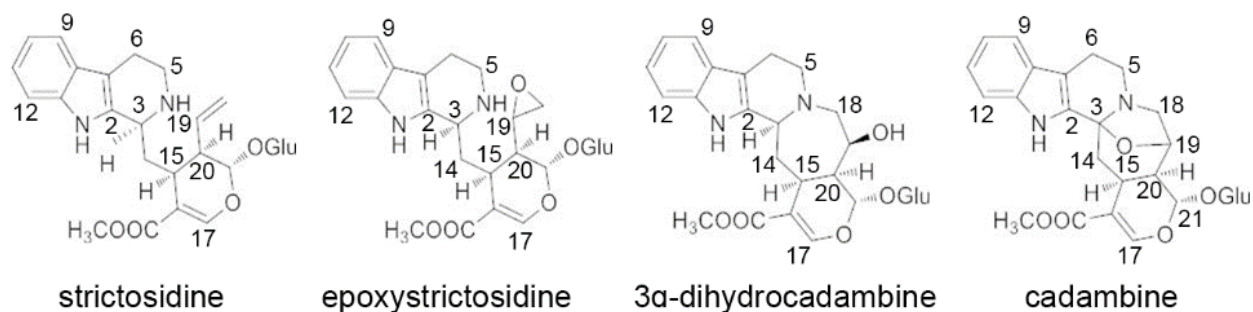
Figure S6 Chemical structures of strictosidine, 3α-dihydrocadambine cadambine and predicted expoxystrictosidine
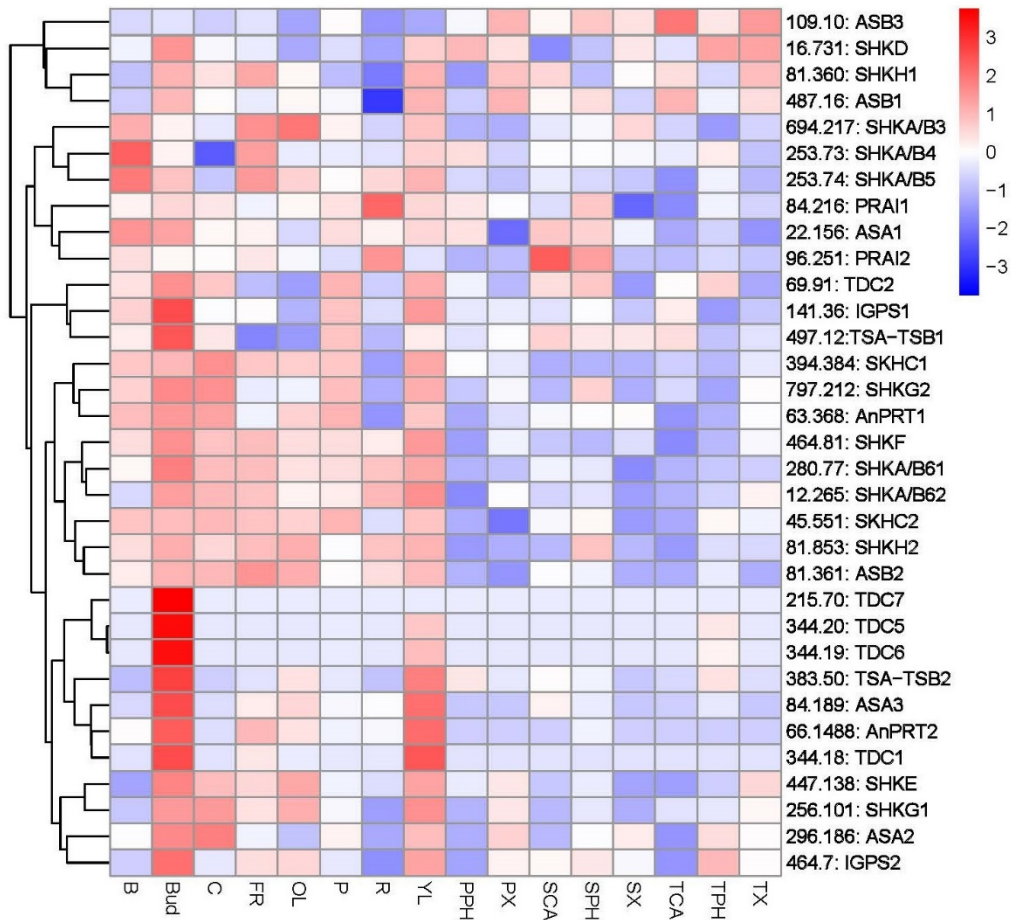
Figure S7 The expression profile of all the predicted biosynthetic genes in

Shikimate pathway. Bark (B), bud, cambium (C), young fruit (FR), old leaves (OL), phloem (P), root (R), young leaves (YL), xylem (primary xylem, PX; transitional xylem, TX; secondary xylem, SX), cambium (transitional cambium, TCA; secondary, SCA) and phloem (primary phloem, PPH; transitional phloem, TPH; secondary phloem, SPH) from the first, second and fourth internodes. The second internode of 1-year-old seedling was identified as the transition from primary growth to secondary growth . AnPRT, anthranilate phosphoribosyltransferase; ASA/B, anthranilate synthase ; IGPS, indole-3-glycerol phosphate synthase; PRAI, N-(5-phospho-beta-D-ribosyl) anthranilate aldose-ketose-isomerase; SHKA/B, 3-deoxy-7-phosphoheptulonate synthase; SKHC,3-dehydroquinate synthase; SHKD, 3-dehydroquinate dehydratase; SHKE, shikimate dehydrogenase; SHKF, shikimate kinase; SHKG, 3-phosphoshikimate 1-carboxyvinyltransferase; SHKH，chorismate synthase；TDC, tryptophan decarboxylase; TSA-TSB,tryptophan synthase.
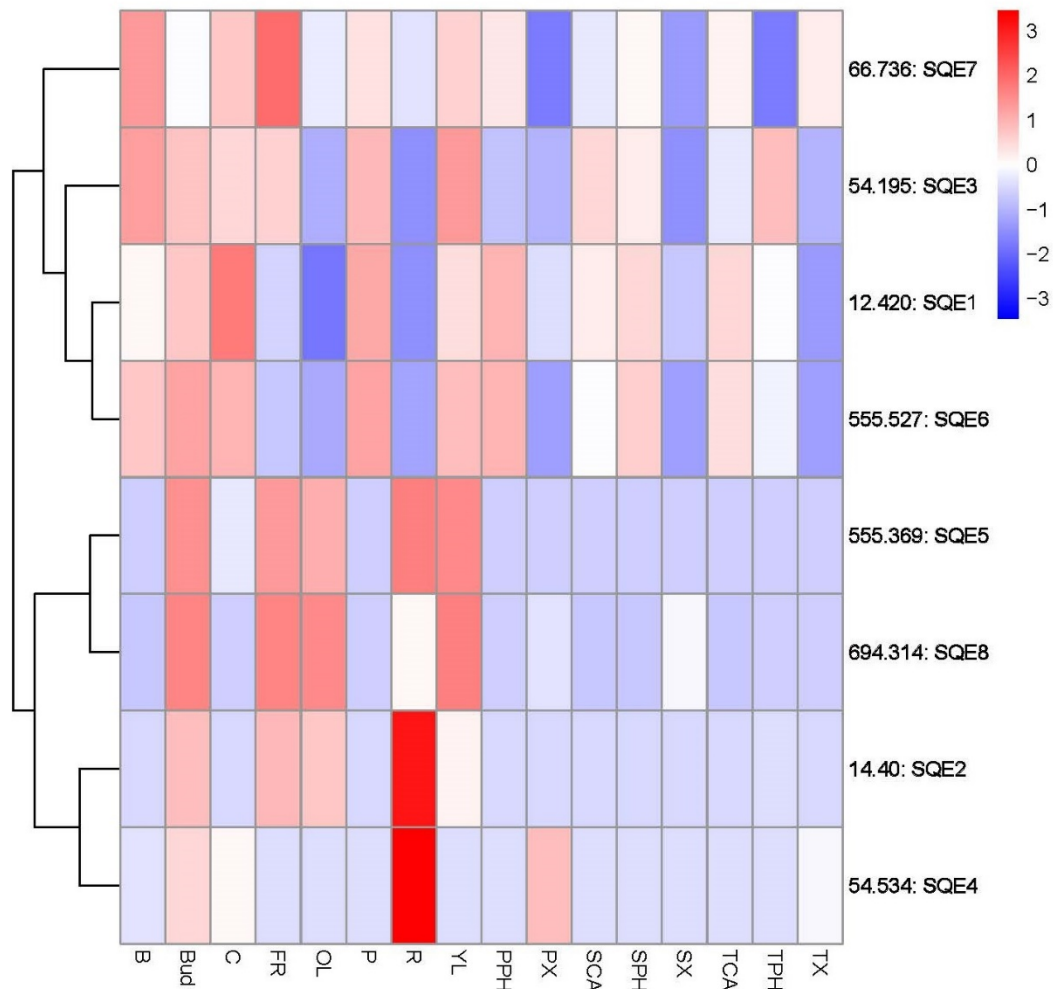
Figure S8 The expression profile of all the predicted squalene epoxidase genes (NcSQEs).
Bark (B), bud, cambium (C), young fruit (FR), old leaves (OL), phloem (P), root (R), young leaves (YL), xylem (primary xylem, PX; transitional xylem, TX; secondary xylem, SX), cambium (transitional cambium, TCA; secondary, SCA) and phloem (primary phloem, PPH; transitional phloem, TPH; secondary phloem, SPH) from the first, second and fourth internodes.
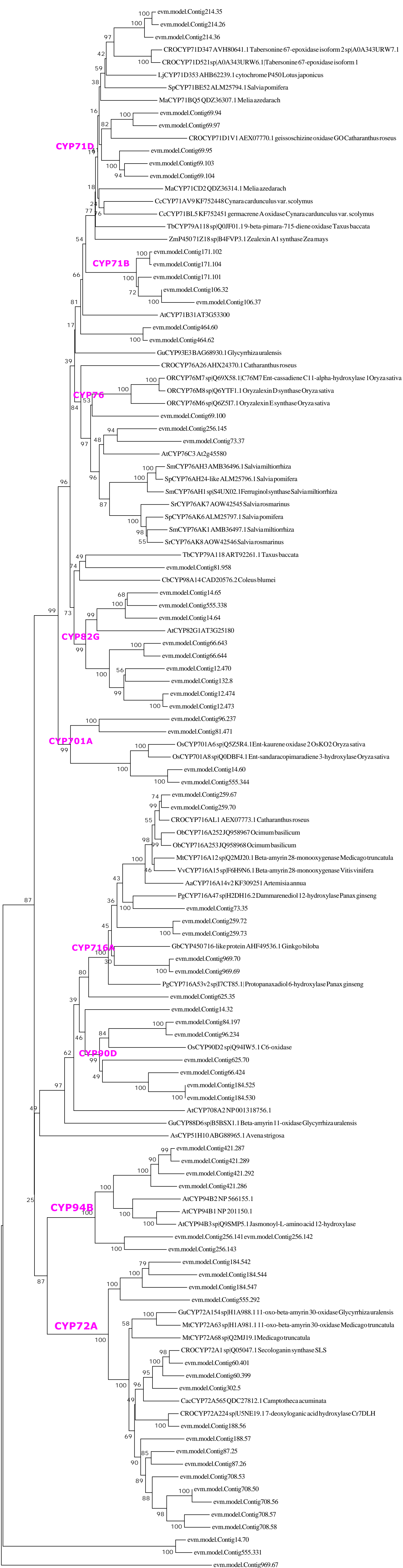
Figure S9. Phylogenetic tree of NcCYPs in BGCs and 52 functionally characterized plant CYP family members involved in terpenoid biosynthesis.

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                                            *         20              *
evm.model.Contig267.36. : MAPTMDT-IPSVEIKDMPE--EAHPMKGGD : 27
evm.model.Contig625.59. : MAPTMDTPTPSLDIKEMPE--EAHPMKGGH : 28
evm.model.Contig81.1046 : M----------ELH-----EFLHMNGGE : 13
CrLAMT_CRO_T028497_LAMT : MVATID----SIEMPALPTAVEAHPMKGGD : 26
Ca_12__768.1_COFAR_LAMT : MENGNH----SAETKEKP---ESHPMNGGD : 23
Ca__XMT1__Q9AVK0.1      : M----------ELQ-----EVLRMNGGE : 13
Cc_XMT1___Cc09_g06970g. : M----------ELQ-----EVLRMNGGE : 13
Ca__MXMT1__XP_027086104 : M----------ELQ-----EVLHMNEGE : 13
CTS1_AB034700_AB034700. : M----------ELQ-----EVLHMNEGE : 13
Cc_MXMT2_Cc00_g24720XMT : M----------ELQ-----EVLHMNEGE : 13
CTS2_AB054841_AB054841. : M----------ELQ-----AVLHMNGGE : 13
CaDXMT1_BAC75663.1_DXMT : M----------ELQ-----EVLHMNGGE : 13
Cc__DXMT1__Cc01_g00720g : M----------ELQ-----EVLHMNGGE : 13
CbSAMT_AAF00108__CbSAMT : M----------DVR-----QVLHMKGGA : 13
PCS1_AB207817_AB207817. : M----------GKVN-----EVLFMNRGE : 14
TCS1_AB031280_AB031280. : MELATA-----GKVN-----EVLFMNRGE : 19
                          M                      M  G


                                            40         *              60
evm.model.Contig267.36. : DLNSYSQNSSYQRGVIDAAKTVIVEAVTEK : 57
evm.model.Contig625.59. : DINSYSQNSCYQKGVIDAAKSVIIEAVTEK : 58
evm.model.Contig81.1046 : DELSYAKNSSQQKLVLMKAKPVLEKCIEEL : 43
CrLAMT_CRO_T028497_LAMT : DSHSYSQNSCYQKGVIDAAKAVIVEAVNEK : 56
Ca_12__768.1_COFAR_LAMT : DSKSYAQNSSYQKGVIEAAKREIVQAIKER : 53
Ca__XMT1__Q9AVK0.1      : GDTSYAKNSAYNQLVLAKVKPVLEQCVREL : 43
Cc_XMT1___Cc09_g06970g. : GDTSYAKNSAYNQLVLAKVKPVLEQCVREL : 43
Ca__MXMT1__XP_027086104 : GDTSYAKNASYN-LALAKVKPFLEQCIREL : 42
CTS1_AB034700_AB034700. : GDTSYAKNASYN-LALAKVKPFLEQCIREL : 42
Cc_MXMT2_Cc00_g24720XMT : GDTSYAKNASYN-LALAKVKPFLEQCIREL : 42
CTS2_AB054841_AB054841. : GDTSYAKNSSYN-LALAKVKPVLEQCIREL : 42
CaDXMT1_BAC75663.1_DXMT : GDTSYAKNSFYN-LFLIRVKPILEQCIQEL : 42
Cc__DXMT1__Cc01_g00720g : GDTSYAKNSSYN-LFLIRVKPVLEQCIQEL : 42
CbSAMT_AAF00108__CbSAMT : GENSYAMNSFIQRQVISITKPITEAAITAL : 43
PCS1_AB207817_AB207817. : GEISYAQNSAFTQKVASMAMPALENAVETL : 44
TCS1_AB031280_AB031280. : GESSYAQNSSFTQQVASMAQPALENAVETL : 49
                          S Cr Y31 ANS Y37 Q38      k        e


                                            *         80              *
evm.model.Contig267.36. : LDLENN-ANFNPSKPFRIADFGCSTGPNTY : 86
evm.model.Contig625.59. : LDLENNITTFDPSKPFHIADFGCSTGPNTY : 88
evm.model.Contig81.1046 : MSTNL-----HLHKCLKIADLGCSSGPNTF : 68
CrLAMT_CRO_T028497_LAMT : LDLENN-PIFDPIKPFRIADFGCSTGPNTF : 85
Ca_12__768.1_COFAR_LAMT : LDIEK-----VWPRRFVIADFGCSTGPNTF : 78
Ca__XMT1__Q9AVK0.1_     : LRANLP----NINKCIKVADLGCASGPNTL : 69
Cc_XMT1___Cc09_g06970g. : LRANLP----NINKCIKVADLGCASGPNTL : 69
Ca__MXMT1__XP_027086104 : LRANLP----NINKCIKVADLGCASGPNTL : 68
CTS1_AB034700_AB034700. : LRANLP----NINKCIKVADLGCASGPNTL : 68
Cc_MXMT2_Cc00_g24720XMT : LRANLP----NINKCIKVADLGCASGPNTL : 68
CTS2_AB054841_AB054841. : LRANLP----NINNCIKVADLGCASGPNTL : 68
CaDXMT1_BAC75663.1_DXMT : LRANLP----NINKCIKVADLGCASGPNTL : 68
Cc__DXMT1__Cc01_g00720g : LRANLP----NINKCFKVGDLGCASGPNTF : 68
CbSAMT_AAF00108__CbSAMT : YSGDT------VTTRLAIADLGCSSGPNAL : 67
PCS1_AB207817_AB207817. : FSKDF-----HLLQALTAADLGCAAGPNTF : 69
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TCS1_AB031280_AB031280. : FSRDF-----HL-QALNAADLGCAAGPNTF :  73
                                        aD GC  GPNt


                                100         *          120
evm.model.Contig267.36. : FAMQNVVEAVGQKYKSLQGK-SQAEFHVFF : 115
evm.model.Contig625.59. : FAMQNVVEAVEQKYKSLK-R-NQPEFHVFF : 116
evm.model.Contig81.1046 : STMLEIIQSIDKACRKLNLE--PPVIQFFL :  96
CrLAMT_CRO_T028497_LAMT  : HAMQNIVESVETKYKSLQ---KTPEFHVFF : 112
Ca_12__768.1_COFAR_LAMT  : LAMQNIVEAVEQKNKSLQQN-PTIDFHVFF : 107
Ca__XMT1__Q9AVK0.1_      : LTVRDIVQSIDKVGQEKKNELERPTIQIFL :  99
Cc_XMT1___Cc09_g06970g.  : LTVRDIVQSIDKVGQEKKNELERPTIQIFL :  99
Ca__MXMT1__XP_027086104  : LTVRDIVQSIDKVGQEEKNELERPTIQIFL :  98
CTS1_AB034700_AB034700.  : LTVRDIVQSIDKVGQEKNELERPTIQIFL  :  98
Cc_MXMT2_Cc00_g24720XMT  : LTVRDIVQSIDKVGQEKNELERPTIQIFL  :  98
CTS2_AB054841_AB054841.  : LTVRDIVQSIDKVGQEKNELERPTIQIFL  :  98
CaDXMT1_BAC75663.1_DXMT  : LTVRDIVQSIDKVGQEKNELERPTIQIFL  :  98
Cc__DXMT1__Cc01_g00720g  : STVRDIVQSIDKVGQEKNELERPTIQIFL  :  98
CbSAMT_AAF00108__CbSAMT  : FAVTELIKTVEELRKKMGRE-NSPEYQIFL :  96
PCS1_AB207817_AB207817.  : AVISTIKRMMEKKCRELYCQ--TLELQVYL :  97
TCS1_AB031280_AB031280.  : AVISTIKRMMEKKCRELNCQ--TLELQVYL : 101


                                  *          140          *
evm.model.Contig267.36. : NDHVNNDFNILFRSLPQDRN---------- : 135
evm.model.Contig625.59. : NDHVNNDFNILFRSLPQKRD---------- : 136
evm.model.Contig81.1046 : NDLIGNDFNAVFKSLPSFYEKLEKENGREY : 126
CrLAMT_CRO_T028497_LAMT  : NDHVNNDFNVLFRSLPPNRE---------- : 132
Ca_12__768.1_COFAR_LAMT  : NDIVDNDFNTLFKSLPSHPR---------- : 127
Ca__XMT1__Q9AVK0.1       : NDLFPNDFNSVFKLLPSFYRKLEKENGRKI : 129
Cc_XMT1___Cc09_g06970g.  : NDLFPNDFNSVFKLLPSFYRKLEKENGRKI : 129
Ca__MXMT1__XP_027086104  : NDLFQNDFNSVFKLLPSFYRKLEKENGRKI : 128
CTS1_AB034700_AB034700.  : NDLFQNDFNSVFKLLPSFYRKLEKENGRKI : 128
Cc_MXMT2_Cc00_g24720XMT  : NDLFQNDFNSVFKLLPSFYRKLEKENGRKI : 128
CTS2_AB054841_AB054841.  : NDLFQNDFNSVFKLLPSFYRKLEKENGRKI : 128
CaDXMT1_BAC75663.1_DXMT  : NDLFQNDFNSVFKSLPSFYRKLEKENGRKI : 128
Cc__DXMT1__Cc01_g00720g  : NDLFQNDFNSVFKLLPSFYRNLEKENGRKI : 128
CbSAMT_AAF00108__CbSAMT  : NDLPGNDFNAIFRSLPIEND--------VD : 118
PCS1_AB207817_AB207817.  : NDLFGNDFNTLFKGLSSQVV----GNKCEE : 123
TCS1_AB031280_AB031280.  : NDLFGNDFNTLFKGLSSEVI----GNKCEE : 127
                           NDl   NDFN  F   Lp


                                160          *          180
evm.model.Contig267.36. : --YFAAGVPGSFYTRVFPKASLHFAHCSYA : 163
evm.model.Contig625.59. : --YFAAGVPGSFYTRVFPKASLHFAHCSYA : 164
evm.model.Contig81.1046 : GSCLVAATPGSFYGRLFPKDSLDFVHSSYS : 156
CrLAMT_CRO_T028497_LAMT  : --FFAAGVPGSFYTRVFPKNSIHFAHCSYA : 160
Ca_12__768.1_COFAR_LAMT  : --YFVAVPGSFYERLFPKASLDLANSSYA  : 155
Ca__XMT1__Q9AVK0.1       : GSCLIGAMPGSFYSRLFPEESMHFLHSCYC : 159
Cc_XMT1___Cc09_g06970g.  : GSCLIGAMPGSFYSRLFPEESMHFLHSCYC : 159
Ca__MXMT1__XP_027086104  : GSCLISAMPGSFYGRLFPEESMHFLHSCYS : 158
CTS1_AB034700_AB034700.  : GSCLISAMPGSFYGRLFPEESMHFLHSCYS : 158
Cc_MXMT2_Cc00_g24720XMT  : GSCLISAMPGSFYGRLFPEESMHFLHSCYS : 158
CTS2_AB054841_AB054841.  : GSCLISAMPGSFYGRLFPEESMHFIHSCYS : 158
CaDXMT1_BAC75663.1_DXMT  : GSCLIGAMPGSFYGRLFPEESMHFLHSCYC : 158
Cc__DXMT1__Cc01_g00720g  : GSCLIGAMPGSFYSRLFPEESMHFLHSCYC : 158
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PCS1_AB207817_AB207817.    : VSCYVMGVPGSFHGRLFPRNSLHLVHSSYS : 153
TCS1_AB031280_AB031280.    : VPCYVMGVPGSFHGRLFPRNSLHLVHSSYS : 157
                                   PGSFy R FP    hf hs  CrY159

                                  *         200        *
evm.model.Contig267.36.    : LHWLSKVPKEIQDKNSP-AFNRGRIHYTGT : 192
evm.model.Contig625.59.    : LHWLSKVPKEIQDKNSP-AFNKGRIHYTGT : 193
evm.model.Contig81.1046    : IHWLSQVPEGLVTESGIPDLNKGNIYVTKT : 186
CrLAMT_CRO_T028497_LAMT    : LHWLSKVPKEIQDKNSL-AYNKGRIHYTGT : 189
Ca_12__768.1_COFAR_LAMT    : LHWLSKVPKEVGDQNSL-AWNKSKTYCSGS : 184
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Cc_XMT1___Cc09_g06970g.    : LQWLSQVPSGLVTELGI-GTNKGSIYSSKA : 188
Ca_MXMT1__XP_027086104     : VHWLSQVPSGLVIELGI-GANKGSIYSSKG : 187
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Cc_MXMT2_Cc00_g24720XMT    : VHWLSQVPSGLVIELGI-GANKGSIYSSKA : 187
CTS2_AB054841_AB054841.    : FHWLSQVPSGLVIELGI-SANKGSIYSSKA : 187
CaDXMT1_BAC75663.1_DXMT    : LHWLSQVPSGLVTELGI-SANKGCIYSSKA : 187
Cc__DXMT1__Cc01_g00720g    : LHWLSQVPSGLVTELGI-SVNKGCIYSSKA : 187
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PCS1_AB207817_AB207817.    : VHWLTQAPKGLTSREGL-ALNKGKIYISKT : 182
TCS1_AB031280_AB031280.    : VHWLTQAPKGLTSREGL-ALNKGKIYISKT : 186
                               CrH162W163             Ng iy
                               CcQ161

                                  220        *        240
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evm.model.Contig625.59.    : EKH-VVKAYFGQFQKDMDAFLKARALEIVG : 222
evm.model.Contig81.1046    : TPAGVHQAYLDQFTKDLMKFLRLRSEEMVP : 216
CrLAMT_CRO_T028497_LAMT    : EKH-VVKAYFGQFQRDFEGFLKARAQEIVV : 218
Ca_12__768.1_COFAR_LAMT    : KKE-VTEAYFAQFRKDLNRFLDARAEELVR : 213
Ca__XMT1__Q9AVK0.1_        : SRLPVQKAYLDQFTKDFTTFLRIHSEELFS : 218
Cc_XMT1___Cc09_g06970g.    : SRLPVQKAYLDQFTKDFTTFLRIHSEELFS : 218
Ca_MXMT1__XP_027086104     : CRPPVQKAYLDQFTKDFTTFLRIHSKELFS : 217
CTS1_AB034700_AB034700.    : CRPPVQKAYLDQFTKDFTTFLRIHSKELFS : 217
Cc_MXMT2_Cc00_g24720XMT    : SRPPVQKAYLDQFTKDFTTFLRIHSKELFS : 217
CTS2_AB054841_AB054841.    : SRPPVQKAYLDQFTKDFTTFLRIHSKELFS : 217
CaDXMT1_BAC75663.1_DXMT    : SRPPIQKAYLDQFTKDFTTFLRIHSEELIS : 217
Cc__DXMT1__Cc01_g00720g    : SRPPIQKAYLDQFTKDFTTFLRIHSEELIS : 217
CbSAMT_AAF00108__CbSAMT    : CPQSVLNAYYKQFQEDHALFLRCRAQEVVP : 201
PCS1_AB207817_AB207817.    : SPPVVKKAYLSQFHEDFTMFLNARSQEVVP : 212
TCS1_AB031280_AB031280.    : SPPVVREAYLSQFHEDFTMFLNARSQEVVP : 216
                               AY   QF D   FL     E

                                  *         260        *
evm.model.Contig267.36.    : GGLMVIQIPGLPSGEVLFSRTGAGMLHGLL : 251
evm.model.Contig625.59.    : GGLMVIQIPGLPSGEVLFSRTGAGMLHALL : 252
evm.model.Contig81.1046    : RGHLLLTLLGKGDE------ADGSGTLDLL : 240
CrLAMT_CRO_T028497_LAMT    : GGLMVIQIPGLPSGEVLFSRTGAGLLHFLL : 248
Ca_12__768.1_COFAR_LAMT    : GGLLVIQLPGVPRGALPFN-TGAGFIQELL : 242
Ca__XMT1__Q9AVK0.1_        : HGRMLLTCICKGVE------LDARNAIDLL : 242
Cc_XMT1___Cc09_g06970g.    : HGRMLLTCICKGVE------LDARNAIDLL : 242
Ca_MXMT1__XP_027086104     : RGRMLLTCICKVDE------FDEPNPLDLL : 241
CTS1_AB034700_AB034700.    : RGRMLLTCICKVDV------FDEPNPLDLL : 241
Cc_MXMT2_Cc00_g24720XMT    : RGRMLLTCICKVDE------YDEPNPLDLL : 241
CTS2_AB054841_AB054841.    : RGRMLLTCICKVDE------YDEPNPLDLL : 241
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CaDXMT1_BAC75663.1_DXMT : RGRMLLTWICKEDE------FENPNSIDLL : 241
Cc__DXMT1__Cc01_g00720g : RGRMLLTFICKEDE------FDHPNSMDLL : 241
CbSAMT_AAF00108__CbSAMT : GGRMVLTILGRRSEDR--ASTECCLIWQLL : 229
PCS1_AB207817_AB207817. : NGCMVLILHGRQSSDP--SEMESCFTWELL : 240
TCS1_AB031280_AB031280. : NGCMVLILRGRQCSDP--SDMQSCFTWELL : 244
                              G            CrP227           CrA241H24L
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                                  280        *        300
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evm.model.Contig625.59. : GASLMELINLGVISEESVDSFNLPQYHPSI : 282
evm.model.Contig81.1046 : GMALNDMIFEGYVEEKLDSFNIPQYIPTV : 270
CrLAMT_CRO_T028497_LAMT : GTSLMELVNKGIINEESVDSFNLPQYHPSV : 278
Ca_12__768.1_COFAR_LAMT : GPCLFEMADLGFISHEKVHSFNLPMYFPSI : 272
Ca__XMT1__Q9AVK0.1_     : EMAINDLVVEGHLEEEKLDSFNLPVYIPSA : 272
Cc_XMT1___Cc09_g06970g. : EMAINDLVVEGHLEEEKLDSFNLPVYIPSA : 272
Ca__MXMT1__XP_027086104 : DMAINDLIVEGLLEEEKLDSFNIPFFTPSA : 271
CTS1_AB034700_AB034700. : DMAINDLIVEGLLEEEKLDSFNIPFFTPSA : 271
Cc_MXMT2_Cc00_g24720XMT : DMAINDLIVEGHLEEEKLASFNLPFFTPSA : 271
CTS2_AB054841_AB054841. : DMAINDLIVEGHLEEEKLASFNLPFFTPSA : 271
CaDXMT1_BAC75663.1_DXMT : EMSINDLVIEGHLEEEKLDSFNVPIYAPST : 271
Cc__DXMT1__Cc01_g00720g : EMSINDLVIEGHLEEEKLDSFNVPIYAPST : 271
CbSAMT_AAF00108__CbSAMT : AMALNQMVSEGLIEEEKMDKFNIPQYTPSP : 259
PCS1_AB207817_AB207817. : AIAIAELVSQGLIDKDKLDTFNVPSYWPSL : 270
TCS1_AB031280_AB031280. : AMAIAELVSQGLIDEDKLDTFNIPSYFASL : 274
                             G     eek d FN P   CrQ273 H275
                                                   CcI266
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                            *          320          *
evm.model.Contig267.36. : EELEMVIEMNNSFTLEKVGALNHPMKNLPF : 311
evm.model.Contig625.59. : EELEMVIEMNNSFTLEKVGALNHPMKNSPF : 312
evm.model.Contig81.1046 : EEIRNIIQKEGSFRILNLEIVQLRFDSSFC : 300
CrLAMT_CRO_T028497_LAMT : EDLEMVIEMNDCFTIERVGTLPHPMKNLPF : 308
Ca_12__768.1_COFAR_LAMT : EELDLVIKGNGHFTAERIKILNHPMQHLPF : 302
Ca__XMT1__Q9AVK0.1_     : EEVKCIVEEEGSFEILYLETFKVLYDAGFS : 302
Cc_XMT1___Cc09_g06970g. : EEVKCIVEEEGSFEILYLETFKVLYDAGFS : 302
Ca__MXMT1__XP_027086104 : EEVKCIVEEEGSCEILYLETFKAHYDAAFS : 301
CTS1_AB034700_AB034700. : EEVKCIVEEEGSCEILYLETFKAHYDAAFS : 301
Cc_MXMT2_Cc00_g24720XMT : EEVKCIVEEEGSFEILYLETFKAHYDAGFS : 301
CTS2_AB054841_AB054841. : EEVKCIVEEEGSFEILYLETFKAHYDAGFS : 301
CaDXMT1_BAC75663.1_DXMT : EEVKCIVEEEGSFEILYLETFKVPYDAGFS : 301
Cc__DXMT1__Cc01_g00720g : EEVKRIVEEEGSFEILYLETFNAPYDAGFS : 301
CbSAMT_AAF00108__CbSAMT : TEVEAEILKEGSFLIDHIEASEIYWSSCTK : 289
PCS1_AB207817_AB207817. : EEVKDIVERDGSFTIDHLEGFELDSLEMQE : 300
TCS1_AB031280_AB031280. : EEVKDIVERDGSFTIDHIEGFDLDSVEMQE : 304
                          ee        gsf              CrP330
```

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                                340        *        360
evm.model.Contig267.36. : D--------------------VQMTSLQVRA : 322
evm.model.Contig625.59. : D--------------------VQMTSSQVRA : 323
evm.model.Contig81.1046 : PDD-----NQGPVNSGFDARAAFVARNMRA : 325
CrLAMT_CRO_T028497_LAMT : D--------------------VQRTSLQVRA : 319
Ca_12__768.1_COFAR_LAMT : D--------------------AKMTCLQTRS : 313
Ca__XMT1__Q9AVK0.1_     : IDD------------EHIKAEYVASSVRA : 319
Cc_XMT1___Cc09_g06970g. : IDD------------EHIKAEYVASSVRA : 319
Ca__MXMT1__XP_027086104 : IDDDYPVRSH-----EQIKAEYVASLIRS : 325
CTS1_AB034700_AB034700. : IDDDYPVRSH-----EQIKAEYVASLIRS : 325
```

```
Cc_MXMT2_Cc00_g24720XMT : IDDDYPVRSHFQVYGDEHIKAEYVASLIRS : 331
CTS2_AB054841_AB054841. : IDDDYPVRSHFQVYGDEHIKAEYVASLIRS : 331
CaDXMT1_BAC75663.1_DXMT : IDDDYQGRSHSPVSCDEHARAAHVASVVRS : 331
Cc__DXMT1__Cc01_g00720g : IDDDYQGRSHSPVSCDEHARAAHVASVVRS : 331
CbSAMT_AAF00108__CbSAMT : DGD-----GGGSV----EEEGYNVARCMRA : 310
PCS1_AB207817_AB207817. : DDK--------------WVRGDKFAKMVRA : 316
TCS1_AB031280_AB031280. : NDK--------------WVRGEKFTKVVRA : 320
```
CrQ_{316} R
CcS_{316}

```
                                  *           380          *
evm.model.Contig267.36. : IMEGILGDHFGEKILDQLFEIYTKKLQENY : 352
evm.model.Contig625.59. : IMEGILTDHFGEKILDPLFEIYTKKLQENY : 353
evm.model.Contig81.1046 : VYGPILATHFGEAIMDDLFHSFAKHTAK-- : 353
CrLAMT_CRO_T028497_LAMT : IMECILTEHFGENILDPLFEIYTKNLQENF : 349
Ca_12__768.1_COFAR_LAMT : IFEGFIKDHFEIDIVDQLFDLFAKKLEESC : 343
Ca__XMT1__Q9AVK0.1      : VYEPILASHFGEAIIPDIFHRFAKHAAK-- : 347
Cc_XMT1___Cc09_g06970g. : VYEPILASHFGEAIIPDIFHRFAKHAAK-- : 347
Ca__MXMT1__XP_027086104 : VYEPILASHFGEAIMPDLFHRLAKHAAK-- : 353
CTS1_AB034700_AB034700. : VYEPILASHFGEAIMPDLFHRLAKHAAK-- : 353
Cc_MXMT2_Cc00_g24720XMT : VYEPILASHFGEAIMPDLFHRLAKHAAK-- : 359
CTS2_AB054841_AB054841. : VYEPILASHFGEAIMPDLFHRLAKHAAK-- : 359
CaDXMT1_BAC75663.1_DXMT : IFEPIVASHFGEAIMPDLSHRIAKNAAK-- : 359
Cc__DXMT1__Cc01_g00720g : IYEPILASHFGEAILPDLSHRIAKNAAK-- : 359
CbSAMT_AAF00108__CbSAMT : VAEPLLLDHFGEAIIEDVFHRYKLLIIE-- : 338
PCS1_AB207817_AB207817. : FTEPIISNQFGQEIMDKLYDKFTHILVS-- : 344
TCS1_AB031280_AB031280. : FTEPIISNQFGPEIMDKLYDKFTHIVVS-- : 348
```
CrI_{320} hFg   I   k

```
                                  400           *
evm.model.Contig267.36. : NVFDKEIRRDADLFLVLKRKSN---- : 374
evm.model.Contig625.59. : NVFDKEIRRDADLFLVLKRKSK---- : 375
evm.model.Contig81.1046 : -FLQMGKGAVKSLVISLAKE------ : 372
CrLAMT_CRO_T028497_LAMT : HVFDKEIRKDADLYLVLKRKGN---- : 371
Ca_12__768.1_COFAR_LAMT : TIFDQEIRKDVDLFVLLKR------- : 362
Ca__XMT1__Q9AVK0.1      : -VLPLGKGFYNNLIISLAKKPEKSDV : 372
Cc_XMT1___Cc09_g06970g. : -VLPLGKGFYNNLIISLAKKPEKSDM : 372
Ca__MXMT1__XP_027086104 : -VLHMGKGCYNNLIISLAKKPEKSDV : 378
CTS1_AB034700_AB034700. : -VLHMGKGCYNNLIISLAKKPEKSDV : 378
Cc_MXMT2_Cc00_g24720XMT : -VLHLGKGCYNNLIISLAKKPEKSDV : 384
CTS2_AB054841_AB054841. : -VLHLGKGCYNNLIISLAKKPEKSDM : 384
CaDXMT1_BAC75663.1_DXMT : -VLRSGKGFYDSLIISLAKKPEKSDV : 384
Cc__DXMT1__Cc01_g00720g : -VLRSGKGFYDSVIISLAKKPEKADM : 384
CbSAMT_AAF00108__CbSAMT : -RMSKEKTKFINVIVSLIRKSD---- : 359
PCS1_AB207817_AB207817. : -DLEAELPKTTSIILVLSKIVG---- : 365
TCS1_AB031280_AB031280. : -DLEAKLPKTTSIILVLSKIDG---- : 369
```
CrD_{359} L

Figure S10. Protein alignment of CrLAMT, CcNMTs and their respective Neolamarckia paralogues. The aligned sequences were from *Coffea arabica* (Ca, C), *Coffea canephora* (Cc), *Catharanthus roseus* (Cr), *Clarkia breweri* (Cb).
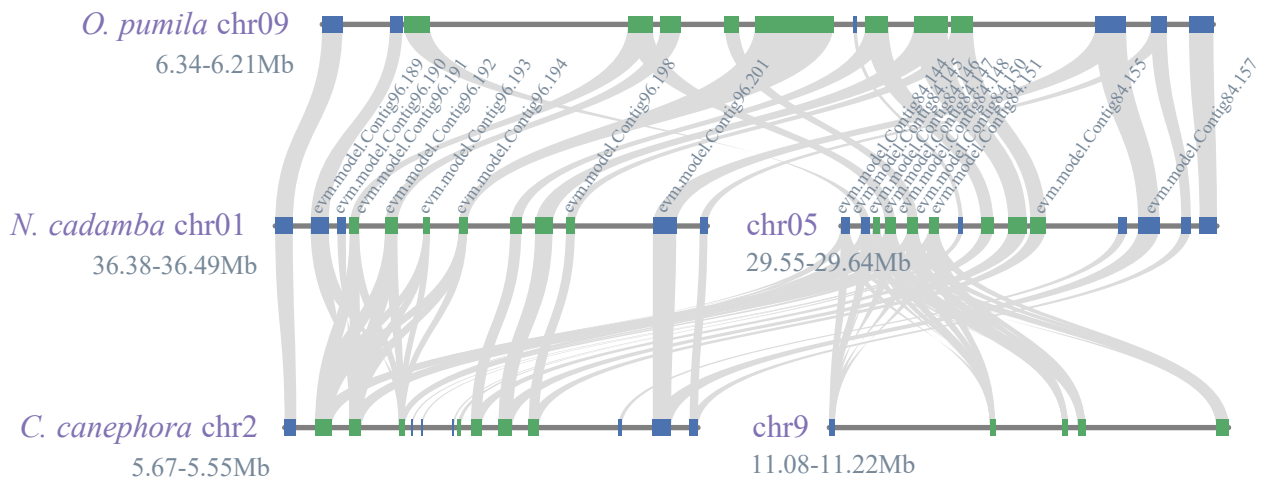
Figure S11 The structure of tandem duplicated NcDLGTs.
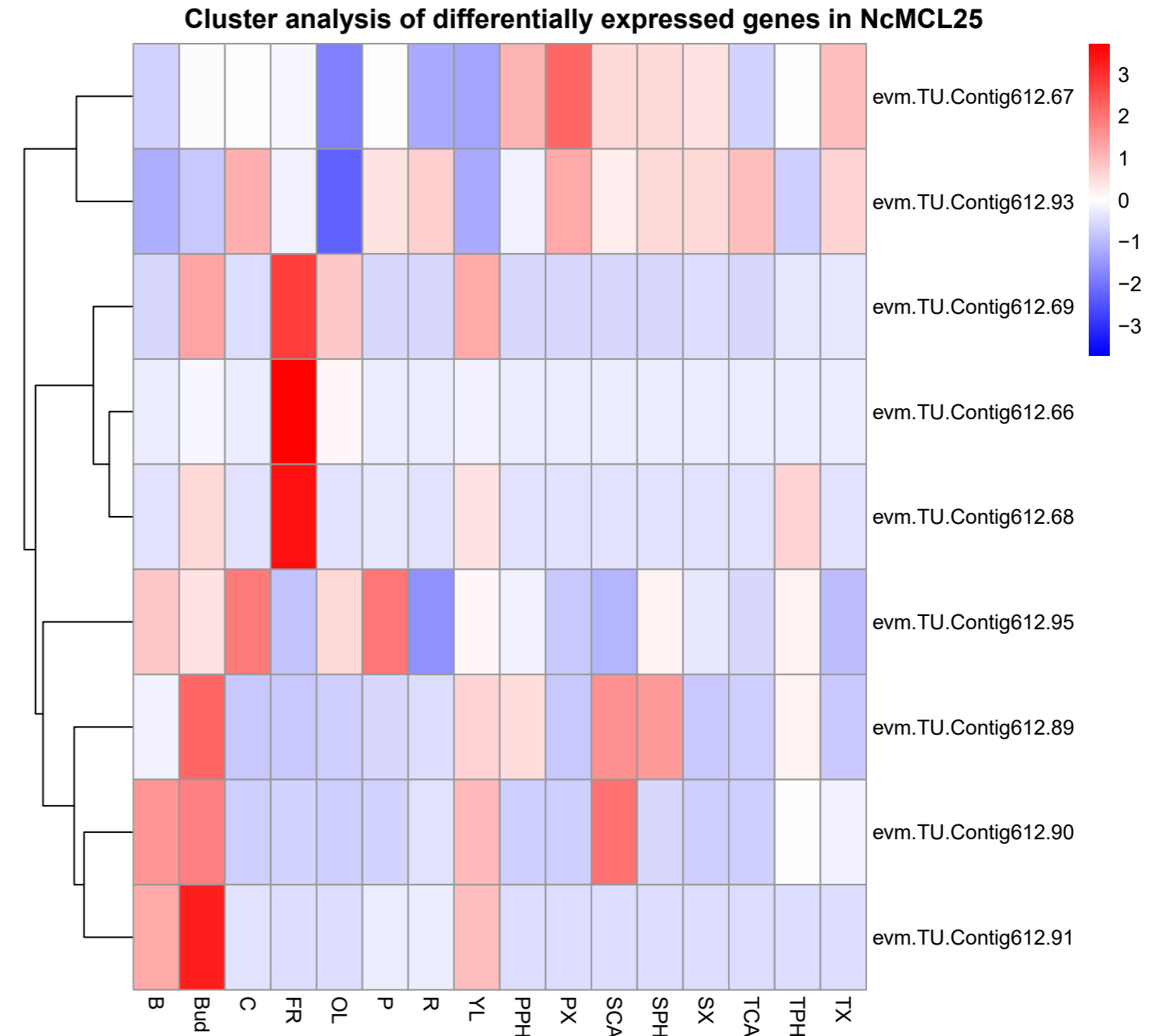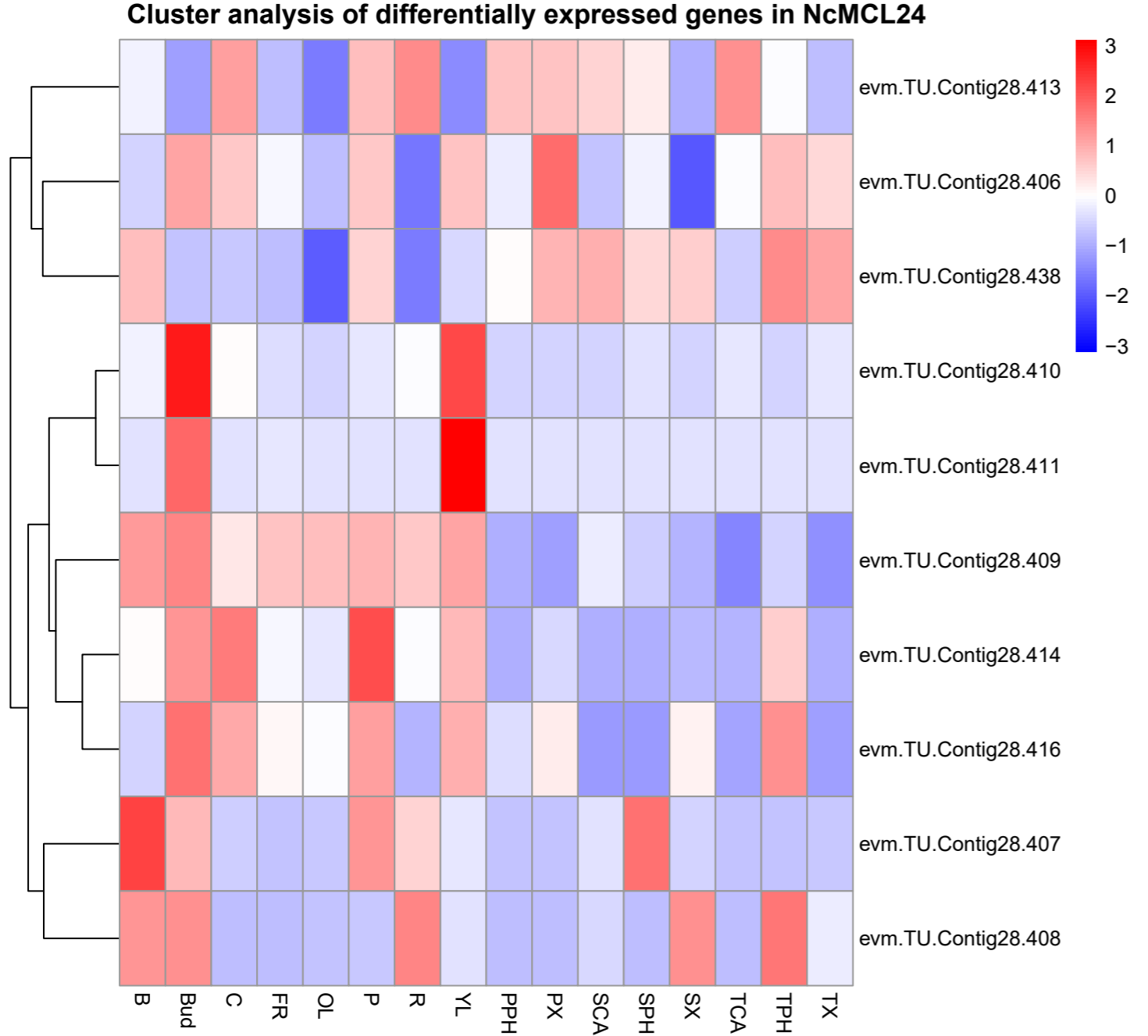
Figure S12 Heat Map of Expression Data of genes in NcMCL24 and NcMCL25. The sixteen tissues of *N. cadamba* were indicated as those in the Figure S8.
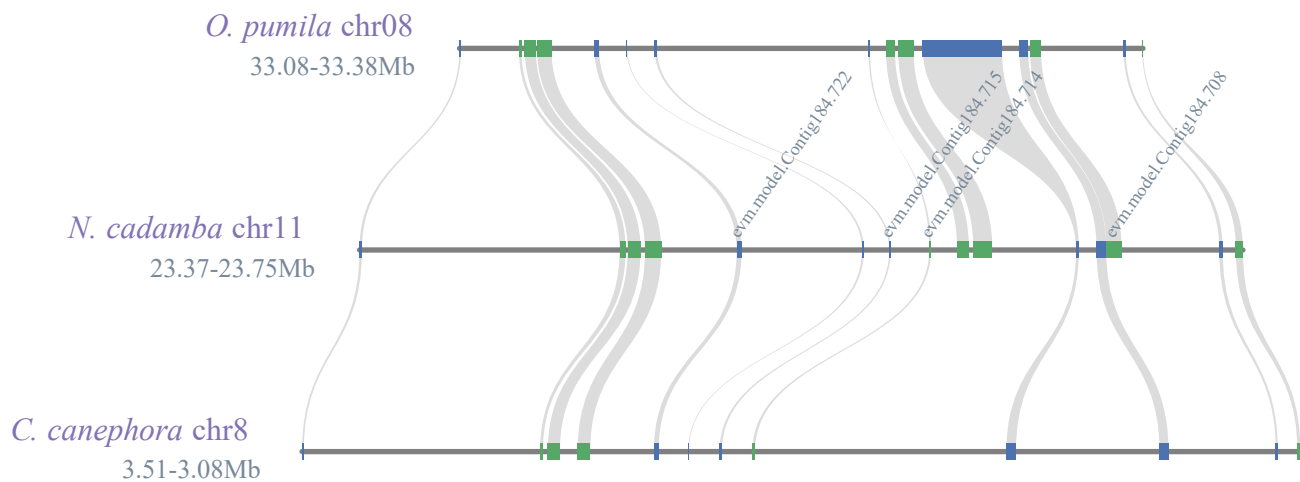
Figure S13 Duplication of NcMYC TFs in tandem order.

Alignment: Untitled

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                                     ....|....| ....|....| ....|....| ....|....| ....|....|
                                             10         20         30         40         50
CrSGD   AAF28800.1                   ---MGSKDDQ SLVVAIS--- ---------- ---------- ----------
RsRG    AAF03675.1                   ---------- ---MATQ--- ---------- ---------- ----------
RsSGD   2JF6_A                       ---MDNTQAE PLVVAIV--- ---------- ---------- ----------
RvSGD   AFI71457                     ---MESNQGE PLVVAIV--- ---------- ---------- ----------
CaacSGD   AES93119.1                 ---------- -MEAQSI--- ---------- ---------- ----------
evm.model.Contig941.1                ---------- ---------- ---------- ---------- ----------
evm.model.Contig941.2                ---------- ---------- ---------- ---------- ----------
evm.model.Contig253.82               ---------- ---------- ---------- ---------- ----------
Opuchr06_g0093690-1.1                ---------- ---------- ---------- ---------- ----------
Opuchr06_g0093740-1.1                ---------- ---------- ---------- ---------- ----------
Opuchr02_g0057620-1.1                ---------- ---------- ---------- ---------- ----------
Opuchr02_g0057880-1.1                ---------- ---------- ---------- ---------- ----------
Opuchr02_g0058000-1.1                ---------- ---------- ---------- ---------- ----------
Opuchr01_g0011710-1.1                ----MEFLGH LLLGILL--- ---IFHVHAV LYVNGDGVFP RIYGLHKIDH
Opuchr01_g0010140-1.1                ---------- ---------- ---MFSQAFA VDDH------ ----------
Opuchr01_g0010230-1.1                ---MGRFLLW FLIFALVHGY GGSIFSQAYA GDGD------ ----------
Opuchr01_g0011680-1.1                ----MEFKFH FLLVLGL--- ---LFLEQAH ADGN------ ----------
Opuchr01_g0012200-1.1                ----MEFPVH VLVVL----- ---LFLSHVY VYCI------ ----------
Opuchr04_g0010120-1.1                MNTLIMSRGM LVLVLLV--- ---TALTVLS SQCA------ ----------
evm.model.Contig521.4                ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.7                ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.8                ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.10               ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.17               ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.9                ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.16               ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.30                ----MEFLGH LFLGAFL--- ---VLSHFHG ASGNWPGVYP TIYGLNTVDR
evm.model.Contig79.29                ----MEFLGH LFLGAFL--- ---VLSHFHG ASGNWPGVYP TIYGLNTVDR
evm.model.Contig79.21                ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.20                ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.19                ---------- ---------- ---------- ---------- ----------
evm.model.Contig139.149              ---------- ---------- ---------- ---------- ----------
evm.model.Contig158.2                ---------- ---------- ---------- ---------- ----------
evm.model.Contig387.54               ----MAVQNS FLVSLLI--- ----LANFLF VSVL------ ----------
evm.model.Contig387.55               ----MALQGS LLLGLLI--- ----LVNFLF SSKL------ ----------
pdb|3PTK|B Chain B  Os4BGlu12        ---AMADITS LYKKAGS--- ---------- ---------- ----------
BAS85953.1 Os03g0703000              ----MAARRA NCALVLV--- ---LALALLA ARDA------ ----------
AtBGLU18 sp|Q9SE50.2                 ---MVRFEKV HLVLGLA--- ---LVLTLVG APTK------ ----------


                                     ....|....| ....|....| ....|....| ....|....| ....|....|
                                             60         70         80         90        100
CrSGD   AAF28800.1                   -PAAEPNGNH SVPIPFAYPS IPIQPRKHNK PIVHRRDFPS DFILGAGGSA
RsRG    AAF03675.1                   -SSAVIDSND ---------- -----ATR-- --ISRSDFPA DFIMGTGSSA
RsSGD   2JF6_A                       -PKPNASTEH --------TN SHLIPVTRSK IVVHRRDFPQ DFIFGAGGSA
RvSGD   AFI71457                     -PKPNASTEQ --------KN SHLIPATRSK IVVHRRDFPQ DFVFGAGGSA
CaacSGD   AES93119.1                 -PLSVHNPSS ---------- ---------- --IHRRDFPP DFIFGAASAA
evm.model.Contig941.1                ---------- ---------- MAGSNN--VM SQISRADFGE EFIFGSASSA
evm.model.Contig941.2                ---------- ---------- MAASS---VM SQISRADFGE DFIFGSASAA
evm.model.Contig253.82               ---------- ---------- MAASN---VI SPISRADFGE EFIFGSASSA
Opuchr06_g0093690-1.1                ----ANFIHI HIVHLVNLCL IVNSNQEMAA SKISRADFGE DFIFGSASSA
Opuchr06_g0093740-1.1                ---------- ----KIRIQE MAASSI--LA SQISRADFGE DFIFGSASFA
Opuchr02_g0057620-1.1                ---------- ---------- -----MGGTP IVIER----- ----------
Opuchr02_g0057880-1.1                ---------- ---------- ---------- MEIHR----- ----------
Opuchr02_g0058000-1.1                ---------- ---------- ---------- MEIHRSEFPV DMIFGAATAA
Opuchr01_g0011710-1.1                DAQPLSPSFG ID-------- ---------- -VLNRSSFPP GFIFGAASSS
Opuchr01_g0010140-1.1                HSIDESSSYE IIT------- ---------- -KFNRSSFPP DFIFGAASAA
Opuchr01_g0010230-1.1                HSIDESPSHE IR-------- ---------- -KFNRSSFPP DFIFGAASAA
Opuchr01_g0011680-1.1                -SKTLSPSYG IH-------- ---------- -KLNRSSFPP GFLFGASTAA
Opuchr01_g0012200-1.1                -AEQFSPNYR TN-------- ---------- -EFNRSSFPP GFLFGASSSA
Opuchr04_g0010120-1.1                -AAVVNAETA AKGEEYLDFL NEGKYHLNST KGSLRKSFAK GFVFGTATSA
evm.model.Contig521.4                ---------- ---------- ---------M AEIHRSDFPH DFIFGAATAA
evm.model.Contig521.7                ---------- ---------- ---------M AEIHRSDFPH DFIFGAATAA
evm.model.Contig521.8                ---------- ---------- ---------- MKMIN----- ----------
```

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evm.model.Contig521.10    ---------- ---------- ----------   MEISRSDFGN NFLFGSATSS
evm.model.Contig521.17    ---------- ---------- ----------   MLMESTDLQ- ------ERSE
evm.model.Contig521.9     ---------- ---------- ---------M   AEIHRSDFPN DFLFGAATAA
evm.model.Contig521.16    ---------- ---------- ----------   MAIGKRQHL- ------AWKE
evm.model.Contig79.30     KAPALSPSFA IN-------- ----------   -ILNRTSFPP GFIFGAASSA
evm.model.Contig79.29     KAPALSPSFA IN-------- ----------   -ILNRTSFPP GFIFGAASSA
evm.model.Contig79.21     MATPESHVFP SDS------- ----------   -PLKRQDFPE GFLFGASASA
evm.model.Contig79.20     MATPESHVFP SDS------- ----------   -PLKRQDFPE GFLFGASASA
evm.model.Contig79.19     ---------- ---------- ----------   ---------- ----------
evm.model.Contig139.149   MATPESHVFP SDS------- ----------   -PLKRQDFPE GFLFGASASA
evm.model.Contig158.2     MATPESHVFP FDS------- ----------   -PLKRQDFPK GFLFGASASA
evm.model.Contig387.54    -SAGSTRPSN VTT------- ----------   -PLKRSSFPP HFIFGAASSA
evm.model.Contig387.55    -SDAQTPSYN ISV------- ----------   -PFNRTSFPP DFIFGAASSA
pdb|3PTK|B Chain B  Os4BGlu12  AAAPFAYNSA GEP------- ----------   -PVSRRSFPK GFIFGTASSS
BAS85953.1 Os03g0703000   -GAAAVPKPN WLG------- ----------   -GLSRAAFPK RFVFGTATSA
AtBGLU18 sp|Q9SE50.2      -AQGPVCGAG LPD------- ----------   -KFSRLNFPE GFIWGTATAA


                          ....|....| ....|....| ....|....| ....|....| ....|....|
                               110        120        130        140        150
CrSGD  AAF28800.1         YQCEGAYNEG NRGPSIWDTF T-NRYPAKIA DGSNGNQAIN SYNLYKEDIK
RsRG   AAF03675.1         YQIEGGARDG GRGPSIWDTF T-HRRPDMIR GGTNGDVAVD SYHLYKEDVN
RsSGD  2JF6_A             YQCEGAYNEG NRGPSIWDTF TRQRSPAKIS DGSNGNQAIN CYHMYKEDIK
RvSGD  AFI71457           YQCEGAYNEG NRGPSIWDTF T-QRTPAKIS DGSNGNQAIN CYHMYKEDIK
CaacSGD  AES93119.1       YQYEGAANEY GRGPSIWDFW T-QRHPGKMV DCSNGNVAID SYHRFKEDVK
evm.model.Contig941.1     YQMEGAAAEG GRGPSIWDTF T-EQTPEKIA DGSNGNVAVD QYHLYKEDVK
evm.model.Contig941.2     YQMEGAAAEG GRGPSIWDTF T-EQTPDKII DGSNGNVAVD QYHLYKEDVK
evm.model.Contig253.82    YQMEGAAAEG GRGPSIWDTF T-EQTPHKVT DGSNGNVAVN QYYLYKEDVK
Opuchr06_g0093690-1.1     YQMEGAASED GRAPSIWDTF T-EQTPEKVI DGSNGNVAAD QYHHYKEDVQ
Opuchr06_g0093740-1.1     YQMEGAAGEG GRGPSIWDTF T-EQTPGKVI DGSNGNVAVD QYHLYKDDVK
Opuchr02_g0057620-1.1     ---------- ---------- -------TIM DSSNAKEACK SYHYYKEDVK
Opuchr02_g0057880-1.1     ---------- ---------- -------SDF PEKFIFGAAT S--AYQEDVK
Opuchr02_g0058000-1.1     YQVEGSLNQG GRGPSSWDEM I-RKDPGSIM DGDNAKMACK SYYYYKEDVK
Opuchr01_g0011710-1.1     YQVEGGWNAD GKGLSNWDYY T-HKFPEKIA DRSNGDVATG SYHRYKEDIK
Opuchr01_g0010140-1.1     FQVEGAWNED GKGPSIWDYF M-HNHPEKIK DHSNGDVAAD SYHLYKEDVE
Opuchr01_g0010230-1.1     FQVEGAWNED GKGPSIWDNF M-HNRPEMVR DHSNGDVAAD SYHLYKEDVK
Opuchr01_g0011680-1.1     YQIEGAWNID GKGPSIWDKF T-HKFPERIK DHSNGDVAID SYHLYKEDVK
Opuchr01_g0012200-1.1     YQLEGAWNVD GKGPSIWDTF T-HRFPDKIK DHNNGDVAAD SYHLYKEDIK
Opuchr04_g0010120-1.1     YQVEGMADKD GRGPSIWDTF I-KAPGREPN NA-SGEVAVD QYHKYKQDID
evm.model.Contig521.4     YQVEGALAEG GRGPSSWDTF T-QRTPGKVY EGQDANIACN SYYLYKEDVK
evm.model.Contig521.7     YQVEGAVAEG GRGPSSWDTL T-QRTP---- ---------- ----------
evm.model.Contig521.8     -----LVINC T--------- ---------- ---------- ----------
evm.model.Contig521.10    YQVEGATEEG GRRPNTWDTM I-RRHPDRIS NYDNANVAID SYHLYKDDVK
evm.model.Contig521.17    -----RVIME T--------- ---------- ---------- ----LHEDVK
evm.model.Contig521.9     YQVEGGVGDG GRGPSSWDTL V-QRTPDKVT EGRNANIACN SYYLYKEDVK
evm.model.Contig521.16    DRWKGKVIDG HNA------- ---------- -----NIACN SYYLYKEDVK
evm.model.Contig79.30     YQVEGGWDAD GKGPSNWDTF T-HKYPEKIA NGSNGDVATD SYHRYKEDIK
evm.model.Contig79.29     YQVEGGWDAD GKGPSNWDTF T-HKYPEKIA NGSNGDVATD SYHRYKEDIK
evm.model.Contig79.21     FQYEGAVDKD GRGPSIWDTF L-KEKYPDIV KN-GGLEAIE HYYQYKDDVR
evm.model.Contig79.20     FQYEGAVDKD GRGPSIWDTF L-KENYPDIV KN-GGLEAIE HYYQYKDDVR
evm.model.Contig79.19     ---------- ---------- -----MADIV QK-GGLEAIR HYYQYKS---
evm.model.Contig139.149   FQYEGAVDKD GRGPSIWDIF L-EEKYPDIV KN-EGLEAIR HYDQYKDDVR
evm.model.Contig158.2     FQYEGAVDKD GRGPSIWDTF L-KEKYPDIV KK-GGLEAIR HYYQYKDDVR
evm.model.Contig387.54    YQYEGAAFED GKGPSIWDTY T-RKYPGKIV DRSNGDVSDD FYHRYKEDVK
evm.model.Contig387.55    YQYEGAAFED GKGPSIWDVF A-HKYPEKIL DHSNGDVADD FYHRYKEDVR
pdb|3PTK|B Chain B  Os4BGlu12  YQYEGGAAEG GRGPSIWDTF T-HQHPEKIA DRSNGDVASD SYHLYKEDVR
BAS85953.1 Os03g0703000   YQVEGMAASG GRGPSIWDAF A-HTPGNVAG NQ-NGDVATD QYHRYKEDVN
AtBGLU18 sp|Q9SE50.2      FQVEGAVNEG CRGPSMWDTF T-KKFPHRCE NH-NADVAVD FYHRYKEDIQ


                          ....|....| ....|....| ....|....| ....|....| ....|....|
                               160        170        180        190        200
CrSGD  AAF28800.1         IMKQTGLESY RFSISWSRVL PGGNL----- SGGVNKDGVK FYHDFIDELL
RsRG   AAF03675.1         ILKNLGLDAY RFSISWSRVL PGGRL----- SGGVNKEGIN YYNNLIDGLL
RsSGD  2JF6_A             IMKQTGLESY RFSISWSRVL PGGRL----- AAGVNKDGVK FYHDFIDELL
RvSGD  AFI71457           IMKQAGLEAY RFSISWSRVL PGGRL----- AAGVNKDGVK FYHDFIDELL
CaacSGD  AES93119.1       IMKKIGLDAY RFSISWSRLL PSGKL----- SGGVNKEGVN FYNDFIDELV
evm.model.Contig941.1     MMKKIGLDAY RFSISWSRVL PGGRL----- RAGVNKAGID YYNNLINELL
evm.model.Contig941.2     IMKKIGLDSY RFSISWPRVL PGGRL----- SAGVNKTGID YYNNLLNELL
```

```
evm.model.Contig253.82         MMKKIGLDAY RFSISWPRVL PGGRL----- SAGVNKAGID YYNNLINELL
Opuchr06_g0093690-1.1          LMKKIGLDAY RFSISWPRVL PGGRL----- SAGVNKAGVE YYNNLINELL
Opuchr06_g0093740-1.1          MMKKIGLDAY RLSISWPRVL PGGRI----- SAGVNKEGIQ YYNNLINELL
Opuchr02_g0057620-1.1          LAKNMGLDSY RFSISWPRVL PGGRL----- NAGINREGIQ YYNNLIDEIL
Opuchr02_g0057880-1.1          LAKNIGIDSY RFSISWSRIL PGGKL----- NGGVNKEGIQ YYNNLIDQLL
Opuchr02_g0058000-1.1          LAKQLGLDAY RFSISWTRVL PGGRL----- SAGVNREGIQ YYNNLIDELL
Opuchr01_g0011710-1.1          LLKAMNTDSY RFSISWSRII PYGKI----- SKGINEKGIE YYDNLINEVI
Opuchr01_g0010140-1.1          LLKGMNMDAY RFSISWPRLL PS-------- ---------- ----------
Opuchr01_g0010230-1.1          LLKGMNMDAY RFSISWPRLL PNGKI----- SGGVNEKG-- ---TLFNLAM
Opuchr01_g0011680-1.1          HLKKMNMDSY RFSISWPRIL PR-------- ---------- ----------
Opuchr01_g0012200-1.1          LLKGMNMDSY RFSISWSRVL PC-------- ---------- ----------
Opuchr04_g0010120-1.1          LMARLNFDAY RFSISWSRIF PNG------- SGKVNWKGVA YYNRLINYML
evm.model.Contig521.4          LLKHLGLDSY RFSISWTRVL PGGRL----- NAGVNKEGIR YYNDLINELL
evm.model.Contig521.7          ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.8          ---------- ---------- ---------- ---------- -YSSRFMDPI
evm.model.Contig521.10         FMKQIGLDAY RFSISWTRVL PGGRL----- NAGVNKEGIK YYNNLINELL
evm.model.Contig521.17         LLKHLGLDSY RFSISWTRVL PGGRL----- NAGVNKEGIR YYNDLINELL
evm.model.Contig521.9          LVKHLGLDSY RFSISWTRVL PGGRL----- NAGVNKEGIR YYNDLINELL
evm.model.Contig521.16         LVTHIGLDSY RFSISWTRIL PGGRL----- NAGVNKEGIR YYNDLINELT
evm.model.Contig79.30          LLKEMNADSY RFSISWSRIL PHGKL----- SKGINEKGIE YYNNLIDELL
evm.model.Contig79.29          LLKEMNADSY RFSISWSRIL PHGKL----- SKGINEKGIE YYNNLIDELL
evm.model.Contig79.21          VIKETGLESY RFSIAWPRIL P--------- ---------- ----------
evm.model.Contig79.20          VIKETGLESY RFSIAWPRIL PKGRRIAPEV GGGINEAGID FYNDLINELL
evm.model.Contig79.19          ---------- ------SRLL HN-------- ---------- -----ILDCR
evm.model.Contig139.149        VIKEMGLKIH RFSISWPRIL PKGRK----- SNGINEEGIN FYKGLIEELR
evm.model.Contig158.2          VIKEMGLKTY RFSISWPRIL PKGRK----- SNGINEEGIN FYKGLIKELR
evm.model.Contig387.54         LMKFIGLNGF RFSISWPRVL PHGKL----- SKGVNKAGIA FYNNLINDLL
evm.model.Contig387.55         LMKYEGLNGF RFSISWSRVL PYGKL----- SKGVNKLGVA FYNNLINELL
pdb|3PTK|B Chain B  Os4BGlu12  LMKDMGMDAY RFSISWTRIL PNGSL----- RGGVNKEGIK YYNNLINELL
BAS85953.1 Os03g0703000        LMKSLNFDAY RFSISWSRIF PDG------- EGRVNQEGVA YYNNLINYLL
AtBGLU18 sp|Q9SE50.2           LMKDLNTDAF RLSIAWPRIF PHGRM----- SKGISKVGVQ FYHDLIDELL


                               ....|....| ...|....| ....|....| ....|....| ....|....|
                                  210        220        230        240        250
CrSGD  AAF28800.1              ANGIKPFATL FHWDLPQALE DEYGGFLSDR IVEDFTEYAE FCFWEFGDKV
RsRG   AAF03675.1              ANGIKPFVTL FHWDVPQALE DEYGGFLSPR IVDDFCEYAE LCFWEFGDRV
RsSGD  2JF6_A                  ANGIKPSVTL PHWDLPQALE DEYGGFLSHR IVDDFCEYAE FCFWEFGDKI
RvSGD  AFI71457                ANGIKPFATL FHWDLPQALE DEYGGFLSHR IVDDFCEYAE FCFWEFGDKI
CaacSGD  AES93119.1            ANGIEPFVTL FHWDLPQALE NEYGGFLSPR IIADYVDFAE LCFWEFGDRV
evm.model.Contig941.1          ANDIQPFITL FHWDVPQALE DEYGGFLNRQ IVNDFREFAE LCFWEFGDRV
evm.model.Contig941.2          ANDIQPFVTL FHWDVPQALE DEYGGFLNRK IVDDFREFAE LCFWEFGDRV
evm.model.Contig253.82         ANGIQPFVTL FHWDVPQALE DEYGGFLNRK IVNDFREFAE LCFWEFGDRV
Opuchr06_g0093690-1.1          ANGIEPYITL FHWDVPQALE NEYGGFLNRK IVDDFREFAE LCFWEFGDRV
Opuchr06_g0093740-1.1          ANGIKPFVTL FHWDVPQALE DEYGGFLSRK IVNDFREFAE LCFWEFGDRV
Opuchr02_g0057620-1.1          ANGIIPFVTL HHFEVPQALE DEYGGFLSKN IVKDFLEFAE LCFWEFGDRV
Opuchr02_g0057880-1.1          ANGIIPFVTL HHFDLPQALE DQYGGFLSEN IVKDFCDFAE LCFWEFGDRV
Opuchr02_g0058000-1.1          ANGIIPFATI HHFEVPQALE DEYGGFLNGK IVNDYLEFAG LCFWEFGDRV
Opuchr01_g0011710-1.1          ANGLTPSVTI FHWELPLALE KEYGGFLSPK IIKDFHDYAN LCFERFGDRV
Opuchr01_g0010140-1.1          ---IKPVVTL FHWDVPQALE EEYNGLLSPN FINDYYDFAN LCFERFGDRV
Opuchr01_g0010230-1.1          HAGIKPVVTL FHFDVPQALE EEYNGLLSHQ IIQDYYDYSN LCFERFGDRV
Opuchr01_g0011680-1.1          ---ITPMVTL FHFDLPQALE DEYGGFLDPQ IVNDFHDFAN LCFERFGYRV
Opuchr01_g0012200-1.1          ---LTPAVTL FHWDLPQALE DEYGGFLSPE IVNDFHDFAK LCFERFGDRV
Opuchr04_g0010120-1.1          KRGITPYANL NHYDLPLALQ DRYNGWLGRE VVKDFADYAE FCFKTFGDRV
evm.model.Contig521.4          ANGIVPYVTL HHFEVPQALE DEYGGFLSPR IVKDFCEFAE LCFWEFGDRV
evm.model.Contig521.7          --GIVPFVTL HHFEVPQALE DEYGGFLSPQ IVDDFCEFAE LCFWEFGDRV
evm.model.Contig521.8          TYGQYPTSML QR--VPSNRL RPFSPEESEK LKGSY-DFLG LNYYTS----
evm.model.Contig521.10         AHGIQPFVTL FHFEVPQTLE DEYGGFLSDK IVKDFSEFAG LCFWEFGDRV
evm.model.Contig521.17         ANGIVPFVTL HHFEVPQALE DEYGGFLSPR IRDDFCEFAE LCFWEFGDRN
evm.model.Contig521.9          ANGIIPYVTL HHFEVPQALE DEYGGFLSPR IVKDFCEFAE LCFWEFGDRV
evm.model.Contig521.16         ANGIVPFVTL HHLEVPQTLE EEYGGFLSPR IVKDFCEFAE LCFWEFGDRV
evm.model.Contig79.30          KNGLQPSVTL FHWDIPQALE DEYGGFLSPK IVDDFHDYAN LCFERFGDRV
evm.model.Contig79.29          KNGLQPSVTL FHWDIPQALE DEYGGFLSPK IVDDFHDYAN LCFERFGDRV
evm.model.Contig79.21          --SIEPMVTL YHWDVPQELE NEYLGFLDRR IVGDFVDYAD LCFSRFGDRV
evm.model.Contig79.20          ANDIEPMVTL YHWDVPQELE NEYLGFLDRR IVGDFVDYAD LCFSRFGDRV
evm.model.Contig79.19          YRAYGDSLSL G---CAPSLE DDTKGSGQAD LY-------- LCFSRFGKEV
evm.model.Contig139.149        KNDIEPMVTL FHWDVPQALE KEYQGFLDKR IVHDFVDYAD LCFSRFGKEV
evm.model.Contig158.2          KNDIEPMVTL FHWDVPQALE NEYKGFLDKR IVRDFVDYAD LCFSRFGKEV
evm.model.Contig387.54         SKGIQPFVTL FHWDVPQALE DEYGGFLSPH IVNDFRDFAD LCFKHFGDRV
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evm.model.Contig387.55          ANGVTPFVTL FHWDPPQALE EEYGGFLNIS IVDDFRDFSE LCFKEFGDRV
pdb|3PTK|B Chain B  Os4BGlu12   SKGVQPFITL FHWDSPQALE DKYNGFLSPN IINDFKDYAE ICFKEFGDRV
BAS85953.1 Os03g0703000         QKGITPYVNL YHYDLPLALE KKYGGWLNAK MADLFTEYAD FCFKTFGNRV
AtBGLU18 sp|Q9SE50.2            KNNIIPLVTV FHWDTPQDLE DEYGGFLSGR IVQDFTEYAN FTFHEYGHKV


                                ....|....| ....|....| ....|....| ....|....| ....|....|
                                        260        270        280        290        300
CrSGD   AAF28800.1              KFWTTFNEPH TYVASGYATG EFAPGRGG-- -----ADG-- ----------
RsRG    AAF03675.1              KHWMTLNEPW TFSVHGYATG LYAPGRGR-- -----TSPEH VNHPTVQHRC
RsSGD   2JF6_A                  KYWTTFNEFH TFAVNGYALG EFAPGRGG-- -----KGD-- ----------
RvSGD   AFI71457                KYWTTFNEPH TFTANGYALG EFAPGRGK-- -----NG--- ----------
CaacSGD  AES93119.1             KNWATCNEPW TYTVSGYVLG NFPPGRGP-- -----SSRET MRSLPALCR-
evm.model.Contig941.1           TNWITLNEPW SFAFGGYATG AFAPGRGA-- -----ATPEH IKDAIPKHRC
evm.model.Contig941.2           KNWITLNEPW AFAFDGYATG TYPPGRGA-- -----ATPEH IKDAIPKHRC
evm.model.Contig253.82          KNWITLNEPW SLAFGGYAIG VQAPGRGA-- -----ATPEH IKDAIPKHRC
Opuchr06_g0093690-1.1           KNWITLNEPW SFALGGYTLG SSAPGRGA-- -----TTPEH SKDYIPQHRC
Opuchr06_g0093740-1.1           KNWITLNEPW SFAFGGYTTG AYAPGRGA-- -----TTPEH VKDAIPKHRC
Opuchr02_g0057620-1.1           KHWVTFNEPW SFILYGYVMG AMPPNRGS-- ---SSEEHAQ LSHVPHKCCF
Opuchr02_g0057880-1.1           KHWVTFNEPW TFISFGYVQG KMPPNRGS-- ---SSKEHAE TTHTVHKGCT
Opuchr02_g0058000-1.1           KHWITFNEPW SFIYYGYVKG TMPPNHGATT ---SAPELAQ LPHIKHKGSS
Opuchr01_g0011710-1.1           KHWVTFNEPW SYSISGYD-- ---------- ---------- -GGTFAPGRC
Opuchr01_g0010140-1.1           KQWITFNEPF ASSVPGYD-- ---------- ---------- -MGIFAPGRC
Opuchr01_g0010230-1.1           KQWITFNEPL SSSGGGYD-- ---------- ---------- -IGIIAPGRC
Opuchr01_g0011680-1.1           KHWITMNEPS GYSYAGYG-- ---------- ---------- -MGFFPPNRC
Opuchr01_g0012200-1.1           KHWITFNEPW AFSSFGYD-- ---------- ---------- -SGIHAPGRC
Opuchr04_g0010120-1.1           KNWFTFNEPR VVAALGYD-- ---------- ---------- -NGFFAPGRC
evm.model.Contig521.4           KFWTTFNEPW TFIYYGYVVG MMPPGRGS-- -----SSTEH TEHNLIRHRC
evm.model.Contig521.7           KFWTTFNEPW TFIYYGYVVG MMPPCRGS-- -----SSTEH TEHKLIRHRC
evm.model.Contig521.8           ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.10          KHWTTLNEPW SFANYAYAVG TFPPNRGS-- -----SSEDH ASYPIVQHRT
evm.model.Contig521.17          ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.9           KFWTTFNEPW SFIYYGYVVG SMPPCRGS-- -----SSTEH TEHKLIQHRC
evm.model.Contig521.16          KFWTTFNEPW TFIYYGYVAG RTPPGRSS-- -----SSTEH TKHSIIRHRC
evm.model.Contig79.30           KYWVTFNEPW SYSLSGYD-- ---------- ---------- -SGLYAPGRC
evm.model.Contig79.29           KYWVTFNEPW SYSLSGYD-- ---------- ---------- -SGLYAPGRC
evm.model.Contig79.21           KHWITFNEPW SFSVGGYTMG TFAPGRGASS NERAQMIFEF PTSRATSKQA
evm.model.Contig79.20           KHWVTFNEPW SFSVGGYTMG TFAPGRGASS NERAQMIFEF PTSRATSKQA
evm.model.Contig79.19           KHWITFNEPW SFSVGGYST- ---------- ---------- --------A
evm.model.Contig139.149         KHWITFNEPW SFSVGGYSMG TFAPGRGAAS NERAQMM--- PTSRATSEQA
evm.model.Contig158.2           KHWITFNEPW SFSVGGYSTG TFAPGRGAAS NERAQMIFDL PTSRATSEKA
evm.model.Contig387.54          KHWTTFNEPW SFSTGGYDSS TI-------- ---------- -TGTLAPGRC
evm.model.Contig387.55          KYWSTFNEPW SFSTGGYDST TA-------- ---------- -IGTIAPGRC
pdb|3PTK|B Chain B  Os4BGlu12   KNWITFNEPW TFCSNGYA-- ---------- ---------- -TGLFAPGRC
BAS85953.1 Os03g0703000         KHWFTFNEPR IVALLGYD-- ---------- ---------- -QGTNPPKRC
AtBGLU18 sp|Q9SE50.2            KHWITFNEPW VFSRAGYD-- ---------- ---------- -NGKKAPGRC


                                ....|....| ....|....| ....|....| ....|....| ....|....|
                                        310        320        330        340        350
CrSGD   AAF28800.1              ---------- --KGEPGKEP YIATHNLLLS HKAAVEVYRK NFQKCQGGEI
RsRG    AAF03675.1              STVAPQCI-- CSTGNPGTEP YWVTHHLLLA HAAAVELYKN KFQRGQEGQI
RsSGD   2JF6_A                  ---------- --EGDPAIEP YVVTHNILLA HKAAVEEYRN KFQKCQEGEI
RvSGD   AFI71457                ---------- --KGDPATEP YLVTHNILLA HKAAVEAYRN KFQKCQEGEI
CaacSGD  AES93119.1             RSILHTHI-- CTDGNPATEP YRVAHHLLLS HAAAVEKYRT KYQTCQRGKI
evm.model.Contig941.1           HCLHSGD--- CEEGDPSTEP YLVAHHLLLA HAEAVKLYRE NFK-AQGGKI
evm.model.Contig941.2           NCLCAGD--- CEAGDPGTEP YLVAHHLLLA HAEAVKIYRE NFQQAQGGKI
evm.model.Contig253.82          YCSQAGD--- CEAGDPSTEP YLVAHHLLLA HAEAVKLYRE YFQ-AQGGKI
Opuchr06_g0093690-1.1           HQSSFAHI-- CDEGDPGTEP YVVSHHLLLA HAEAVKLYRE NFQ-AQGGKI
Opuchr06_g0093740-1.1           HCPYADDS-- CEDGDPGREP YLVAHVLLA HAEAVKLYRE YFK-AQGGKI
Opuchr02_g0057620-1.1           HHQCPQK--- SDNGNPGVEP YTVSHNLLMA HAEAFLLYKT KFKG-QGGKI
Opuchr02_g0057880-1.1           RHGYPLI--- CDKGDPGVEP YTVSHNLLMA HAQAFNLYKT KFKA-QGGKI
Opuchr02_g0058000-1.1           HQDHSIL--- VENGDPGVEP YTVSHLLMA HAKAFHLYKS KFKG-QGGQI
Opuchr01_g0011710-1.1           SAWKQNN--- CTGGNSGTEP YLVSHNQLLA HADAVQLYRT KYQAHQKGKI
Opuchr01_g0010140-1.1           SSWKNNN--- CTTGDSSTEP YIVMHHILLA HAHAVKLYKT KYQVNQKGII
Opuchr01_g0010230-1.1           SCWRNNN--- CTAGDSSTEP YIVTHNILLA HAHAVRLYKT KYQDHQKGII
Opuchr01_g0011680-1.1           SSWMNNN--- CSGGDSSTEP YIVSHHLLLA HAKAAKLYKT KFQAHQKGVI
Opuchr01_g0012200-1.1           SSWMNKN--- CTGGNSGTEP YIVAHQLLA HADAVKLYKT KYQSHQKGII
Opuchr04_g0010120-1.1           SKAFG----N CTAGNSATEP YIVAHNLILC HASAAQRYRE KYQEKQKGKI
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evm.model.Contig521.4     PCERAFI--- CETGDPGFEP YEVSRNLLLA HAEAVKLYKK KFKA-QAGKI
evm.model.Contig521.7     HHECALI--- CENGNPGVEP YVASRHLLLA HAAAVQLYKK KFKV-EK---
evm.model.Contig521.8     ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.10    DKSFAQI--- CENGDPGREP YIVAHNLLLA HAEAVRIYRE KFQETQGGKI
evm.model.Contig521.17    ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.9     QHECAFI--- CENGDPGVEP YVASRHLLLA HAAAVQLYKK NFKA-QGGKI
evm.model.Contig521.16    HHDHPAL--- CENGDPGVEP YVASRHLLLA HAKAVQIYKN KFKA-QGGKI
evm.model.Contig79.30     SSWMQNN--- CSGGDSGTEP YVVTHYQLLA HVEAVELYKK KYQATQKGKI
evm.model.Contig79.29     SSWMQNN--- CSGGDSGTEP YVVTHYQLLA HVEAVELYKK KYQATQKGKI
evm.model.Contig79.21     TIDTGAP--- -KAGNPGTEP YIVSHHQLLA HAAAVKLYRE KYQKKQKGKI
evm.model.Contig79.20     TIDTGAP--- -KAGDPGTEP YIVSHHQLLA HAAAVKLYRE RYQKKQKGKI
evm.model.Contig79.19     SIDTGAP--- -KEGNPGTEP YIVSHHQLLA HAAAVKLYRA KYQVCNIHVL
evm.model.Contig139.149   SKATGAP--- -KEGNPGTEP YIVSHYQLLA HAKTVKLYRE KYQGERKGII
evm.model.Contig158.2     SIDTGAP--- -KEGNPGTEP YIVSHHQLLA HAAAVKLYRE KYQGERKGNI
evm.model.Contig387.54    SAWLNKG--- CPAGDSATEP YVVGHNILLS HAVAVKLYRE TYKASQRGQI
evm.model.Contig387.55    SSWLNK---- CPAGDSSTEP YLVAHHIILC HATVAKLYKE KYKPSQKGEI
pdb|3PTK|B Chain B  Os4BGlu12  SPWEKGN--- CSVGDSGREP YTACHHQLLA HAETVRLYKA KYQALQKGKI
BAS85953.1 Os03g0703000   TKCA------ -AGGNSATEP YIVAHNFLLS HAAAVARYRT KYQAAQQGKV
AtBGLU18 sp|Q9SE50.2       SPYIPGYGQH CQDGRSGYEA YQVSHNLLLS HAYAVDAFRN CKQCAG-GKI


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                               360        370        380        390        400
CrSGD  AAF28800.1          GIVLNSM-WM EPLN-ETKED IDARERGLDF MLGWFIEPLT TGEYPKSMRA
RsRG  AAF03675.1           GISHATQ-WM EPWDENSASD VEAAARALDF MLGWFMEPIT SGDYPKSMKK
RsSGD  2JF6_A              GIVLNSM-WM EPLS-DVQAD IDAQKRALDF MLGWFLEPLT TGDYPKSMRE
RvSGD  AFI71457            GIVLNST-WM EPLN-DVQAD IDAHKRALDF MLGWFIEPLT TGDYPKSMRE
CaacSGD  AES93119.1        GIVLNVT-WL EPFSEWCPND RKAAERGLDF KLGWFLEPVI NGDYPQSMQN
evm.model.Contig941.1      GITLVSK-WW EPLN-DTPQD KEALERAADF MLGWFMSPIT FGDYPKRMRD
evm.model.Contig941.2      GITLVSQ-WW EPLN-DTPKD KEALERAVDF MFGWFMSPIT FGDYPKRMRD
evm.model.Contig253.82     GITLVSQ-WW EPLN-DTPQD KEALERAADF MFGWFMSPIT FGDYPKRMRD
Opuchr06_g0093690-1.1      GITLVSQ-WW EPLH-DTPQD KEAVERAADF MFGWFMSPIT YGEYPKRMRD
Opuchr06_g0093740-1.1      GITLVSQ-WW EPLN-DTPQD KEALERAADF MFGWFMSPIS YGDYPKRMRD
Opuchr02_g0057620-1.1      GITLNSH-WF VPKTNDCQAD EDAIPRQVDF EFGWFMGPIT YGQYPKSMLD
Opuchr02_g0057880-1.1      GITLVTR-WF VPLT-DTPAD KDAAQRQLDF DFGWFMDPIT YGQYPKSMLD
Opuchr02_g0058000-1.1      GITLVTG-WY EPLT-DSPAD KEAVKRQLDF VFGWFMNPIT YGHYPNIMLE
Opuchr01_g0011710-1.1      GIVLVST-WM VPLRN-TARD KRAAIRALDF MFGWFMNPLV YGDYPPSMRV
Opuchr01_g0010140-1.1      GITLVAT-WM VPYSN-SSAD KQATIRAMDF RMGWNLSPLV YGEYPKSMQT
Opuchr01_g0010230-1.1      GISVVTS-WL VPYSK-SPAD KQATSRALDF QIGWNLSPLV YGEYPKSMQT
Opuchr01_g0011680-1.1      GITLVSI-WV VPYSN-SLDD RHAVDRFLEF SLGGFMDPLF FGDYPKSMRT
Opuchr01_g0012200-1.1      GITLNSM-WM VPNSN-SLDD YRASIRMLDF MLGWFMDPLV FGDYPYSMTT
Opuchr04_g0010120-1.1      GILLDFV-WY EPLNESSKAD IAAAQRARDF HIGWFMHPLV YGEYPQNLQT
evm.model.Contig521.4      GITLVTH-WY DPLT-NSESD KEAAQRAMDF EFGWFMDPIT YGQYPTGMLQ
evm.model.Contig521.7      ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.8      ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.10     GITLVTH-WF EPLN-DTEDD KEAANRAFDF KFGWFMEPVT YGRYPKRMTD
evm.model.Contig521.17     --TQNTN-LS D--------- ---------- -----IDAIT N---------
evm.model.Contig521.9      GITLVTH-WY EPRS-NSDSD KEAAQRAMDF EFGWFMDPIT YGQYPTNMLQ
evm.model.Contig521.16     GITLNTD-WY EPL--NAETD KEAAQRAMDF QFGWFMDPIT SGQYPISMLQ
evm.model.Contig79.30      GITLVST-WM VPFSN-SPLD KRAAVRALDF MFGWFMNPLV YGKYPVSMQI
evm.model.Contig79.29      GITLVST-WM VPFSN-SPLD KRAAVRALDF MFGWFMNPLV YGKYPVSMQI
evm.model.Contig79.21      GITLLSN-WA IPYHD-TKED QDAAQRALDF MFGWFMDPIT YGDYPSTMRS
evm.model.Contig79.20      GITLLSN-WA IPYHD-TKED QDAAQRALDF MFGWFMDPIT YGDYPSTMRS
evm.model.Contig79.19      SLQLISFSIH IPSTL-SPKK KFSKNRSLHF RF---MDPIT YGDYPSSMQS
evm.model.Contig139.149    GITLVSN-WT VPYHN-TQED IEAAQRALDF MFGWFMDPIT YGDYPSSMRS
evm.model.Contig158.2      GITLVSN-WT VPYHN-TQED IAAAQRALDF MFGWFMDPIT YGHYPKSMRS
evm.model.Contig387.54     GIVLVTN-WM IPYSN-RTAD VKAAQRALDF FYGWFLDPIT YGDYPKSMRS
evm.model.Contig387.55     GIVLVTN-WM IPYSN-TTAD AIATRRGLDF FLGWFLDPFT YGDYPKSMRD
pdb|3PTK|B Chain B  Os4BGlu12  GITLVSH-WF VPFSR-SKSN NDAAKRAIDF MFGWFMDPLI RGDYPLSMRG
BAS85953.1 Os03g0703000    GIVLDFN-WY EALSN-STED QAAAQRARDF HIGWYLDPLI NGHYPQIMQD
AtBGLU18 sp|Q9SE50.2        GIAHSPA-WF EPQDLEHVGG --SIERVLDF ILGWHLAPTT YGDYPQSMKD


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                               410        420        430        440        450
CrSGD  AAF28800.1          LVGS-RLPEF STEVSEKLTG CYDFIGMNYY TTTYVSNADK IP---DTPGY
RsRG  AAF03675.1           FVGS-RLPKF SPEQSKMLKG SYDFVGLNYY TASYVTNAST NSSGSNNFSY
RsSGD  2JF6_A              LVKG-RLPKF SADDSEKLKG CYDFIGMNYY TATYVTNAVK SNS--EKLSY
RvSGD  AFI71457            IVKG-RLPRF SPEDSEKLKG CYDFVGMNYY TATYVTNAAK SNS--EKLSY
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CaacSGD   AES93119.1            LVKQ-RLPKF SEEESKLLKG SFDFIGINYY TSNYAKDAPQ AGS-DGKLSY
evm.model.Contig941.1           IVKS-RLPKF SKEESENLRK SFDFLGLNYY TSQYVTDASG IES--ELVSY
evm.model.Contig941.2           IVKS-RLPKF SKEESNNLRK SYDFLGLNYY TSQYVTDASG TKS--ELLSY
evm.model.Contig253.82          IVKS-RLPKF SKEESENLKK SFDFLGLNYY TSQYVTDASG TKS--ELLSY
Opuchr06_g0093690-1.1           IVKS-RLPKF SKEEAQMLKG SFDFLGLNYY TSQYVTDASG TKS--DVLSY
Opuchr06_g0093740-1.1           IVQS-RLPKF SEEESQTLKG SYDFLGLNYY TSQYVTDGSG TKS--DLLSY
Opuchr02_g0057620-1.1           LVPHERLQPF SDEESKILKG SYDFLGLNYY TSVFVADSPK SNG--A-PSY
Opuchr02_g0057880-1.1           LVPEDRLQPF SAEESKKLKG TYDFLGLNYY TSSFAADAPN LKG--P-PSY
Opuchr02_g0058000-1.1           LVPADRLQPF SDEESKILEG SYDFLGLNYY TSSFVGDALL SFG--PRPSY
Opuchr01_g0011710-1.1           LVGN-RLPRF TVYQTKLLIG SYDFLGLNYY TAFYISNVN- TTS-KVNLSY
Opuchr01_g0010140-1.1           LVGN-RLPKF TKEASNLLKG SFDFLGLNYY TTTYVKDTSR NKS--SHLSY
Opuchr01_g0010230-1.1           LVGN-RLPKF TKEESNLLKG SFDFLGLNYY TANYVKDNSN FKP--SNLSY
Opuchr01_g0011680-1.1           LVGH-RLPKF TKKQSEEVKG SYDFIGLNYY TAYYVIDQSH TTG-VRNKS-
Opuchr01_g0012200-1.1           LVGN-RLPKF TKDQSELLKG SYDFIGMNYY TAFYAIDASL TNDNMGNASY
Opuchr04_g0010120-1.1           IVAD-RLPKF TKEEVKMVKG SFDYVGINQY TAYYMYDPHQ GKP--KDIGY
evm.model.Contig521.4           RVPASRLRPF SPEESEKLKG SYDFLGLNYY TSLYATDSST GKS--GPPSY
evm.model.Contig521.7           ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.8           ---------- ---------- ---------- --LYATDSST GKS--GPPSY
evm.model.Contig521.10          NVPSDRLRPF TAEESAKLKG SYDFLGLNYY TGTYATNDPA SAK--GPPSY
evm.model.Contig521.17          ------VHSF VKMEILALS- ---------- -----REASD G-------TL
evm.model.Contig521.9           RVPASRLQPF SPEETEKLKG SYDFLGLNYY TSLYATDSST GKS--GPPSY
evm.model.Contig521.16          RVPPNRLQPF SPKESEELKG SYDFLGLNYY TSQYATDSST GKS--GPPSY
evm.model.Contig79.30           LVGN-RLPKF TKEQSKKLIG SYDFLGLNYY TAQYAAHIP- TPPNKVNLSY
evm.model.Contig79.29           LVGN-RLPKF TKEQSKKLIG SYDFLGLNYY TAQYAAHIP- TPPNKVNLSY
evm.model.Contig79.21           LVGP-RLPRF TSTESELLKG SFDFLGFNYY TANYVKNAPK SES---DPDY
evm.model.Contig79.20           LVGS-RLPRF APNESELLKG SFDFLGFNYY TANYVKNAPK SES---DPDY
evm.model.Contig79.19           LVCN-RLPMF SETESELLKC SFDFLGFNYY TANYVKNAPN SGS---D--Y
evm.model.Contig139.149         LVGN-RLPMF SKTESELLKG SFDFLGFNYY TANYVKNAPN SGS---H--Y
evm.model.Contig158.2           LVGN-RLPMF SETESELLKC SFDFLGFNYY TANYVKNAPN SGS---D--Y
evm.model.Contig387.54          IIGR-RLPKF TPEQKKLLKG SIDILGVNYY TSNYVSNIRS ANS--VNISF
evm.model.Contig387.55          SVGN-RLPKF TPKESELVKG SLDFLGLNYY TSNYVADIPF ANT--VNISY
pdb|3PTK|B Chain B  Os4BGlu12   LVGN-RLPQF TKEQSKLVKG AFDFIGLNYY TANYADNLPP SNG--LNNSY
BAS85953.1 Os03g0703000         LVKD-RLPKF TPEQARLVKG SADYIGINQY TASYMKGQQL MQQ--TPTSY
AtBGLU18 sp|Q9SE50.2            RVGH-RLPKF TEAEKKLLKG STDYVGMNYY TSVFAKEISP -DP--KSPSW
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                                     460        470        480        490        500
CrSGD   AAF28800.1              ETDARINKNI FVKKVDGKEV RIGEP----- -----CYGGW QHVVPSGLYN
RsRG    AAF03675.1              NTDIHVTY-- ---ETDRNGV PIGPQ----- ----SGSDW LLIYPEGIRK
RsSGD   2JF6_A                  ETDDQVTK-T FERNQK---- PIGHA----- -----LYGGW QHVVPWGLYK
RvSGD   AFI71457                ETDDHVDK-T FDRVVDGKSV PIGAV----- -----LYGEW QHVVPWGLYK
CaacSGD   AES93119.1            NTDSKVEI-- --THERKKDV PIGPL----- -----GGSNW VYLYPEGIYR
evm.model.Contig941.1           VTDQKVKT-- --QAVGPDGK TE-------- -IGPKAGSNW LHIYPVGIYK
evm.model.Contig941.2           VSDQQ----- ---------- ---------- -----AGTTW VYNYPIGLYK
evm.model.Contig253.82          VTDQQVKT-- --QAVGPDGK TE-------- -IGPVAGSNW LYIYPVGIYK
Opuchr06_g0093690-1.1           VTDQQVTT-- --QATDLDGK PIGPMGLTQF HFGAQGGSSW LYIYPTGIYK
Opuchr06_g0093740-1.1           VTDQQVKT-- --QVVGPDGK TE-------- -IGPKAGSSW LYIYPVGIYK
Opuchr02_g0057620-1.1           LTDSLTKC-- --ENVDINGN PVGDE----- -----TGSSW IYLYPEGLYE
Opuchr02_g0057880-1.1           LTDPRTNI-- --QNNDLNGN PIGPD----- -----IGSPW IYMYPKGLYE
Opuchr02_g0058000-1.1           QTDSRTVC-- --KDHDLHGN PIGPP----- -----IGSPW IYLCPKGLYE
Opuchr01_g0011710-1.1           NTDQHVALS- ----VERDNV LIGEK----- ----SGSDW LHVYPKGLWN
Opuchr01_g0010140-1.1           RTDVQANSSI ----VMRNGK LIGKE----- -----AASSW LHFYPKGLRK
Opuchr01_g0010230-1.1           STDAQADSGI ----VMRNGK LIGKE----- -----G---- FEFY-IGSFK
Opuchr01_g0011680-1.1           SSDSQTRITA ----VSRNGT LIGEE----- -----FGSGN IHFYPSGIQK
Opuchr01_g0012200-1.1           TTDSKARVT- ----VERNGK LIGDA----- -----YGDSW IHYYPRGIWK
Opuchr04_g0010120-1.1           QQEWNAGFAY ----E-RKGV PIGPR----- -----AYSYW LYDVPWGLYK
evm.model.Contig521.4           ITDMHTDT-- --KDTSADGK LIGPK----- -----TDSGW IYICPEGIYK
evm.model.Contig521.7           ---------- ---------- ---------- ------DIGW IYIYPEGIYK
evm.model.Contig521.8           ITDMHTDT-- --PGLNNFSK MILFYFD--- ---FQTDSGW IYIFPEGIYK
evm.model.Contig521.10          ITDWHVKT-- --QPAAADGK TLIGAS---- -----TSSGW IYLYPTGIFK
evm.model.Contig521.17          IGPKVKNI-- --IYMSADGN LNGPKT---- ----ETDASW IYICPEGIYK
evm.model.Contig521.9           ITDMHTDT-- --PDKNADGK LIGPA----- -----TDSGW IYICPEGIYK
evm.model.Contig521.16          ITDMHTDT-- --TGEASDGT LIGPK----- -----TDASW IYICPEGIYK
evm.model.Contig79.30           STDQHVNLT- ----SERNGT LIGAQ----- -----AGSIW LHVYPSGIRE
evm.model.Contig79.29           STDQHVNLT- ----SERNGT LIGAQ----- -----AGSIW LHVYPSGIRE
evm.model.Contig79.21           RRDSQAECT- ----PFRDGV PIGER----- -----AASDW LYVYPKGIME
evm.model.Contig79.20           RRDSQAECT- ----PFRDGV PIGER----- -----AASDW LYVYPKGIME
evm.model.Contig79.19           KLDSQAECT- ----PFRDGV AIGER----- -----AASDW LYVYPKGIME
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evm.model.Contig139.149        KLDSQAECT- ----PFRDGV PIGER----- -----AASDW LYVYPKGIME
evm.model.Contig158.2          KLDSQAECT- ----PFRDGV PIGER----- -----AASDW LYVYPKGIME
evm.model.Contig387.54         STDLHVNLT- ----SERNGK LIGAP----- -----TGVSI FYDYPPGLTE
evm.model.Contig387.55         TTDTRTNMT- ----QERNGK FIGAP----- -----TGAGI LFVYPRGLTE
pdb|3PTK|B Chain B  Os4BGlu12  TTDSRANLT- ----GVRNGI PIGPQ----- -----AASPW LYVYPQGFRD
BAS85953.1 Os03g0703000        SADWQVTYVF ----A-KNGK PIGPQ----- -----ANSNW LYIVPWGMYG
AtBGLU18 sp|Q9SE50.2           TTDSLVDWDS ----KSVDGY KIGSK----- -----PFNGK LDVYSKGLRY


                                 ....|....| ....|....| ....|....| ....|....| ....|....|
                                        510        520        530        540        550
CrSGD   AAF28800.1             LLVYTKEKYH VPVIYVSECG VVEENRTNIL LTEGKTNILL TEARHDKLRV
RsRG    AAF03675.1             ILVYTKKTYN VPLIYVTENG VDDVK----- ----NTNLTL SEARKDSMRL
RsSGD   2JF6_A                 LLVYTKETYH VPVLYVTSG MVEEN----- ----KTKILL SEARRDAERT
RvSGD   AFI71457               LLVYTKETYH VPVLYVTSG MVEEN----- ----KTKILL SEARRDPERT
CaacSGD AES93119.1             LLDWMRKKYN NPLVYITENG VDDKN----- ----DTKLTL SEARHDETRR
evm.model.Contig941.1          LLKYVKSRYE DPVIFITENG VDEVN----- ----DLKLTV SKARMDKTRI
evm.model.Contig941.2          LLKYIKSRYE DPVIFITENG VDEMN----- ----DPKLTV SKARTDKIRI
evm.model.Contig253.82         LLKYIKSRYE DPIIYITENG VDEVN----- ----DLKLTV SKARTDKMRI
Opuchr06_g0093690-1.1          LLKYVKLRYN DPLIFITENG IDEVN----- ----DPKLTV SKARLDKVRV
Opuchr06_g0093740-1.1          LLKYIKSHYN DPIIYITENG VDEEN----- ----DFRLTV SNSRKDKIRI
Opuchr02_g0057620-1.1          LLCHIKKTYK DPPIYITENG VDEMS----- ----DPKKSV SEARADPERI
Opuchr02_g0057880-1.1          LLCYIKKHYK DPPIYITENG VDEIS----- ----DLKKTV CEARVDPERI
Opuchr02_g0058000-1.1          LLSYIKKTYN DPPIYITENG VDEVS----- ----DYKKIV TEAREDPNRI
Opuchr01_g0011710-1.1          LLIYIKNYK NPIIYITENG VDEKNN---- -----ATLTL KQALQDNFRI
Opuchr01_g0010140-1.1          MLLYVKHRYQ DPIIYITENG VDEYDN---- -----PSLPL ETALKDYFRI
Opuchr01_g0010230-1.1          LASFLSKRNP E--------G VDENDD---- -----ASLPL KTALEDYYRI
Opuchr01_g0011680-1.1          LLLYIKRKYK NPIIYITENG VDDTHN---- -----SSMKF -EALNDSFRI
Opuchr01_g0012200-1.1          LLLYIKRKYH NPIIYITENG VNGIDN---- -----STLLS -NELNDNFRI
Opuchr04_g0010120-1.1          AVTYVKETYG NPTMILAENG R-DDPGN--- -----LTLPS --GLNDTARI
evm.model.Contig521.4          LLGYIKKRYN DPPIYITENG VAESN----- ----DYKKTV SEARADETRI
evm.model.Contig521.7          LLCYIKKRYN DPPVYITENG VYEMS----- ----DYNKTV CEARADETRI
evm.model.Contig521.8          LLCYIKKRYN DPPIYITENG VAESN----- ----DYEKTV SEARVDETRI
evm.model.Contig521.10         LLSKIKTYYN DPPIYITENG VADAG----- ----DPEGKI ANARVDDIRI
evm.model.Contig521.17         LLCYIKKQYN DPPIYITENG VYEMN----- ----DYNKTV CEACADETRI
evm.model.Contig521.9          LLGYIKKRYN DPPIYITENG VAETN----- ----DYKKTV CAARSDETRI
evm.model.Contig521.16         LLCHIKKRYN DPPIYITENG VAENN----- ----DYKKTV SEARVDETRI
evm.model.Contig79.30          LLLYIKRKYQ NPIIYITENG IDELND---- -----PNLSL KEALQDSFRI
evm.model.Contig79.29          LLLYIKRKYQ NPIIYITENG IDELND---- -----PNLSL KEALQDSFRI
evm.model.Contig79.21          HVDYIRQKYN NPTVYITENG RDEMNQ---- -----KDLSY WISLFDHKRI
evm.model.Contig79.20          HVDYIRQKYN NPTVYITENG RDEMNQ---- -----KDLSY WISLFDHERI
evm.model.Contig79.19          HVDYIRKKYK NPPIYITENG RDELNQ---- -----PELSY WVSLFDYKRI
evm.model.Contig139.149        HVDYIRKKYK NPPIYITENG RDELNQ---- -----PELSY WVSLFDHKRI
evm.model.Contig158.2          HVDYIRKKYK NPPIYITENG RDELNQ---- -----PELSY WVSLFDYKRI
evm.model.Contig387.54         LLVYTKKKYK NPIIYITENG IGDSN----- ------IKTV KEGVNDPQRI
evm.model.Contig387.55         LLVYIKEKYK NPTIYITENG LAEVN----- ------IDTV EQGVNDTQRI
pdb|3PTK|B Chain B  Os4BGlu12  LLLYVKENYG NPTVYITENG VDEFNN---- -----KTLPL QEALKDDARI
BAS85953.1 Os03g0703000        CVNYIKQKYG NPTVVITENG M-DQPAN--- -----LSRDQ --YLRDTTRV
AtBGLU18 sp|Q9SE50.2           LLKYIKDNYG DPEVIIAENG YGEDLGE--- -----KHNDV NFGTQDHNRK


                                 ....|....| ....|....| ....|....| ....|....| ....|....|
                                        560        570        580        590        600
CrSGD   AAF28800.1             DFLQSHLASV RDAIDDG-VN VKGFFVWSFF DNFEWNLGYI CRYGIIHVDY
RsRG    AAF03675.1             KYLQDHIFNV RQAMNDG-VN VKGYFAWSLL DNFEWGEGYG VRFGIIHIDY
RsSGD   2JF6_A                 DYHQKHLASV RDAIDDG-VN VKGYFVWSFF DNFEWNLGYI CRYGIIHVDY
RvSGD   AFI71457               DYHQKHLASV RDAIDDG-VN VKGYFVWSFF DNFEWNLGFI GRYGIIHVDY
CaacSGD AES93119.1             DYHEKHLRFL HYATHEG-AN VKGYFAWSFM DNFEWSEGYS VRFGMIYIDY
evm.model.Contig941.1          KYHHDHLAYV KQAIDNDKVK VKGYFIWSLL DNFEWGDGFS VRFGIIHVNY
evm.model.Contig941.2          KYHHDHLEYV KQAMVIDKVK VKGYFIWSLL DNFEWTEGYS VRFGIIYVNY
evm.model.Contig253.82         KYHHDHLEYV KQAIDIDKVQ VKGYFIWSLL DNFEWSDGYS VRFGIIYVNY
Opuchr06_g0093690-1.1          EYHRDHLAQI KEAMDVDKVN VKAYFIWSLL DNFEWGEGYS VRFGIIHVNY
Opuchr06_g0093740-1.1          QYHHDHLEYV KQAINIDKVK VQGYFIWSLL DNFEWAEGFS VRFGIIHVNY
Opuchr02_g0057620-1.1          KYHTEHLKVV KRAMLEDRVN VKGYFIWSLI DNFEWTGGYA SRFGLVYVDF
Opuchr02_g0057880-1.1          KYHTEHLKEI KRAMVEDRVN MKGYFLWSLI DNFEWTEGYA SRFGLVYVEF
Opuchr02_g0058000-1.1          KYLTEHLKAI KKAIVEKRVN VKGYFVWSLM DNFEWTEGYQ DRFGLMYVEF
Opuchr01_g0011710-1.1          QYYKHLQFL RKAIKNG-VR VKGYYGWSIL DNFEWADGYT VRFGINYVNF
Opuchr01_g0010140-1.1          KYYHHLRFL YKAIKDG-VK VRGYFGWSVL DNLEWADGYT VRFGLNFVDF
Opuchr01_g0010230-1.1          KYYYRHLRFL HKAIEEG-VK VRGYFGWSIM DNLEWTYGYT VRFGLNYVDF
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Opuchr01_g0011680-1.1        KYHHAHLSFL HKAILDG-VQ VKGYHAWSLV DNFEWISGFT SHYGLNLVDF
Opuchr01_g0012200-1.1        KYFHGHLSYL HKAILDG-AR VKGFYGWSIM DNFEWSSGFT ARFGLNFVDF
Opuchr04_g0010120-1.1        SYYKGYLAEL RKTIDDG-AN VIGYFAWSLL DNFEWRLGYT SRFGIVYVDF
evm.model.Contig521.4        TYHSGHLKEI KRAMVEQRVN VKAYFIWSLL DNFEWTDGYR VRFGLVYVNF
evm.model.Contig521.7        TYHSGHLKEI KRAMDEQRAN VKAYFAWSLL DNFEWTDGYT LRFGLVYVNF
evm.model.Contig521.8        TYHSGHLKEM KRAMVEQRVN VKAYFVWSLL DNFEWSSGYT LRFGLVYCNF
evm.model.Contig521.10       NYHREHLKEV KHAINENGVD VKGYFIWSLV DNFEWTAGYK DRFGIVYINY
evm.model.Contig521.17       TYHRGHLKEI KRAMVEQRVN VKAYFVLSLL DNFEWTDGYT LLFGLVYVNF
evm.model.Contig521.9        TYHSGHLKEI KRAMDELRVN VKAYFVWSLL DNFEWSDGYR IRFGLVYVNF
evm.model.Contig521.16       TYHRGHLKEI KHAMVEQRVN VKGYFIWSLL DNFEWSSGYT LRFGLAYVNF
evm.model.Contig79.30        KYYYRHLLYI KKAIDEG-VQ VKGYYGWSIM DNMEWADGYR VRFGINFVDF
evm.model.Contig79.29        KYYYRHLLYI KKAIHEG-VQ VKGYYGWSIM DNMEWADGYT VRFGINFVDF
evm.model.Contig79.21        SYHYKHLQFL KKAITNG-AN VKGYLIWSLM DNLEWSSGFK TRFGMNFIDF
evm.model.Contig79.20        SYHYKHLQFL KKAIANG-AN VKGYLIWSLM DNLEWSSGFK TRFGMNFIDF
evm.model.Contig79.19        SYHYRHLQYL KQAISNG-AD VKGYLVWSLM DNLEWSSGFK TRFGMNFIDF
evm.model.Contig139.149      SYHYRHLQYL KQAISNG-AD VKGYLVWSLM DNLEWSSGFK TRFGMNFIDF
evm.model.Contig158.2        SYHYRHLQYL KKAISNG-AD VKGYLVWSLM DNLEWSSGFK TRFGMNFIDF
evm.model.Contig387.54       RFYRGHLSAA KAAIKVG-VN VKGFFAWTFL DTFEWSSGYT LRFGINFVDF
evm.model.Contig387.55       RFYHGHFKAL KAAIDKG-VD VKGFFAWTFL DTFEWGSGLG MRFGINFIDY
pdb|3PTK|B Chain B  Os4BGlu12 EYYHKHLLSL LSAIRDG-AN VKGYFAWSLL DNFEWSNGYT VRFGINFVDY
BAS85953.1 Os03g0703000      HFYRSYLTQL KKAIDEG-AN VAGYFAWSLL DNFEWLSGYT SKFGIVYVDF
AtBGLU18 sp|Q9SE50.2         YYIQRHLLSM HDAICKDKVN VTGYFVWSLM DNFEWQDGYK ARFGLYYIDF
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                                 610        620        630        640        650
CrSGD   AAF28800.1          KT--FQRYPK DSAIWYKN-F ISEGFVTN-- -------TAK KRFREEDKLV
RsRG    AAF03675.1          NDN-FARYPK DSAVWLMNSF HKNISKLP-- -------AVK RSIREDDEEQ
RsSGD   2JF6_A              KS--FERYPK ESAIWYKN-F IAGKSTTS-- -------PAK RR-REEAQ-V
RvSGD   AFI71457            NS--FERCPK ESAIWYKN-F IAGVSTTS-- -------PAK RR-REEAEGV
CaacSGD  AES93119.1         KND-LARYPK DSAIWYKN-- --FLTKTE-- -------KTK KR-QLDHKEL
evm.model.Contig941.1       KDGY-ARYPK ESALWFMN-F LKKSNGVS-- --DVSQPAKP TKRALDCGEF
evm.model.Contig941.2       KDGY-ARHPK ESALWFMN-F LKKSNGVS-- --QVSQTTKP TKRALDDGEL
evm.model.Contig253.82      KDGY-ARYPK ESALWFMN-F LNKTNGVG-- --ELSRPTKP TKRALDDGKL
Opuchr06_g0093690-1.1       RDGN-ARYPK LSALWFMN-F LNKNNSVN-- --EVQQPAKG TKRELENGD-
Opuchr06_g0093740-1.1       KDGY-ARYPK ESALWFIN-F LNKTNSVN-- --ELPQPSKG TKRVLDNGES
Opuchr02_g0057620-1.1       VNDDRSRFPK ESATWYMN-F LSKKRKSV-- ----APGRSP SNGVMEDGG-
Opuchr02_g0057880-1.1       KNEDRSRFPK DSASWYMN-F LDKKHR---- ----SAGYSP SNGSKEDDAC
Opuchr02_g0058000-1.1       KTEDRPRCPK DSGLWYMN-F LCRRFKPIIP IEYGAVGYAP QNGLIEDAAN
Opuchr01_g0011710-1.1       KT--LQRFRK LSSFWFERFL SR------- ---------- ----------
Opuchr01_g0010140-1.1       KNG-MKRYPK LSAKWFKSFL QK------- ---------- ----------
Opuchr01_g0010230-1.1       RNG-LERYPK LSAKWFGKFL QK------- ---------- ----------
Opuchr01_g0011680-1.1       NDG-LKRYPK LSAKWFQRFL TKY------ ---------- ----------
Opuchr01_g0012200-1.1       KDG-LKRYPK LSAKWFQSFL QK------- ---------- ----------
Opuchr04_g0010120-1.1       ET--LKRYPK MSAYWFKKFM HPLVYGEYPQ NLQTIVADRL PKFTKEEVKM
evm.model.Contig521.4       KDDHLSRYPK ESALWFMN-F LDKKSR---- ----PTEYAA TGGLLVNHAM
evm.model.Contig521.7       KDDQLSRYPK ESALWFTE-F SRQDE----- ---------- ----------
evm.model.Contig521.8       KDDQLSRYPK ESALWFMN-F LDRKSR---- ----PAEYVY QEAYLSIMRW
evm.model.Contig521.10      NDADLTRYPK ESAIWFMN-F LKKKKR---- ---LSIDNEE TNGLAANNTQ
evm.model.Contig521.17      KDDQLSRYPK ESALWFMN-F LDKKNR---- ----LAEYAP TGGLLVNHAM
evm.model.Contig521.9       RDDQLSRYPK ESAFWFMN-F LDKKSR---- ----PPPYAS QGGLLANQVM
evm.model.Contig521.16      KDDNLSRYPK ESALWFMN-F LNKKNR---- ----PAEYAP RGGTVVNHGK
evm.model.Contig79.30       KT--LKRYRK LSAHWFERFL RNEFRTMVNK YYFFLCFLAL ILRFSNSQPK
evm.model.Contig79.29       KT--LKRYRK LSAHWFERFL RK------- ---------- ----------
evm.model.Contig79.21       QNN-LKRYPK LSSGWFKFFL LEDVQPKAEE L--------- ----------
evm.model.Contig79.20       QND-LKRYPK LSSGWFKFF- LEDVPLEAEE L--------- ----------
evm.model.Contig79.19       QNG-LKRYPK LSSGWFMFFL HDDVQPKVEE P--------- ----------
evm.model.Contig139.149     QNN-LKRYPK LSSGWFKFFL HYDVQPRVEE L--------- ----------
evm.model.Contig158.2       QNG-LKRYPK LSSGWFMFFL HDDVQPKVEE L--------- ----------
evm.model.Contig387.54      KNG-LKRYPK RSALWLKGFL K--------- ---------- ----------
evm.model.Contig387.55      KNN-LKRYPK RSALWLKRFL LK-------- ---------- ----------
pdb|3PTK|B Chain B  Os4BGlu12 NDG-RKRYPK NSAHWFKKFL LK-------- ---------- ----------
BAS85953.1 Os03g0703000     NT--LERHPK ASAYWFRDML KH-------- ---------- ----------
AtBGLU18 sp|Q9SE50.2        QNN-LTRHQK VSGKWYSEFL KP-------Q FPTSKLREEL ----------
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                                 660        670        680        690        700
CrSGD   AAF28800.1          ELVKKQKY-- ---------- ---------- ---------- ----------
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RsRG    AAF03675.1          VSSKRLRK-- ---------- ---------- ---------- ----------
RsSGD   2JF6_A              ELVKRQKT-- ---------- ---------- ---------- ----------
RvSGD   AFI71457            ELVKRQKT-- ---------- ---------- ---------- ----------
CaacSGD   AES93119.1        DNIPQKK--- ---------- ---------- ---------- ----------
evm.model.Contig941.1       ASNSVVEENP KK-------- ---------- -------KVL KV--------
evm.model.Contig941.2       ASNSIVEENP KKGPQAS--- ---------- PMAVEMKAAL EAVNFCHKEG
evm.model.Contig253.82      EANAMVEEKP KK-------- ---------- -------KVL KV--------
Opuchr06_g0093690-1.1       ------KDKP NK-------- ---------- -------KVL KI--------
Opuchr06_g0093740-1.1       VSESSDQEIP KK-------- ---------- -------KIL KV--------
Opuchr02_g0057620-1.1       ---------- ---------- ---------- ---RLPSKRP RNA-------
Opuchr02_g0057880-1.1       KNPSDVSPTP GIISGEI--- ---------- VVHRPPSKRA RN--------
Opuchr02_g0058000-1.1       KVASQVSAFK S--NEIV--- ---------- AYESTPSKRQ RKV-------
Opuchr01_g0011710-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0010140-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0010230-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0011680-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0012200-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr04_g0010120-1.1       VKGSFDYVGI NQYTAYYMYD RHQGKPKDIG YEQEWNAGFA CRDDPGNLTL
evm.model.Contig521.4       DIVPTPPLAL EKYG-----P KSLE------ LVRDSPNKRL RSN-------
evm.model.Contig521.7       ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.8       TLYPLHHPW RNMGQSRLRP KYNREPANPN SIRQTAKSRP KQDWSMVGVS
evm.model.Contig521.10      ELSQSKSPAH AKDLP----- ---------- -SNEAPAKRA RKR-------
evm.model.Contig521.17      DIVPTPLLAL EKYG-----P KSGE------ LVRDSVNKRL RAN-------
evm.model.Contig521.9       DIVSAPQLAL EKYW-----A KVGG------ TCCS------ ----------
evm.model.Contig521.16      DIVSTPPLAL EKYG-----P KSGEL----- LVRDSPNKRL RAN-------
evm.model.Contig79.30       ISPTYNIKTF NRSNFPTDFV FGSATSAYQN EGAANEGGKG PSIWDTYTKN
evm.model.Contig79.29       ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.21       ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.20       ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.19       ---------- ---------- ---------- ---------- ----------
evm.model.Contig139.149     ---------- ---------- ---------- ---------- ----------
evm.model.Contig158.2       ---------- ---------- ---------- ---------- ----------
evm.model.Contig387.54      ---------- ---------- ---------- ---------- ----------
evm.model.Contig387.55      ---------- ---------- ---------- ---------- ----------
pdb|3PTK|B Chain B   Os4BGlu12    ---------- ---------- ---------- ---------- ----------
BAS85953.1 Os03g0703000     ---------- ---------- ---------- ---------- ----------
AtBGLU18 sp|Q9SE50.2        ---------- ---------- ---------- ---------- ----------


                            ....|....| ....|....| ....|....| ....|....| ....|....|
                                  710        720        730        740        750
CrSGD   AAF28800.1          ---------- ---------- ---------- ---------- ----------
RsRG    AAF03675.1          ---------- ---------- ---------- ---------- ----------
RsSGD   2JF6_A              ---------- ---------- ---------- ---------- ----------
RvSGD   AFI71457            ---------- ---------- ---------- ---------- ----------
CaacSGD   AES93119.1        ---------- ---------- ---------- ---------- ----------
evm.model.Contig941.1       ---------- ---------- ---------- ---------- ----------
evm.model.Contig941.2       WKGFILEGGF SSHSS----- ---------- ---------- ----------
evm.model.Contig253.82      ---------- ---------- ---------- ---------- ----------
Opuchr06_g0093690-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr06_g0093740-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr02_g0057620-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr02_g0057880-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr02_g0058000-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0011710-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0010140-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0010230-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0011680-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr01_g0012200-1.1       ---------- ---------- ---------- ---------- ----------
Opuchr04_g0010120-1.1       PAGLNDTARI SYYKGYLAEL RKTIDDGANV IGYFAWSLLD NFEWRLGYTS
evm.model.Contig521.4       ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.7       ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.8       TRSGKKKEEE EGERKVEGMV LEAYDVMLFL A--------- ----------
evm.model.Contig521.10      ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.17      ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.9       ---------- ---------- ---------- ---------- ----------
evm.model.Contig521.16      ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.30       YPGLSYPLPL FVCFIMLAKK NQLDVRLLKE SGFDAYRFSI SWPRLLPQGN
evm.model.Contig79.29       ---------- ---------- ---------- ---------- ----------
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evm.model.Contig79.21      ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.20      ---------- ---------- ---------- ---------- ----------
evm.model.Contig79.19      ---------- ---------- ---------- ---------- ----------
evm.model.Contig139.149    ---------- ---------- ---------- ---------- ----------
evm.model.Contig158.2      ---------- ---------- ---------- ---------- ----------
evm.model.Contig387.54     ---------- ---------- ---------- ---------- ----------
evm.model.Contig387.55     ---------- ---------- ---------- ---------- ----------
pdb|3PTK|B Chain B  Os4BGlu12  ---------- ---------- ---------- ---------- ----------
BAS85953.1 Os03g0703000    ---------- ---------- ---------- ---------- ----------
AtBGLU18 sp|Q9SE50.2       ---------- ---------- ---------- ---------- ----------


                           ....|....| ....|....| ....|....| ..
                                760        770        780
CrSGD   AAF28800.1         ---------- ---------- ---------- --
RsRG    AAF03675.1         ---------- ---------- ---------- --
RsSGD   2JF6_A             ---------- ---------- ---------- --
RvSGD   AFI71457           ---------- ---------- ---------- --
CaacSGD   AES93119.1       ---------- ---------- ---------- --
evm.model.Contig941.1      ---------- ---------- ---------- --
evm.model.Contig941.2      ---------- ---------- ---------- --
evm.model.Contig253.82     ---------- ---------- ---------- --
Opuchr06_g0093690-1.1      ---------- ---------- ---------- --
Opuchr06_g0093740-1.1      ---------- ---------- ---------- --
Opuchr02_g0057620-1.1      ---------- ---------- ---------- --
Opuchr02_g0057880-1.1      ---------- ---------- ---------- --
Opuchr02_g0058000-1.1      ---------- ---------- ---------- --
Opuchr01_g0011710-1.1      ---------- ---------- ---------- --
Opuchr01_g0010140-1.1      ---------- ---------- ---------- --
Opuchr01_g0010230-1.1      ---------- ---------- ---------- --
Opuchr01_g0011680-1.1      ---------- ---------- ---------- --
Opuchr01_g0012200-1.1      ---------- ---------- ---------- --
Opuchr04_g0010120-1.1      RFGIVYVDFE TLKRYPKMSA YWFKKLLYRG HY
evm.model.Contig521.4      ---------- ---------- ---------- --
evm.model.Contig521.7      ---------- ---------- ---------- --
evm.model.Contig521.8      ---------- ---------- ---------- --
evm.model.Contig521.10     ---------- ---------- ---------- --
evm.model.Contig521.17     ---------- ---------- ---------- --
evm.model.Contig521.9      ---------- ---------- ---------- --
evm.model.Contig521.16     ---------- ---------- ---------- --
evm.model.Contig79.30      RS-------- ---------- ---------- --
evm.model.Contig79.29      ---------- ---------- ---------- --
evm.model.Contig79.21      ---------- ---------- ---------- --
evm.model.Contig79.20      ---------- ---------- ---------- --
evm.model.Contig79.19      ---------- ---------- ---------- --
evm.model.Contig139.149    ---------- ---------- ---------- --
evm.model.Contig158.2      ---------- ---------- ---------- --
evm.model.Contig387.54     ---------- ---------- ---------- --
evm.model.Contig387.55     ---------- ---------- ---------- --
pdb|3PTK|B Chain B  Os4BGlu12  ---------- ---------- ---------- --
BAS85953.1 Os03g0703000    ---------- ---------- ---------- --
AtBGLU18 sp|Q9SE50.2       ---------- ---------- ---------- --
```

Figure S14 Protein alignment of CrSGD, RsSGD, RvSGD, RsRG and their respective Neolamarckia and Ophiorrhiza paralogues. Accession numbers: CrSGD (AAF28800.1) from *Catharanthus roseus*, RsSGD (CAC83098.1) and RsRG (AAF03675.1) from *Rauvolfia serpentina*, RvSGD (AFI71457) from *R. verticillata*. Previously reported active-site residues of RsSGD and RsRG were framed or showed with bright colors. The amino acid sequences from *N. cadamba* (evm.model) , *Camptotheca acuminate* (Caac), *Ophiorrhiza pumila* (Op), *Arabidopsis thaliana* (At) and *Oryza sativa* (Os).