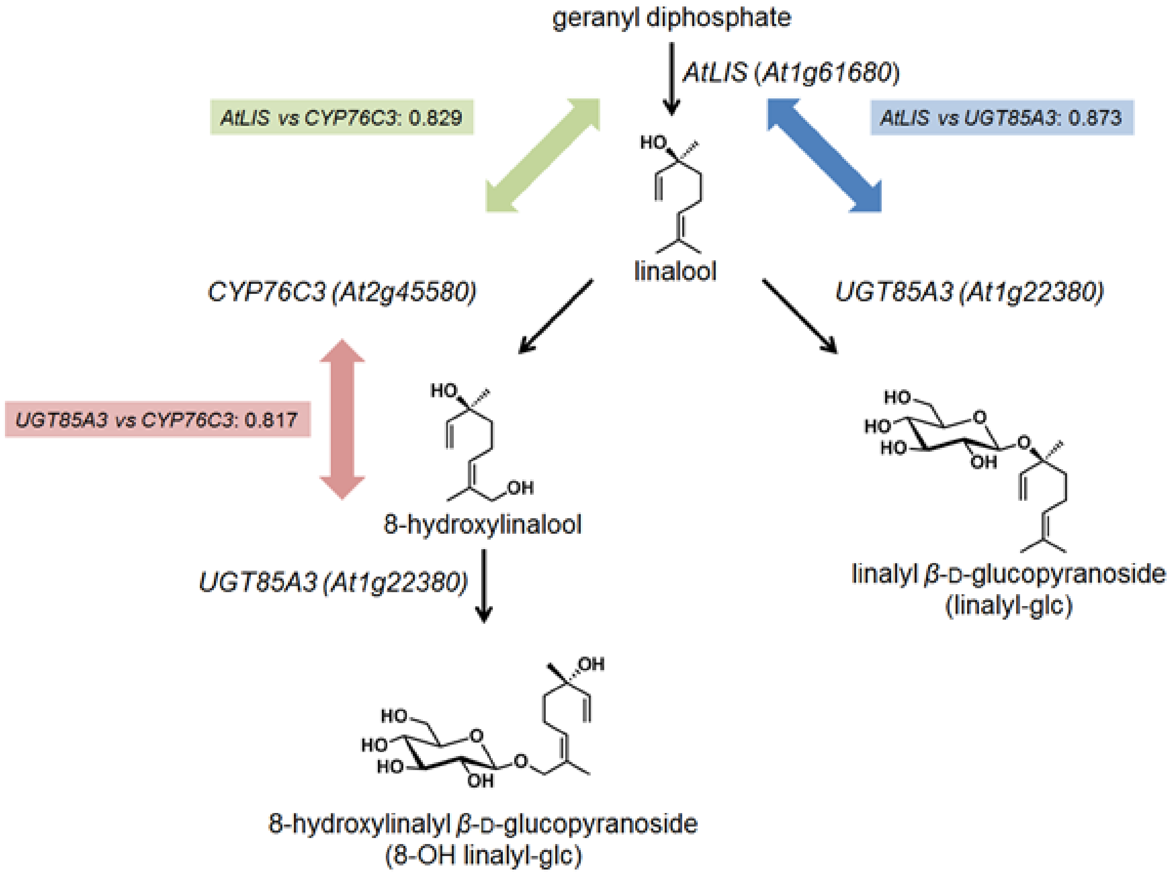
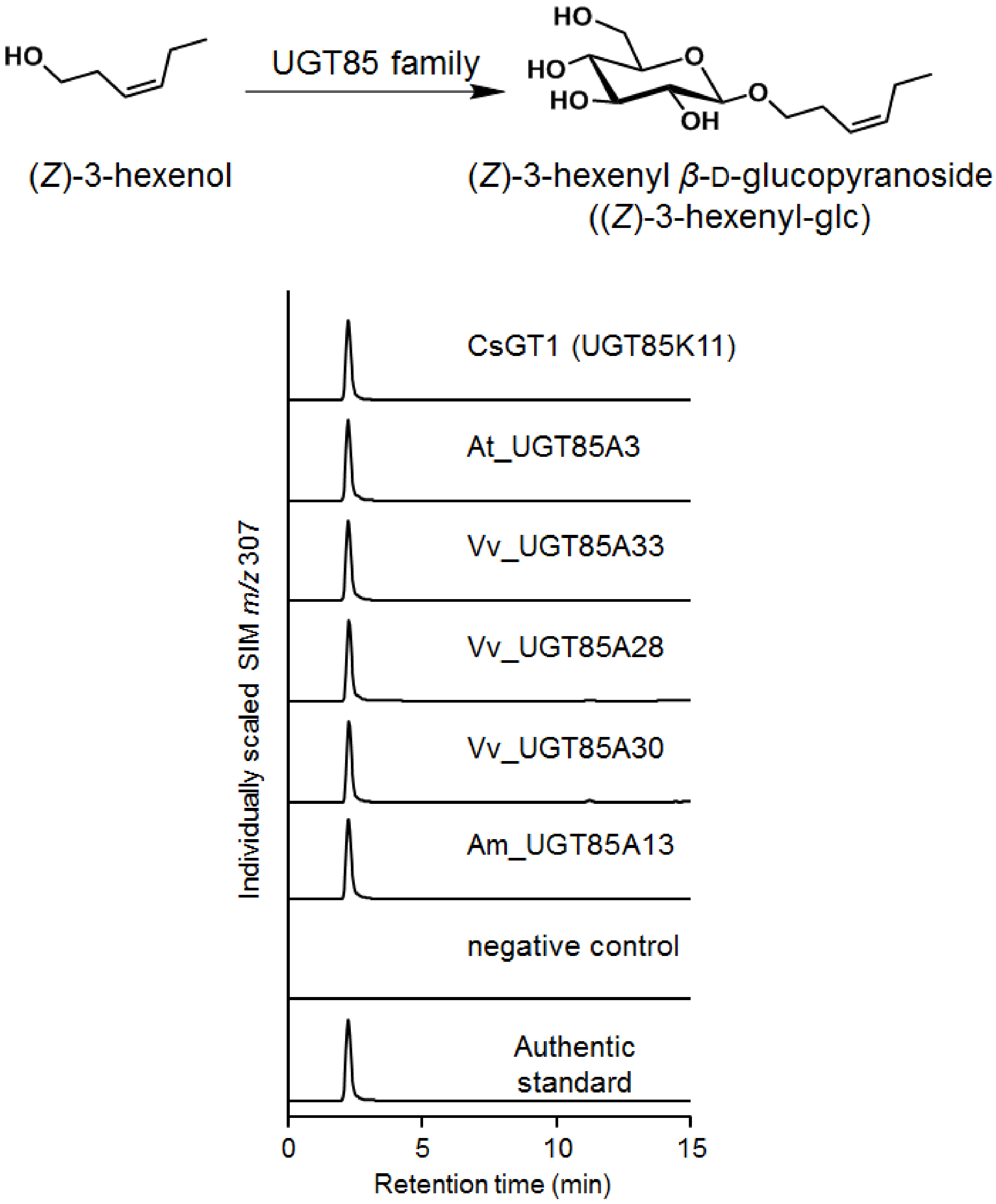
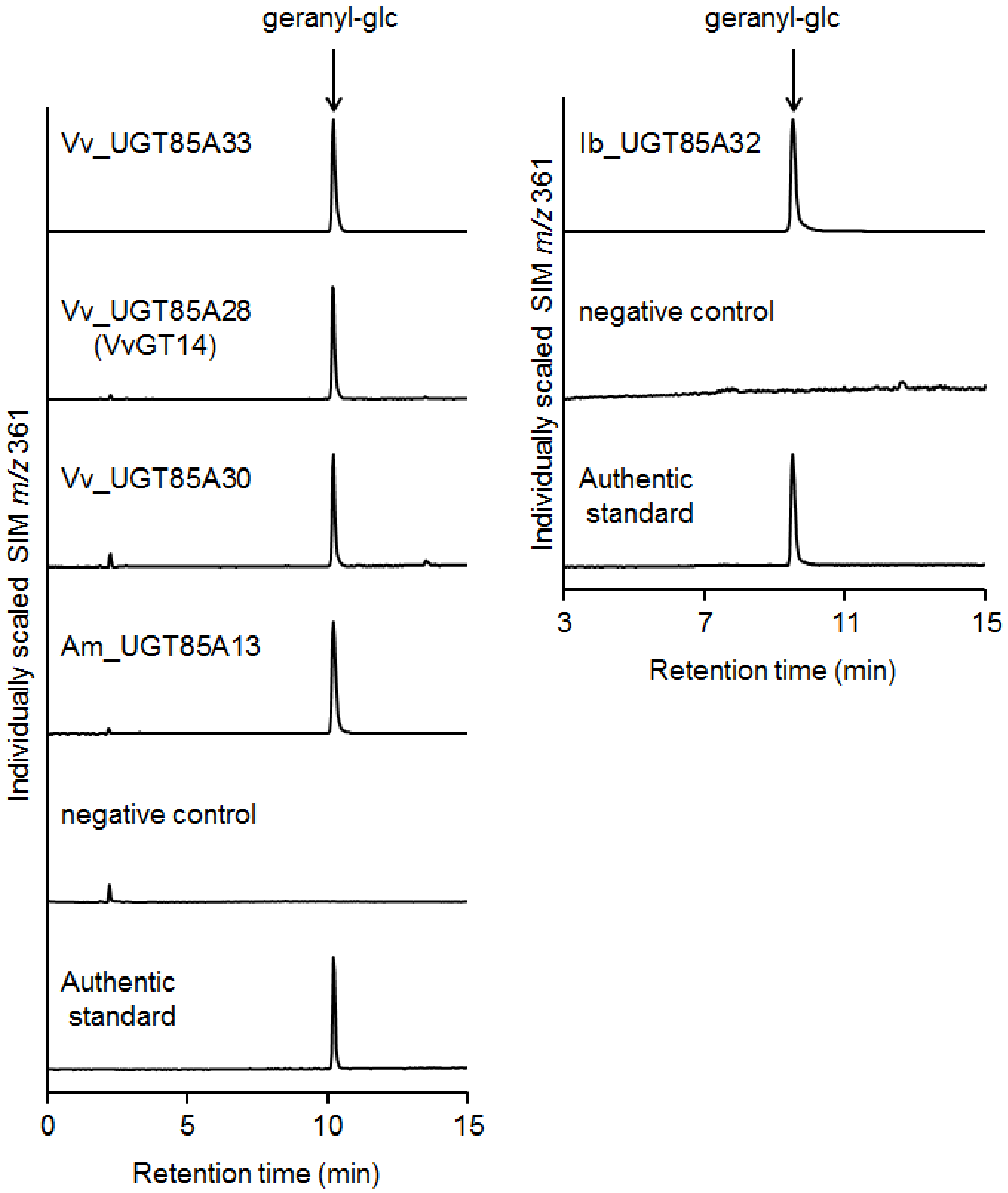
Supplemental Figures



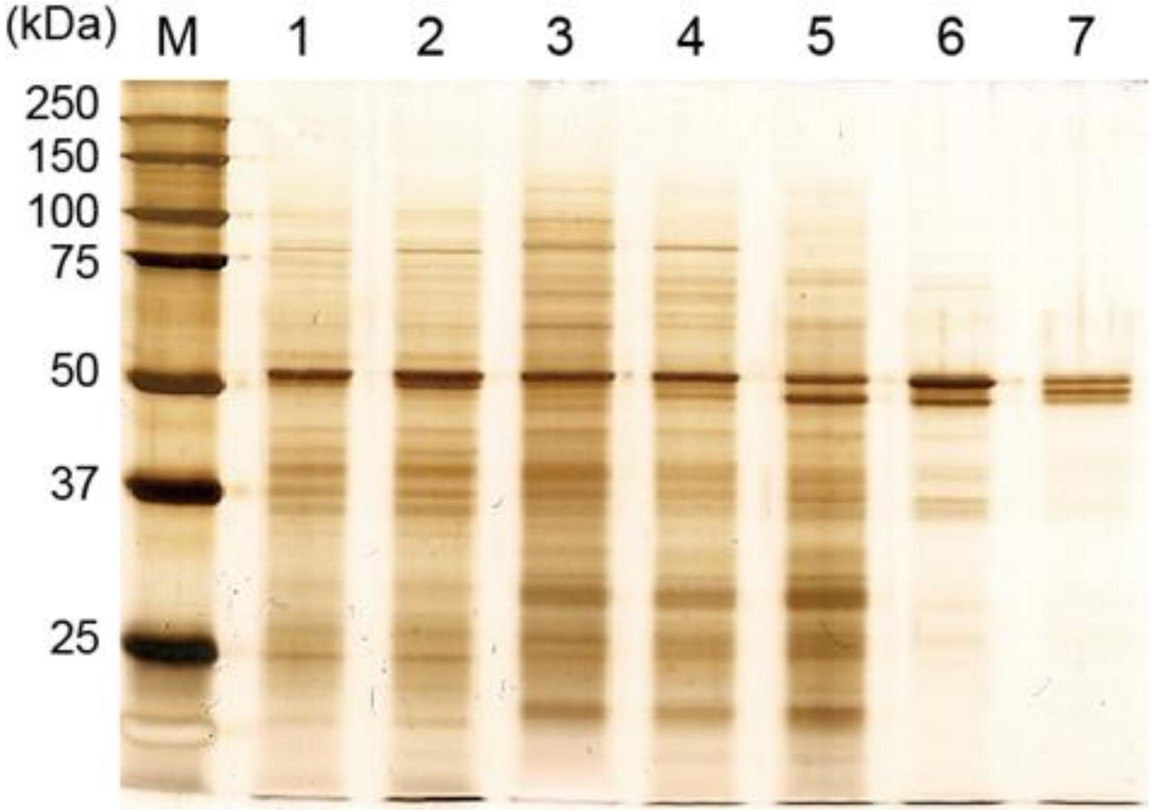
Supplemental Figure S1. **Co-expression analysis of AtLIS, CYP76Cs and UGT85A3 by ATTDII (Gene coexpression database, http://atted.jp/) with Ver. C4.1.**



Supplemental Figure S2. Enzymatic activity of CsGT1 homologs for (*Z*)-3-hexenol. *In vitro* characterization of UGT85s toward (*Z*)-3-hexenol with tea plant (CsGT1; UGT85K11), Arabidopsis (At_UGT85A3), grapevine (*Vitis vinifera*: Vv_UGT85A33, Vv_UGT85A28, Vv_UGT85A30) and snapdragon (*Antirrhinum majus*: Am_UGT85A13). LC-MS analysis of the enzymatic product of CsGT1 (UGT85K11), At_UGT85A1, At_UGT85A3, Vv_UGT85A33, Vv_UGT85A28, Vv_UGT85A30 and Am_UGT85A13 compared to the authentic standard ((*Z*)-3-hexenol).



Supplemental Figure S3. Enzymatic activity of CsGT1 homologs for geraniol. *In vitro* characterization of UGT85As toward geraniol with grapevine (*Vitis vinifera*: Vv_UGT85A33, Vv_UGT85A28, Vv_UGT85A30), sweet potato (*Ipomoea batatas*: Ib_UGT85A32), snapdragon (*Antirrhinum majus*: Am_UGT85A13). LC-MS analysis of the enzymatic product of Vv_UGT85A33, Vv_UGT85A28, Vv_UGT85A30 and Am_UGT85A13 and Ib_UGT85A32 compared to the authentic standard (geranyl-glu).



Supplemental Figure S4. Purified enzymes catalyzing the second xylosyltransferase (CsGT2). SDS-PAGE analysis of each active fraction obtained from purification steps. Lane 1; crude enzyme, lane 2; ammonium sulfate, lane 3; HiTrap DEAE FF, lane 4; HiTrap Q FF , lane 5; Macro-prep Ceramic Hydroxyapatite Type III, lane 6; HiTrap Blue HP, lane 7; Mono Q 5/50 GL. SDS-PAGE was staining by a silver staining methods (Sil-best stain one, Nacalai, Kyoto, Japan)

A)

Sequence	Charge	Observed *m/z*	*Mr* (Calc)
FPEVEKVELEEALPK	+3	586.3224	1755.9294
GLVVEGWAPQAR	+2	641.852	1281.6829
EEIEEIAHGLELSMVNFIWVVRFPEVEK	+4	840.4036	3357.6948

B)

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  1 ENEHSEIIQW  LDNKGEYSTL  FVSFGSEYFM  SKEEIEEIAH  GLELSMVNFI
 51 WVVRFPEVEK  VELEEALPKG  FIDRVGERGL  VVEGWAPQAR  ILTHSSTGGF
101 VSHCEWNSVL  ESLKFGVPMV  AIPMQYEQPL  NAKLVEEVGV  AAEVNRDING
151 RLNREEIAQV  IRKVVVEKSG  EDIRIKARIF  GDKIRMKGDE  EIDEAVEVLL
201 QLCKDVKLLK  NSNFIEIFKW  VEKVFYFYFI  LFYWVVWYTN  SLIRLYTSRR
251 STNIVFDHVV  LVLDLVALFF  IYIYRFTIIG  VIVSSFCSID  TGGILNMV
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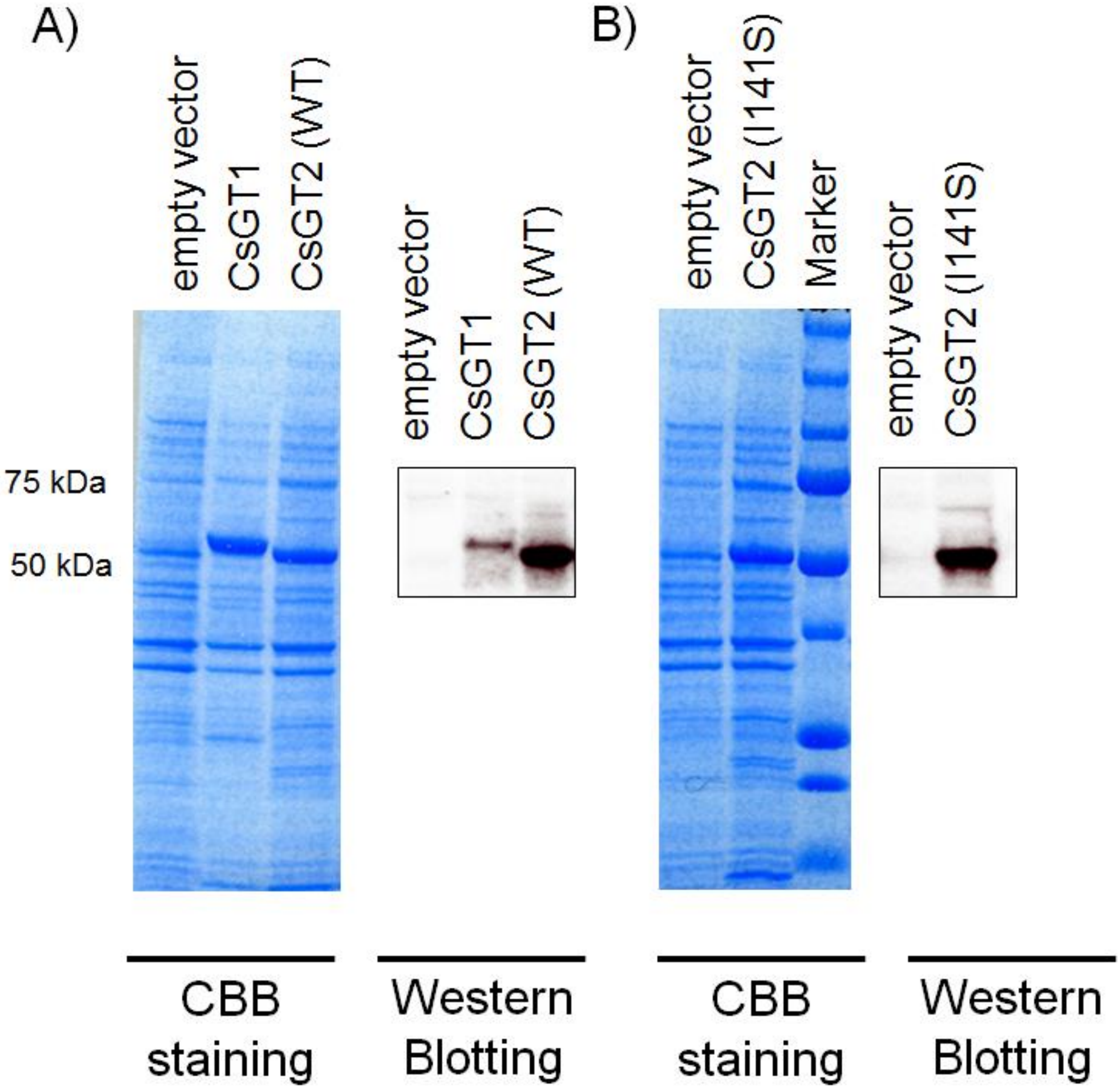
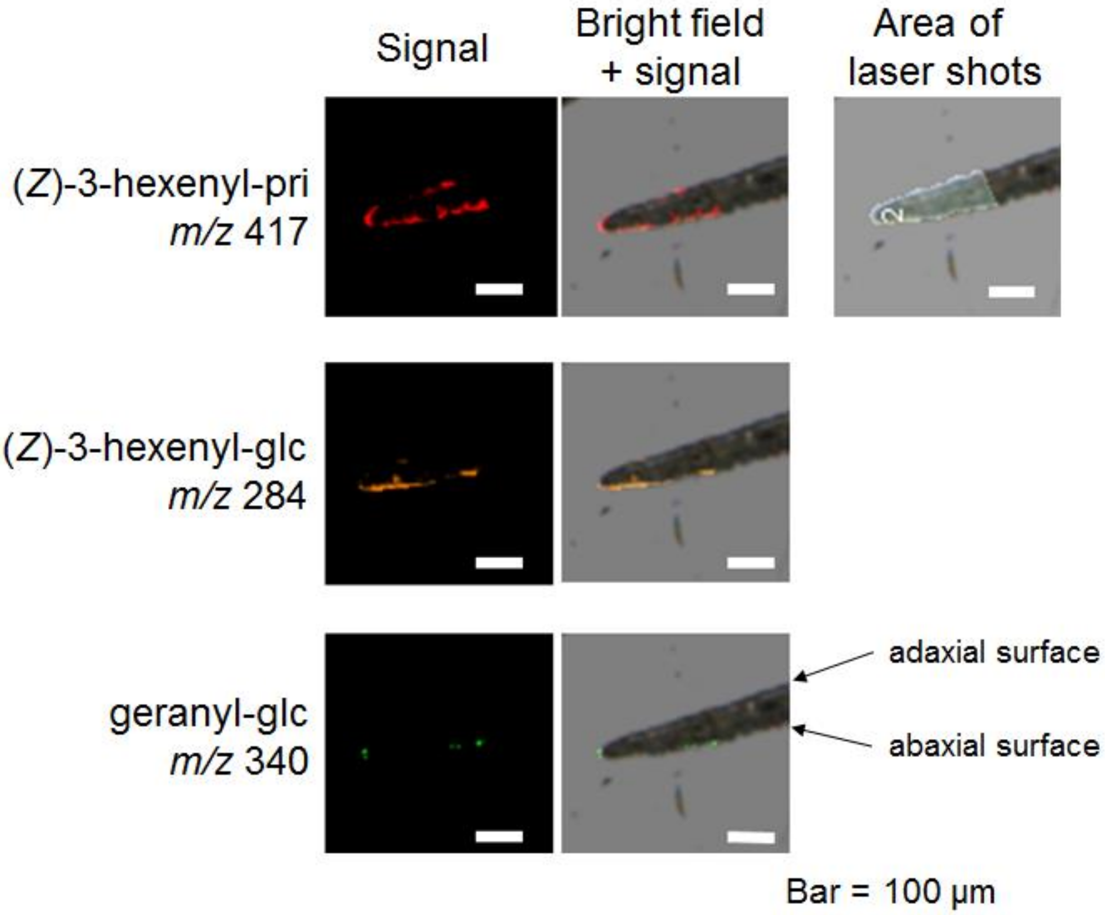
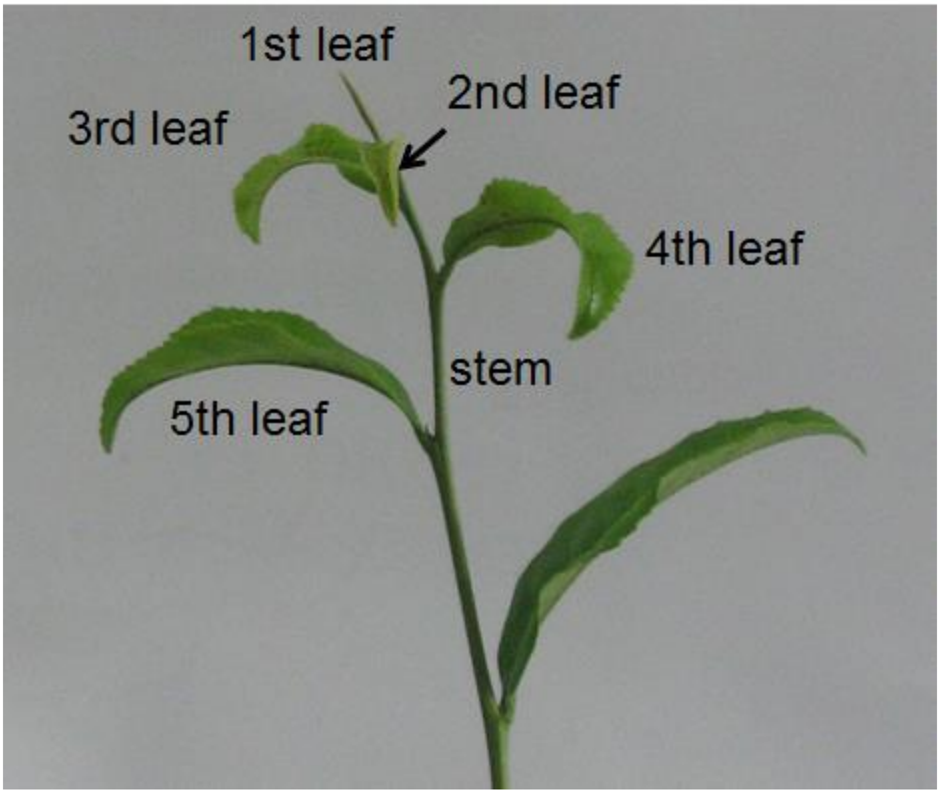
Supplemental Figure S5. Partial peptide sequence of the CsGT2. LC-MS/MS analysis of the partial peptide sequences of CsGT2 (UGT94P1) that purified from tea leaves. A) Three peptide sequences were exactly identified with tea EST database contig 13. B) Predicted amino acid sequence of tea EST database contig 134. Red letters show identical peptides with tea EST database and LC-MS/MS analytical results.



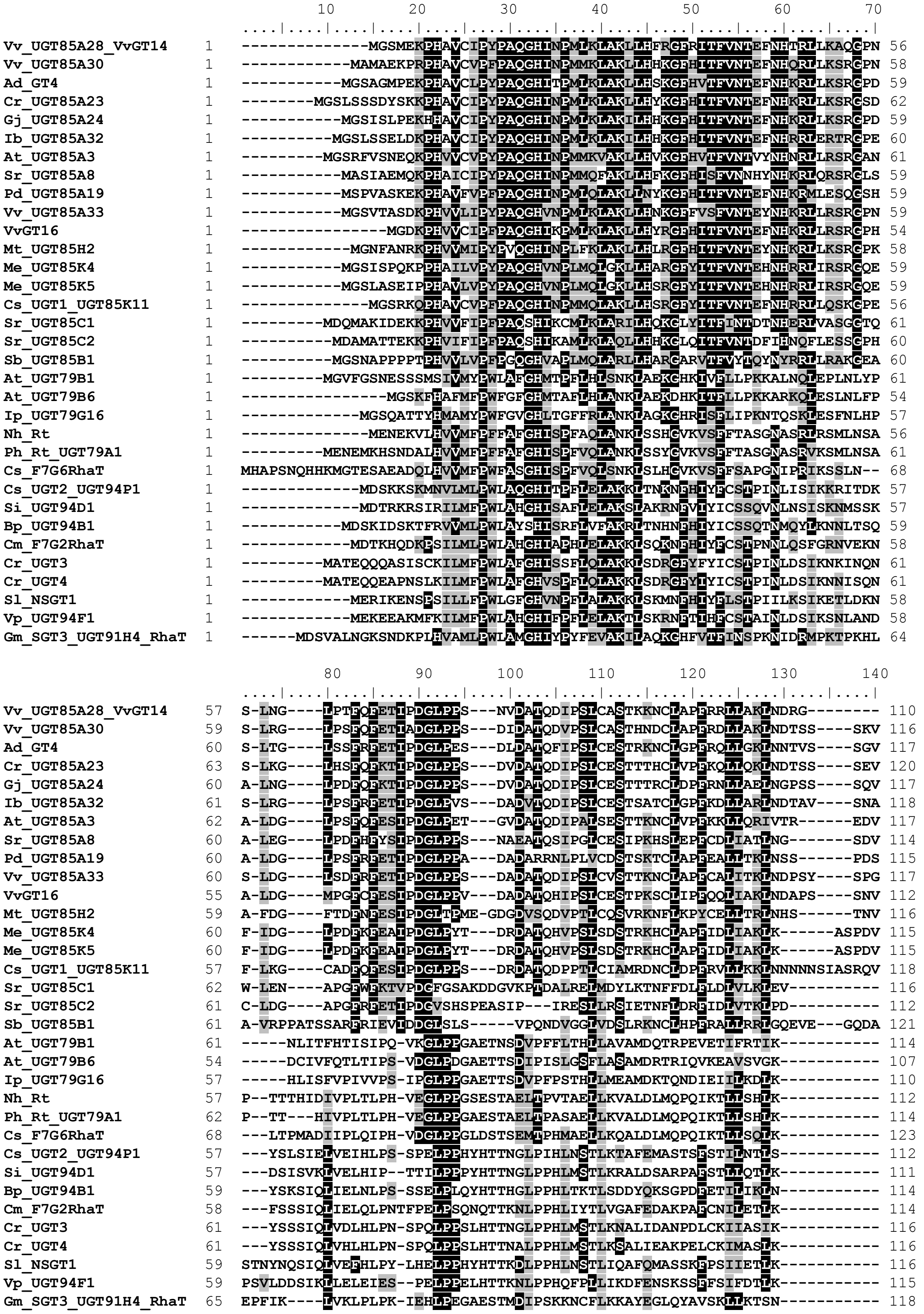
Supplemental Figure S6. Recombinant proteins of a series of CsGTs. Specific bands responsible of CsGT1 and CsGT2 (A), and CsGT2-I141S proteins (B) were detected around the size marker of 50kDa in SDS-PAGE, are roughly consistent with the estimated molecular size of CsGT1 (55.7 kDa) and CsGT2 (51.1 kDa), respectively. These specific bands were immunologically confirmed to be the recombinant CsGTs by Western blotting analysis.



Supplemental Figure S7. Imaging MS of young fresh leaves of *C.sinensis*. Specific signal (red; *m/z* 417) corresponding to (*Z*)-3-hexenyl-pri. Specific signal (orange; *m/z* 284) corresponding to (*Z*)-3-hexenyl-glc. Specific signal (green; *m/z* 340) corresponding to geranyl-glc.



Supplemental Figure S8. Harvesting individual tissues for quantification of endogenous aroma glycosides and quantitative real-time PCR (qRT-PCR) of CsGTs and β-PD. The young and mature developmental stages of leaves and stems were defined as follows: young leaves, which are the first, second, and third leaves (plucking part for high grade tea products); mature leaves, which are the fourth and fifth leaves; stem, which are green young non-lignified part between the 3rd leaf and 5th leaf; branch, which are brown lignified old part.



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Ad_GT4                1   -----------MGSAGMPEKPHAVCLPYPAQGHITPMLKLAKLLHSKGFHVTFVNTEFNHKRLLKSRGPD 59
Cr_UGT85A23           1   --------MGSLSSSDYSKKPHAVCIPYPAQGHINPMLKLAKLLHYKGFHITFVNTEFNHKRLLKSRGSD 62
Gj_UGT85A24           1   -----------MGSISLPEKHHAVCIPYPAQGHINPMLKLAKILHHKGFHITFVNTEFNHKRLLKSRGPD 59
Ib_UGT85A32           1   ----------MGSLSSELDKPHAVCIPYPAQGHINPMLKLAKILHHKGFHITFVNTEFNHRRLERTRGPE 60
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Sr_UGT85A8            1   -----------MASIAEMQKPHAICIPYPAQGHINPMMQFAKLLHFKGFHISFVNNHYNHKRLQRSRGLS 59
Pd_UGT85A19           1   -----------MSPVASKEKPHAVFVPFPAQGHINPMLQLAKLLNYKGFHITFVNTEFNHKRMLESQGSH 59
Vv_UGT85A33           1   -----------MGSVTASDKPHVVLIPYPAQGHVNPMLKLAKLLHNKGFFVSFVNTEYNHKRLLRSRGPN 59
VvGT16                1   ----------------MGDKPHVVCIPFPAQGHIKPMLKLAKLLHYRGFHITFVNTEFNHKRLLRSRGPH 54
Mt_UGT85H2            1   ------------MGNFANRKPHVVMIPYPVQGHINPLFKLAKLLHLRGFHITFVNTEYNHKRLLKSRGPK 58
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Me_UGT85K5            1   -----------MGSLASEIPPHAVLVPYPAQGHVNPLMQLGKLLHSRGFYITFVNTEHNHRRLIRSRGQE 59
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Sr_UGT85C1            1   ---------MDQMAKIDEKKPHVVFIPFPAQSHIKCMLKLARILHQKGLYITFINTDTNHERLVASGGTQ 61
Sr_UGT85C2            1   ----------MDAMATTEKKPHVIFIPFPAQSHIKAMLKLAQLLHHKGLQITFVNTDFIHNQFLESSGPH 60
Sb_UGT85B1            1   ----------MGSNAPPPPTPHVVLVPFPGQGHVAPLMQLARLLHARGARVTFVYTQYNYRRLLRAKGEA 60
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Ip_UGT79G16           1   -------------MGSQATTYHMAMYPWFGVGHLTGFFRLANKLAGKGHRISFLIPKNTQSKLESFNLHP 57
Nh_Rt                 1   --------------MENEKVLHVVMFPFFAFGHISPFAQLANKLSSHGVKVSFFTASGNASRLRSMLNSA 56
Ph_Rt_UGT79A1         1   ---------MENEMKHSNDALHVVMFPFFAFGHISPFVQLANKLSSYGVKVSFFTASGNASRVKSMLNSA 61
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Si_UGT94D1            1   -------------MDTRKRSIRILMFPWLAHGHISAFLELAKSLAKRNFVIYICSSQVNLNSISKNMSSK 57
Bp_UGT94B1            1   -----------MDSKIDSKTFRVVMLPWLAYSHISRFLVFAKRLTNHNFHIYICSSQTNMQYLKNNLTSQ 59
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Sl_NSGT1              1   ------------MERIKENSPSILLFPWLGFGHVNPFLALAKKLSKMNFHIYFLSTPIILKSIKETLDKN 58
Vp_UGT94F1            1   ------------MEKEEAKMFKILMFPWLAHGHIFPFLELAKTLSKRNFTIHFCSTAINLDSIKSNLAND 58
Gm_SGT3_UGT91H4_RhaT  1   ------MDSVALNGKSNDKPLHVAMLPWLAMGHIYPYFEVAKILAQKGHFVTFINSPKNIDRMPKTPKHL 64

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Gj_UGT85A24           60  A-LNG----LPDFQFKTIPDGLPPS---DVDATQDIPSLCESTTTRCLDPFRNLLAELNGPSS----SQV 117
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At_UGT85A3            62  A-LDG----LPSFQFESIPDGLPET---GVDATQDIPALSESTTKNCLVPFKKLLQRIVTR------EDV 117
Sr_UGT85A8            60  A-LEG----LPDFHFYSIPDGLPPS---NAEATQSIPGLCESIPKHSLEPFCDLIATLNG-------SDV 114
Pd_UGT85A19           60  A-LDG----LPSFRFETIPDGLPPA---DADARRNLPLVCDSTSKTCLAPFEALLTKLNSS------PDS 115
Vv_UGT85A33           60  S-LDG----LSDFRFETIPDGLPPS---DADATQDIPSLCVSTTKNCLAPFCALITKLNDPSY----SPG 117
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Mt_UGT85H2            59  A-FDG----FTDFNFESIPDGLTPME-GDGDVSQDVPTLCQSVRKNFLKPYCELLTRLNHS------TNV 116
Me_UGT85K4            60  F-IDG----LPDFKFEAIPDGLPYT---DRDATQHVPSLSDSTRKHCLAPFIDLIAKLK------ASPDV 115
Me_UGT85K5            60  F-IDG----LPDFKFEAIPDGLPYT---DRDATQHVPSLSDSTRKHCLAPFIDLIAKLK------ASPDV 115
Cs_UGT1_UGT85K11      57  F-LKG----CADFQFESIPDGLPPS---DRDATQDPPTLCIAMRDNCLDPFRVLLKKLNNNNNSIASRQV 118
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Sr_UGT85C2            61  C-LDG----APGFRFETIPDGVSHSPEASIP---IRESLLRSIETNFLDRFIDLVTKLPD---------- 112
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At_UGT79B6            54  -----DCIVFQTLTIPS-VDGLPDGAETTSDIPISLGSFLASAMDRTRIQVKEAVSVGK----------- 107
Ip_UGT79G16           57  -----HLISFVPIVVPS-IPGLPPGAETTSDVPFPSTHLLMEAMDKTQNDIEIILKDLK----------- 110
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Bp_UGT94B1            59  ---YSKSIQLIELNLPS-SSELPLQYHTTHGLPPHLTKTLSDDYQKSGPDFETILIKLN----------- 114
Cm_F7G2RhaT           58  ---FSSSIQLIELQLPNTFPELPSQNQTTKNLPPHLIYTLVGAFEDAKPAFCNILETLK----------- 114
Cr_UGT3               61  ---YSSSIQLVDLHLPN-SPQLPPSLHTTNGLPPHLMSTLKNALIDANPDLCKIIASIK----------- 116
Cr_UGT4               61  ---YSSSIQLVHLHLPN-SPQLPPSLHTTNALPPHLMSTLKSALIEAKPELCKIMASLK----------- 116
Sl_NSGT1              59  STNYNQSIQLVEFHLPY-LHELPPHYHTTKDLPPHLNSTLIQAFQMASSKFPSIIETLK----------- 116
Vp_UGT94F1            59  PSVLDDSIKLLELEIES--PELPPELHTTKNLPPHQFPLLIKDFENSKSSFFSIFDTLK----------- 115
Gm_SGT3_UGT91H4_RhaT  65  EPFIK----LVKLPLPK-IEHLPEGAESTMDIPSKKNCFLKKAYEGLQYAVSKLLKTSN----------- 118
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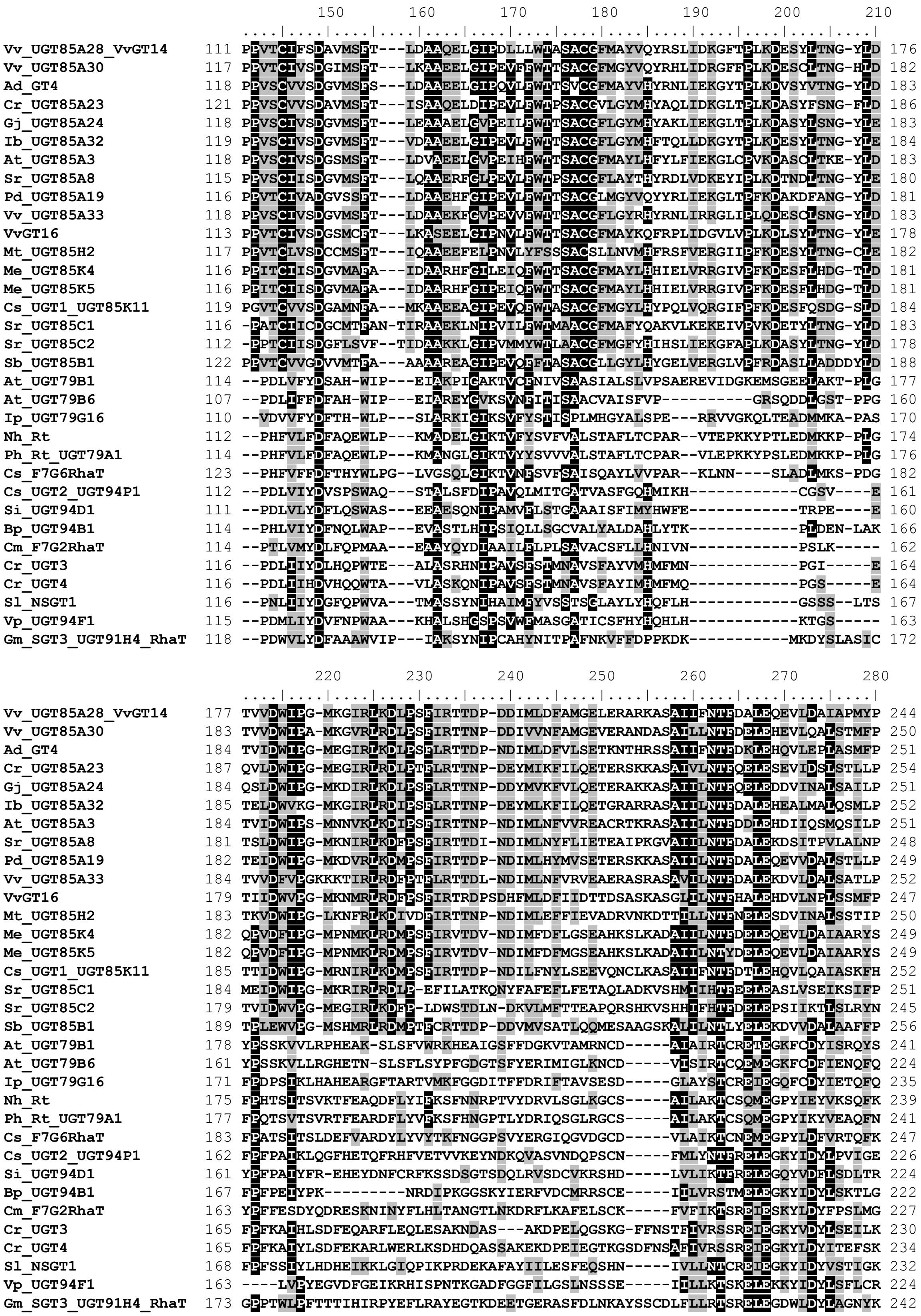
Supplemental Figure S9. Multiple sequence alignment of protein sequences of UGT-glucosyltransferase OG2 and OG8 family. The alignment was performed using ClustalW2.1.



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Vv_UGT85A30           117 PPVTCIVSDGIMSFT---LKAAEELGIPEVFFWTTSACGFMGYVQYRHLIDRGFFPLKDESCLTNG-HLD 182
Ad_GT4                118 PPVSCVVSDGVMSFS---LDAAEELGIPQVLFWTTSVCGFMAYVHYRNLIEKGYTPLKDVSYVTNG-YLD 183
Cr_UGT85A23           121 PPVSCVVSDAVMSFT---ISAAQELDIPEVLFWTPSACGVLGYMHYAQLIDKGLTPLKDASYFSNG-FLD 186
Gj_UGT85A24           118 PPVSCIVSDGVMSFT---LEAAAELGVPEILFWTTSACGFLGYMHYAKLIEKGLTPLKDASYLSNG-YLE 183
Ib_UGT85A32           119 PPVSCIVSDGVMSFT---VDAAEELGIPEVLFWTTSACGFLGYMHFTQLLDKGYTPLKDESYLTNG-YLE 184
At_UGT85A3            118 PPVSCIVSDGSMSFT---LDVAEELGVPEIHFWTTSACGFMAYLHFYLFIEKGLCPVKDASCLTKE-YLD 183
Sr_UGT85A8            115 PPVSCIISDGVMSFT---LQAAERFGLPEVLFWTPSACGFLAYTHYRDLVDKEYIPLKDTNDLTNG-YLE 180
Pd_UGT85A19           116 PPVTCIVADGVSSFT---LDAAEHFGIPEVLFWTTSACGLMGYVQYYRLIEKGLTPFKDAKDFANG-YLD 181
Vv_UGT85A33           118 PPVSCIVSDGVMSFT---LDAAEKFGVPEVVFWTTSACGFLGYRHYRNLIRRGLIPLQDESCLSNG-YLD 183
VvGT16                113 PPVTCIVSDGSMCFT---LKASEELGIPNVLFWTTSACGFMAYKQFRPLIDGVLVPLKDLSYLTNG-YLE 178
Mt_UGT85H2            117 PPVTCLVSDCCMSFT---IQAAEEFELPNVLYFSSSACSLLNVMHFRSFVERGIIPFKDESYLTNG-CLE 182
Me_UGT85K4            116 PPITCIISDGVMAFA---IDAARHFGILEIQFWTTSACGFMAYLHHIELVRRGIVPFKDESFLHDG-TLD 181
Me_UGT85K5            116 PPITCIISDGVMAFA---IDAARHFGIPEIQFWTTSACGFMAYLHHIELVRRGIVPFKDESFLHDG-TLD 181
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Sr_UGT85C1            116 -PATCIICDGCMTFAN-TIRAAEKLNIPVILFWTMAACGFMAFYQAKVLKEKEIVPVKDETYLTNG-YLD 183
Sr_UGT85C2            112 -PPTCIISDGFLSVF--TIDAAKKLGIPVMMYWTLAACGFMGFYHIHSLIEKGFAPLKDASYLTNG-YLD 178
Sb_UGT85B1            122 PPVTCVVGDVVMTFA---AAAAREAGIPEVQFFTASACGLLGYLHYGELVERGLVPFRDASLLADDDYLD 188
At_UGT79B1            114 --PDLVFYDSAH-WIP---EIAKPIGAKTVCFNIVSAASIALSLVPSAEREVIDGKEMSGEELAKT-PLG 177
At_UGT79B6            107 --PDLIFFDFAH-WIP---EIAREYGVKSVNFITISAACVAISFVP----------GRSQDDLGST-PPG 160
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Cm_F7G2RhaT           114 --PTLVMYDLFQPMAA---EAAYQYDIAAILFLPLSAVACSFLLHNIVN------------PSLK----- 162
Cr_UGT3               116 --PDLIIYDLHQPWTE---ALASRHNIPAVSFSTMNAVSFAYVMHMFMN------------PGI-----E 164
Cr_UGT4               116 --PDLIIHDVHQQWTA---VLASKQNIPAVSFSTMNAVSFAYIMHMFMQ------------PGS-----E 164
Sl_NSGT1              116 --PNLIIYDGFQPWVA---TMASSYNIHAIMFYVSSTSGLAYLYHQFLH------------GSSS--LTS 167
Vp_UGT94F1            115 --PDMLIYDVFNPWAA---KHALSHGSPSVWFMASGATICSFHYHQHLH------------KTGS----- 163
Gm_SGT3_UGT91H4_RhaT  118 --PDWVLYDFAAAWVIP---IAKSYNIPCAHYNITPAFNKVFFDPPKDK-----------MKDYSLASIC 172

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Vv_UGT85A30           183 TVVDWIPA-MKGVRLRDLPSFIRTTNP-DDIVVNFAMGEVERANDASAILLNTFDELEHEVLQALSTMFP 250
Ad_GT4                184 TVIDWIPG-MEGIRLKDLPSFLRTTDP-NDIMLDFVLSETKNTHRSSAIIFNTFDKLEHQVLEPLASMFP 251
Cr_UGT85A23           187 QVLDWIPG-MEGIRLRDLPTFLRTTNP-DEYMIKFILQETERSKKASAIVLNTFQELESEVIDSLSTLLP 254
Gj_UGT85A24           184 QSLDWIPG-MKDIRLKDLPSFLRTTNP-DDYMVKFVLQETERAKKASAIILNTFQELEDDVINALSAILP 251
Ib_UGT85A32           185 TELDWVKG-MKGIRLRDIPSFLRTTNP-DEYMLKFILQETGRARRASAIILNTFDALEHEALMALQSMLP 252
At_UGT85A3            184 TVIDWIPS-MNNVKLKDIPSFIRTTNP-NDIMLNFVVREACRTKRASAIILNTFDDLEHDIIQSMQSILP 251
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Pd_UGT85A19           182 TEIDWIPG-MKDVRLKDMPSFIRTTDP-NDIMLHYMVSETERSKKASAIILNTFDALEQEVVDALSTLLP 249
Vv_UGT85A33           184 TVVDFVPGKKKTIRLRDFPTFLRTTDL-NDIMLNFVRVEAERASRASAVILNTFDALEKDVLDALSATLP 252
VvGT16                179 TIIDWVPG-MKNMRLRDFPSFIRTRDPSDHFMLDFIIDTTDSASKASGLIILNTFHALEHDVLNPLSSMFP 247
Mt_UGT85H2            183 TKVDWIPG-LKNFRLKDIVDFIRTTNP-NDIMLEFFIEVADRVNKDTTILLNTFNELESDVINALSSTIP 250
Me_UGT85K4            182 QPVDFIPG-MPNMKLRDMPSFIRVTDV-NDIMFDFLGSEAHKSLKADAIILNTFDELEQEVLDAIAARYS 249
Me_UGT85K5            182 QPVDFIPG-MPNMKLRDMPSFIRVTDV-NDIMFDFMGSEAHKSLKADAIILNTYDELEQEVLDAIAARYS 249
Cs_UGT1_UGT85K11      185 TTIDWIPG-MRNIRLKDMPSFIRTTDP-NDILFNYLSEEVQNCLKASAIIFNTFDTLEHQVLQAIASKFH 252
Sr_UGT85C1            184 MEIDWIPG-MKRIRLRDLP-EFILATKQNYFAFEFLFETAQLADKVSHMIIHTFEELEASLVSEIKSIFP 251
Sr_UGT85C2            179 TVIDWVPG-MEGIRLKDFP-LDWSTDLN-DKVLMFTTEAPQRSHKVSHHIFHTFDELEPSIIKTLSLRYN 245
Sb_UGT85B1            189 TPLEWVPG-MSHMRLRDMPTFCRTTDP-DDVMVSATLQQMESAAGSKALILNTLYELEKDVVDALAAFFP 256
At_UGT79B1            178 YPSSKVVLRPHEAK-SLSFVWRKHEAIGSFFDGKVTAMRNCD-----AIAIRTCRETEGKFCDYISRQYS 241
At_UGT79B6            161 YPSSKVLLRGHETN-SLSFLSYPFGDGTSFYERIMIGLKNCD-----VISIRTCQEMEGKFCDFIENQFQ 224
Ip_UGT79G16           171 FPDPSIKLHAHEARGFTARTVMKFGGDITFFDRIFTAVSESD-----GLAYSTCREIEGQFCDYIETQFQ 235
Nh_Rt                 175 FPHTSITSVKTFEAQDFLYIFKSFNNRPTVYDRVLSGLKGCS-----AILAKTCSQMEGPYIEYVKSQFK 239
Ph_Rt_UGT79A1         177 FPQTSVTSVRTFEARDFLYVFKSFHNGPTLYDRIQSGLRGCS-----AILAKTCSQMEGPYIKYVEAQFN 241
Cs_F7G6RhaT           183 FPATSITSLDEFVARDYLYVYTKFNGGPSVYERGIQGVDGCD-----VLAIKTCNEMEGPYLDFVRTQFK 247
Cs_UGT2_UGT94P1       162 FPFPAIKLQGFHETQFRHFVETVVKEYNDKQVASVNDQPSCN-----FMLYNTFRELEGKYIDYLPVIGE 226
Si_UGT94D1            161 YPFPAIYFR-EHEYDNFCRFKSSDSGTSDQLRVSDCVKRSHD-----LVLIKTFRELEGQYVDFLSDLTR 224
Bp_UGT94B1            167 FPFPEIYPK---------NRDIPKGGSKYIERFVDCMRRSCE-----IILVRSTMELEGKYIDYLSKTLG 222
Cm_F7G2RhaT           163 YPFFESDYQDRESKNINYFLHLTANGTLNKDRFLKAFELSCK-----FVFIKTSREIESKYLDYFPSLMG 227
Cr_UGT3               165 FPFKAIHLSDFEQARFLEQLESAKNDAS---AKDPELQGSKG-FFNSTFIVRSSREIEGKYVDYLSEILK 230
Cr_UGT4               165 FPFKAIYLSDFEKARLWERLKSDHDQASSAKEKDPEIEGTKGSDFNSAFIVRSSREIEGKYLDYITEFSK 234
Sl_NSGT1              168 FPFSSIYLHDHEIKKLGIQPIKPRDEKAFAYIILESFEQSHN-----IVLLNTCREIEGKYIDYVSTIGK 232
Vp_UGT94F1            163 ----LVPYEGVDFGEIKRHISPNTKGADFGGFILGSLNSSSE-----IILLKTSKELEKKYIDYLSFLCR 224
Gm_SGT3_UGT91H4_RhaT  173 GPPTWLPFTTTIHIRPYEFLRAYEGTKDEETGERASFDLNKAYSSCDLFLLRTSRELEGDWLDYLAGNYK 242
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Supplemental Figure S9. *continued.*

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                                   290       300       310       320       330       340       350
                            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Vv_UGT85A28_VvGT14      245 P-IYTIGPLQLLPDQIHD-----SELKLIGSNLWKEEPECLKWLDSKEPNSVVYVNYGS-ITVMTPQQLI 307
Vv_UGT85A30             251 P-IYTIGPLQLLLNQMPD-----NDLKSIESNLWKEEPGCLEWLDAKEPESVVYVNFGS-VTVMTPQQLV 313
Ad_GT4                  252 P-IYTIGPLNLLMNQIKE-----ESLKMIGSNLWKEEPMCIEWLNSKEPKSVVYVNFGS-ITVMTPNQLV 314
Cr_UGT85A23             255 P-IYPIGPLQILQNQVDD-----ESLKVLGSNLWKEEPECLEWLDTKDPNSVVYVNFGS-ITVMTNDQLI 317
Gj_UGT85A24             252 P-IYTIGPLQFLQKEVKD-----ERLSVLGSNLWKEEPECLDWLDSKDPNSVVYVNFGS-ITVMTPGQLV 314
Ib_UGT85A32             253 P-VYAVGPLQFLQTQVKD-----SNVRALASNLWKEDTSCLEWLDTKEPNSVVYVNYGS-ITVMTPDQLL 315
At_UGT85A3              252 P-VYPIGPLHLLVNREIEE---DSEIGRMGSNLWKEETECLGWLNTKSRNSVVYVNFGS-ITIMTTAQLL 316
Sr_UGT85A8              249 Q-IYTIGPLHMMQ-QYVDH---DERLKHIGSNLWKEDVSCINWLDTKKPNSVVYVNFGS-ITVMTKEQLI 312
Pd_UGT85A19             250 P-IYSIGPLQLPYSEIPSE---YNDLKAIGSNLWAENTECLNWLDTKEPNSVVYVNFGS-TTVMTNEQLV 314
Vv_UGT85A33             253 P-VYSIGPLQHLVDQISD-----DRLKSMGSNLWKEQTDCLQWLDSKEPNSVVYVNFGS-ITVMTSQQLT 315
VvGT16                  248 T-ICTVGPLPLLLNQIPDD-------NSIESNLWREETECLQWLNSKQPNSVVYVNFGS-ITVMTPEQLV 308
Mt_UGT85H2              251 S-IYPIGPLPSLLKQTPQ----IHQLDSLDSNLWKEDTECLDWLESKEPGSVVYVNFGS-ITVMTPEQLL 314
Me_UGT85K4              250 KNIYTVGPFILLEKGIPEI-----KSKAFRSSLWKEDLSCLEWLDKREPDSVVYVNYGC-VTTITNEQLN 313
Me_UGT85K5              250 KNIYTVGPFILLEKGIPEI-----KSKAFRSSLWKEDLSCIEWLDKREPDSVVYVNYGC-VTTITNEQLN 313
Cs_UGT1_UGT85K11        253 N-IYTIGPLSLLSKQVIDG-----EFKSLNSSLWKEDTKCLQWLDTKEPNSVVYVNYGS-ITVMTDQHLK 315
Sr_UGT85C1              252 N-VYTIGPLQLLLNKITQKETNN-----DSYSLWKEEPECVEWLNSKEPNSVVYVNFGS-LAVMSLQDLV 314
Sr_UGT85C2              246 H-IYTIGPLQLLLDQIPEEKKQTGITSLHGYSLVKEEPECFQWLQSKEPNSVVYVNFGS-TTVMSLEDMT 313
Sb_UGT85B1              257 P-IYTVGPLAEVIASSDSAS---AGLAAMDISIWQEDTRCLSWLDGKPAGSVVYVNFGS-MAVMTAAQAR 321
At_UGT79B1              242 KPVYLTG----PVLPGSQP------------NQPSLDPQWAEWLAKFNHGSVVFCAFGSQPVVNKIDQFQ 295
At_UGT79B6              225 RKVLLTG----PMLPEPDN------------SKP-LEDQWRQWLSKFDPGSVIYCALGS-QIILEKDQFQ 276
Ip_UGT79G16             236 KPVLLAG----PALPVP--------------SKSTMEQKWSDWLGKFKEGSVIYCAFGS-ECTLRKDKFQ 286
Nh_Rt                   240 KPVLLVG----PVV-PDPP------------SGK-LEEKWDAWLNKFEAGTVIYCSFGS-ETFLKDDQIK 290
Ph_Rt_UGT79A1           242 KPVFSNR----TRS-SGPA------------SGK-LEEKWATWLNKFEGGTVIYCSFGS-ETFLTDDQVK 292
Cs_F7G6RhaT             248 KPVLLTG----PLVNPEPP------------SGE-LEERWANWLGKFPPKSVIYCSFGS-ETFLTVDQIK 299
Cs_UGT2_UGT94P1         227 KKVVPVG----PLVQGIDD------------DE-NEHSEIIQWLDNKGEYSTLFVSFGS-EYFMSKEEIE 278
Si_UGT94D1              225 KRFVPVG----PLVQEVGC------------DMENEGNDIIEWLDGKDRRSTVFSSFGS-EYFLSANEIE 277
Bp_UGT94B1              223 KKVLPVG----PLVQEASL------------LQ-DDHIWIMKWLDKKEESSVVFVCFGS-EYILSDNEIE 274
Cm_F7G2RhaT             228 NEIIPVG----PLIQEP--------------TFKVDDTKIMDWLSQKEPRSVVYASFGS-EYFPSTDEIH 278
Cr_UGT3                 231 SKVIPVCPVIS-LNNNDQG------------QGNKDEDEIIQWLDKKSHRSSVFVSFGS-EYFLNMQEIE 286
Cr_UGT4                 235 RKVMPVCLANSPDNNNHQE------------QSNKDGDELIQWLETKSERSSVFVSFGS-EYFLNKQEFE 291
Sl_NSGT1                233 KELIPIGPLIREAMIDEEE----------------DWGTIQSWLDKKDQLSCVYVSFGS-ESFLSKQEIE 285
Vp_UGT94F1              225 KQIIPTG-------LLIAN------------SDEKDEPEIMQWLDEKSERSTVYISFGS-ECFLSKEQIE 274
Gm_SGT3_UGT91H4_RhaT    243 VPVVPVGLLPPSMQIRDVE----------EEDNNPDWVRIKDWLDTQESSSVVYIGFGS-ELKLSQEDLT 301

                                   360       370       380       390       400       410       420
                            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Vv_UGT85A28_VvGT14      308 EFAWGLANSNQSFLWILRPDLVSG----ESAILPPEFVAETED----RGLLAGWCPQEQVLTHQAIGGFL 369
Vv_UGT85A30             314 EFAWGLANANLKFLWIIRPDLVAG----DAAILPADFVAQTKE----RSLLASWCPQERVLTHPAIGGFL 375
Ad_GT4                  315 EFAWGLANSNQSFLWIIRPDLVVG----ESAVLPPEFVAVTKE----RGMLASWAPQEEVLAHSSVGGFL 376
Cr_UGT85A23             318 EFAWGLANSKQNFLWIIRPDLISG----ESSILGEEFVEETKE----RGLIASWCHQEQVINHPAIGGFL 379
Gj_UGT85A24             315 EFAWGLANSKQTFLWIIRPDLVSG----DSAILPPEFLEETKD----RGLLASWCPQEQVLSHPAIGGFL 376
Ib_UGT85A32             316 EFAWGLANSKKPFLWIVRPDLVTG----EAAIIPPEFLEETKD----RGMLSSWCSQEQVLNHPAIGGFL 377
At_UGT85A3              317 EFAWGLAATGKEFLWVMRPDSVAG----EEAVIPKEFLAETAD----RRMLTSWCPQEKVLSHPAVGGFL 378
Sr_UGT85A8              313 EFGWGLANSKKDFLWITRPDIVGG----NEAMIPAEFIEETKE----RGMVTSWCSQEEVLKHPSIGVFL 374
Pd_UGT85A19             315 EFSWGLANSKKPFLWIIRPGLVAG----ETAVVPPEFLEETKE----RGMLASWCPQEQVLLHSAIGGFL 376
Vv_UGT85A33             316 EFAWGLANSNKPFLWIIRPDLVVG----DSALLPPEFVTETKD----RGMLASWCPQEQVLKHPAIGGFL 377
VvGT16                  309 EFAWGLANSHKPFLWIIRPDLVVG----DSVILPPEFVNETIQ----RGLMAGWCPQEKVLNHPSVGGFL 370
Mt_UGT85H2              315 EFAWGLANCKKSFLWIIRPDLVIG----GSVIFSSEFTNEIAD----RGLIASWCPQDKVLNHPSIGGFL 376
Me_UGT85K4              314 EFAWGLANSKHPFLWIVRPDVVMG----ESAVLPEEFYEEIKD----RGLLVSWVPQDRVLQHPAVGVFL 375
Me_UGT85K5              314 EFAWGLANSKHPFLWIVRPDVVMG----ESAVLPEEFYEAIKD----RGLLVSWVPQDRVLQHPAVGVFL 375
Cs_UGT1_UGT85K11        316 EFAWGLANSKHPFLWIVRPDIVMG----DSAILPEHFVEETKD----RGLLVSWCPQEQVLSHPSIGVFL 377
Sr_UGT85C1              315 EFGWGLVNSNHYFLWIIRANLIDG----KPAVMPQELKEAMNE----KGFVGSWCSQEEVLNHPAVGGFL 376
Sr_UGT85C2              314 EFGWGLANSNHYFLWIIRSNLVIG----ENAVLPPELEEHIKK----RGFIASWCSQEKVLKHPSVGGFL 375
Sb_UGT85B1              322 EFALGLASCGSPFLWVKRPDVVEG----EEVLLPEALLDEVAR---GRGLVVPWCPQAAVLKHAAVGLFV 384
At_UGT79B1              296 ELCLGLESTGFPFLVAIKPPSGVS---TVEEALPEGFKERVQ--GR-GVVFGGWIQQPLVLNHPSVGCFV 359
At_UGT79B6              277 ELCLGMELTGLPFLVAVKPPKGSS---TIQEALPKGFEERVK--AR-GVVWGGWVQQPLILAHPSIGCFV 340
Ip_UGT79G16             287 ELLWGLELTGMPFFAALKPPFETE---SVEAAIPEELKEKIQ--GR-GIVHGEWVQQQLFLQHPSVGCFV 350
Nh_Rt                   291 ELALGLEQTGLPFFLVLNFPANVDASAELNRGLPEGFRERVK--EK-GVIHSGWVQQQHILAHTSVGCYV 357
Ph_Rt_UGT79A1           293 ELALGLEQTGLPFFLVLNFPANVDVSAELNRALPEGFLERVK--DK-GIIHSGWVQQQNILAHSSVGCYV 359
Cs_F7G6RhaT             300 ELAIGLEITGLPFFLVLNFPPNVDGQSELVRTLPPGFMDRVK--DR-GVVHTGWVQQQLILRHESVGCYV 366
Cs_UGT2_UGT94P1         279 EIAHGLELSMVNFIWVVRFP-EVE-KVELEEALSKGFIDRVG--ER-GLVVEGWAPQARILTHSSTGGFV 343
Si_UGT94D1              278 EIAYGLELSGLNFIWVVRFPHGDE-KIKIEEKLPEGFLERVE--GR-GLVVEGWAQQRRILSHPSVGGFL 343
Bp_UGT94B1              275 DIAYGLELSQVSFVWAIRAK----------TSALNGFIDRVG--DK-GLVIDKWVPQANILSHSSTGGFI 331
Cm_F7G2RhaT             279 DIAIGLLLTEVNFIWAFRLH-PDE-KMTIEEALPQGFAEEIERNNK-GMIVQGWVPQAKILRHGSIGGFL 345
Cr_UGT3                 287 EIAIGLELSNVNFIWVLRFP-KGE-DTKIEEVLPEGFLDRVK--TK-GRIVHGWAPQARILGHPSIGGFV 351
Cr_UGT4                 292 EISLGLELSNVNFIWVLRFP-KGE-DKKIEQVLPEGYLERVE--GR-GRIVQGWAPQAKILGHPNIGGFV 356
Sl_NSGT1                286 EIAKGLELSKVNFIWTIKFP-KGV-NKTIEEMVPQGFLESTK--GK-GMVIEGWAPQSLILNHSSIGGFI 350
Vp_UGT94F1              275 EVAKGLELSNVNFIWIIRFPEGKN-SMTVENALPEGFLERVK--GR-GMVIWKFAPQTRILAHKSIGGFV 340
Gm_SGT3_UGT91H4_RhaT    302 ELAHGIELSNLPFFWALKNLKEGV------LELPEGFEERTKE---RGIVWKTWAPQLKILAHGAIGGCM 362
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Supplemental Figure S9. *continued.*

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                                430       440       450       460       470       480       490
                         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Vv_UGT85A28_VvGT14   370 THNGWNSTIEGLCAGVPMICWPFFAEQQTNCRYCCTEWGVGMEIDSD-----VKRDEVAKLVRELMVGEK 434
Vv_UGT85A30          376 THSGWNSTIEGLCGGVPMICWPFFAEQMTNCRYCCTEWGVGMEIGND-----VTRDEVESLVRGLMEGEK 440
Ad_GT4               377 THCGWNSTLESISSGVAVVCWPFFAEQQTNCWYCCGELGIGMEIDSD-----VKREEVERLVRELMVGEK 441
Cr_UGT85A23          380 THNGWNSTIESISSGVPMICWPFFAEQQTNCRFCCNKWGIGMEINSD-----VKRDEVESLVKELMVGEK 444
Gj_UGT85A24          377 THSGWNSTLESICSGVPMICWPFFAEQQTNCWFCCTKWYNGLEIDNN-----VKRDEVESLVTELMVGEK 441
Ib_UGT85A32          378 THNGWNSTLESICSGVPMLCWPFFAEQQTNCHYACSKWGIGKEIDSN-----VKRDEVEKLVRELMEGEK 442
At_UGT85A3           379 THCGWNSTLESLSCGVPMVCWPFFAEQQTNCKFSCDEWEVGIEIGGD-----VKRGEVEAVVRELMDGEK 443
Sr_UGT85A8           375 THSGWNSTIESISNGVPMICWPFFAEQQTNCRYCCVEWEIGLEIDTD-----VKREEVEAQVREMMDGSK 439
Pd_UGT85A19          377 THSGWNSTLEALCGGVPLICWPFFAEQQTNVRYSCTQWGIGIEIDGE-----VKRDYIDGLVRTLMDGEE 441
Vv_UGT85A33          378 THSGWNSTSESICGGVPLICWPFFAEQQTNCRYSCSEWGIGMEIDNN-----VKRVEVEKLVRELMDGEK 442
VvGT16               371 THSGWNSTIESICAGVPMICWPFFAEQQTNCRYACTEWGVGMEIDNN-----VERDEVEKLVKELMEGEK 435
Mt_UGT85H2           377 THCGWNSTTESICAGVPMLCWPFFADQPTDCRFICNEWEIGMEIDTN-----VKREELAKLINEVIAGDK 441
Me_UGT85K4           376 SHCGWNSTIECISGGKPMICWPFFAEQQTNCKYACDVWKTGVELSTN-----LKREELVSIIKEMMETEI 440
Me_UGT85K5           376 SHCGWNSTIECISGGKPMICWPFFAEQQTNCKYACDVWKTGVELSTN-----LKREELVSIIKEMMETEI 440
Cs_UGT1_UGT85K11     378 THCGWNSTLESICGGVPIICWPFFAEQQTNCRYACTEWGIGMEVNHD-----VKRNEIVALINEMLEGDK 442
Sr_UGT85C1           377 THCGWGSIIESLSAGVPMLGWPSIGDQRANCRQMCKEWEVGMEIGKN-----VKRDEVEKLVRMLMEGLE 441
Sr_UGT85C2           376 THCGWGSTIESLSAGVPMICWPYSWDQLTNCRYICKEWEVGLEMGTK-----VKRDEVKRLVQELMG-EG 439
Sb_UGT85B1           385 SHCGWNSLLEATAAGQPVLAWPCHGEQTTNCRQLCEVWGNGAQLPRE-----VESGAVARLVREMMVGDL 449
At_UGT79B1           360 SHCGFGSMWESLMSDCQIVLVPQHGEQILNARLMTEEMEVAVEVER-EKKGWFSRQSLENAVKSVMEEGS 428
At_UGT79B6           341 SHCGFGSMWEALVNDCQIVFIPHLGEQILNTRLMSEELKVSVEVKR-EETGWFSKESLSGAVRSVMDRDS 409
Ip_UGT79G16          351 SHCGWASLSEALVNDCQIVLLPQVGDQIINARIMSVSLKVGVEVEKGEEDGVFSRESVCKAVKAVMDEKS 420
Nh_Rt                358 CHAGFSSVIEAFMNDCQVVMLPQKGDQLLNAKLVSGDMKAGVEVNRRDEDGYFSKDDIEEAVEKVMVEK- 426
Ph_Rt_UGT79A1        360 CHAGFSSVIEALVNDCQVVMLPQKGDQILNAKLVSGDMEAGVEINRRDEDGYFGKEDIKEAVEKVMVDVE 429
Cs_F7G6RhaT          367 CHSGFSSVTEAVISDCQLVLLPLKGDQFLNSKLVAGDLKAGVEVNRRDHDGHFGKEDIFKAVKTVMVDVN 436
Cs_UGT2_UGT94P1      344 SHCGWNSVLESLKFGVPMVAIPMQYEQPLNAKLVEEVG-VAAEVNRD-INGRLNREEIAQVIRKVVVEKS 411
Si_UGT94D1           344 SHCGWSSVMEGVYSGVPIIAVPMHLDQPFNARLVEAVG-FGEEVVRS-RQGNLDRGEVARVVKKLVMGKS 411
Bp_UGT94B1           332 SHCGWSSTMESIRYGVPIIAMPMQFDQPYNARLMETVG-AGIEVGRD-GEGRLKREEIAAVVRKVVVEDS 399
Cm_F7G2RhaT          346 SHCGWGSVVEGMVFGVPIIGVPMAYEQPSNAKVVVDNG-MGMVVPRDKINQRLGGEEVARVIKHVVLQEE 414
Cr_UGT3              352 SHCGWNSVMESIQIGVPIIAMPMNLDQPFNARLVVEIG-VGIEVGRD-ENGKLKRERIGEVIKEVAIGKK 419
Cr_UGT4              357 SHCGWNSVMESIEIGVPIIAIPMITDQPFNARLAVEIG-VGVEVRRE-ENGKVKRESVAEAIKEVVVMGK 424
Sl_NSGT1             351 THCGWNSILESMSFGIPIIAMPMNHDQPLNSRLVEELG-IGVEILRG-ENGKIMKEEVAKGIRKVIEEKP 418
Vp_UGT94F1           341 SHCGWSSITESVYFGVPIIAMPMKFEQVVNGVVVVEVG-VGVEVEKDGSGQYLGEEVAKALDKVFGDNEF 409
Gm_SGT3_UGT91H4_RhaT 363 SHCGSGSVIEKVHFGHVLVTLPYLLDQCLFSRVLEEKQ-VAVEVPRSEKDGSFTRVDVAKTLRFAIVDEE 431

                                500       510       520       530       540
                         ....|....|....|....|....|....|....|....|....|....|....|...
Vv_UGT85A28_VvGT14   435 GKVMKKKTMEWKHRAEVATTGPDGSSYLNLEKIFEQVLL------------------- 473
Vv_UGT85A30          441 GKEMKKKAMEWKRMAEAATTTPAGSSYSNLDKMINQVLLSKSPC-------------- 484
Ad_GT4               442 GKEMKERAMGWKRLAEEATQSSSGSSFLNLDKLVHQVLLSPRP--------------- 484
Cr_UGT85A23          445 GKEMKKKALEWKNIAEVTTTKPDGSSYSNLEKLIKVLKSKPSH--------------- 487
Gj_UGT85A24          442 GMDMKKKALEWKNKAEEAAKSSGGSSYSNLEKVVQVLLSK------------------ 481
Ib_UGT85A32          443 GGEMKKKAMEWKKLAEEAATSSIGSSHINIDKLINLHLLPPKY--------------- 485
At_UGT85A3           444 GKKMREKAVEWRRLAEKATKLPCGSSVINFETIVNKVLLGKIPNT------------- 488
Sr_UGT85A8           440 GKMMKNKALEWKKKAEEAVSIGG-SSYLNFEKLVTDVLLRK----------------- 479
Pd_UGT85A19          442 GKKMRKKALEWKKLAEDATSPKG-SSYLALENVVSKVLLSPRD--------------- 483
Vv_UGT85A33          443 GKEMKKKVMEWKKLAEEATRPGG-SSYDNFNKLLRNVLSKK----------------- 482
VvGT16               436 GKSMKKAAMEWRTKAEEAT-APCGSSYLNLDKLVDILLTKP----------------- 475
Mt_UGT85H2           442 GKKMKQKAMELKKKAEENTRPGG-CSYMNLNKVIKDVLLKQN---------------- 482
Me_UGT85K4           441 GRERRRRAVEWRKKAEEAISVGG-VSYNNFDTFIKEVILQQQTQ-------------- 483
Me_UGT85K5           441 GRERRRRAVEWRKKAEEATSVGG-VSYNNFDRFIKEAILQHKTK-------------- 483
Cs_UGT1_UGT85K11     443 GKQMRKKALKLKKEAEEATDVGG-LSYNNFDRLIKEALHYCEQY-------------- 485
Sr_UGT85C1           442 GERMRKKALEWKKSATLATCCNGSSSLDVEKLANEIKKLSRN---------------- 483
Sr_UGT85C2           440 GHKMRNKAKDWKEKARIAIAPNGSSSLNIDKMVKEITVLARN---------------- 481
Sb_UGT85B1           450 GKEKRAKAAEWKAAAEAAARKGGASWRNVERVVNDLLLVGGKQ--------------- 492
At_UGT79B1           428 -EIGEKVRKNHDKWRCVLTDSGFSDGYIDKFEQNLIELVKS----------------- 468
At_UGT79B6           409 -ELGNWARRNHVKWKESLLRHGLMSGYLNKFVEALEKLVQNINLE------------- 453
Ip_UGT79G16          420 -EIGREVRGNHDKLRGFLMNADLDSKYMDSFNQKLQDLLG------------------ 459
Nh_Rt                426 -----VIRENQKKWKEFLLNKDTHSKFVEDLVHDMMAMAKLSTT-------------- 465
Ph_Rt_UGT79A1        430 KDPGKLIRENQKKWKEFLLNKDIQSKYIGNLVNEMTAMAKVSTT-------------- 473
Cs_F7G6RhaT          437 KEPGASIRANQKWWREFLLNGQIQDKFIADFVKDLKALA------------------- 475
Cs_UGT2_UGT94P1      412 GEDIRIKARIFGDKIRMKGDEEIDEAVEVLLQLCKDVKLLKN---------------- 453
Si_UGT94D1           412 GEGLRRRVEELSEKMREKGEEEIDSLVEELVTVVRRRERSNLKSENSMKKLNVMDDGE 469
Bp_UGT94B1           400 GESIREKAKELGEIMKKNMEAEVDGIVIENLVKLCEMNN------------------- 438
Cm_F7G2RhaT          415 AKQIRRKANEISESMKKIGDAQMSVVVEKLLQLVKKSE-------------------- 452
Cr_UGT3              420 GEKLRKTAKDLGQKLRDREKQDFDELAATLKQLCV----------------------- 454
Cr_UGT4              425 VEKLRKTANDFSKKMKNREKEELDEVVGLLKQLRNGPSSSPMSE-------------- 468
Sl_NSGT1             419 RKQIHLKAMQLSEKIKLKAIDEGVKKLLKLLY-------------------------- 450
Vp_UGT94F1           410 SKEVRYRASNLSDKIRENEEQEEDKVAEQLMSLCAKNKLQKCD--------------- 452
Gm_SGT3_UGT91H4_RhaT 432 GSALRENAKEMGKVFSSEELHNKYIQDFIDALQKYRIPSAS----------------- 472
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Supplemental Figure S9. *continued.*