

# Supplementary Materials

## Figure S1

A

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      *      20      *      40      *      60      *      80      *
Ciclev10020814m : ATGGGTTCAACCAGTTCAGAAACTCAAATAAGTCCAGCCCAAGGCTCGGATGAAGAGGCAAACCTCTGGCCATGCAATTAACCAGTGCCTCAGT : 95
CrOMT2          : ATGGGTTCAACCAGTTCAGAAACTCAAATAAGTCCAGCCCAAGGCTCGGATGAAGAGGCAAACCTCTGGCCATGCAATTAACCAGTGCCTCAGT : 95
HM641694.1     : ATGGGTTCAACCAGTTCAGAAACTCAAATAAGTCCAGCCCAAGGCTCGGATGAAGAGGCAAACCTCTGGCCATGCAATTAACCAGTGCCTCAGT : 95
                ATGGGTTCAACCAGTTCAGAAACTCAAATAAGTCCAGCCCAAGGCTCGGATGAAGAGGCAAACCTCTGGCCATGCAATTAACCAGTGCCTCAGT

      100      *      120      *      140      *      160      *      180      *
Ciclev10020814m : CTTGCCTATGGTTCTCAAATCAGCCATTGAGCTTGATCTTTTAGAGATCATCGCTAAAGCTGGGCCAGATGCTTTCATGTCTCCAAAAGACATAG : 190
CrOMT2          : CTTGCCTATGGTTCTCAAATCAGCCATTGAGCTTGATCTTTTAGAGATCATCGCTAAAGCTGGGCCAGATGCTTTCATGTCTCCAAAAGACATAG : 190
HM641694.1     : CTTGCCTATGGTTCTCAAATCAGCCATTGAGCTTGATCTTTTAGAGATCATCGCTAAAGCTGGGCCAGATGCTTTCATGTCTCCAAAAGACATAG : 190
                CTTGCCTATGGTTCTCAAATCAGCCATTGAGCTTGATCTTTTAGAGATCATCGCTAAAGCTGGGCCAGATGCTTTCATGTCTCCAAAAGACATAG

      200      *      220      *      240      *      260      *      280
Ciclev10020814m : CTTTCAGCTGCCACAAAGAACCAGATGCCATATCGTCTGATCGTATATTGCGCTTCTGGCGAGCTATTAGCTCTTAATGTCTCTTTG : 285
CrOMT2          : CTTTCAGCTGCCACAAAGAACCAGATGCCATATCGTCTGATCGTATATTGCGCTTCTGGCGAGCTATTAGCTCTTAATGTCTCTTTG : 285
HM641694.1     : CTTTCAGCTGCCACAAAGAACCAGATGCCATATCGTCTGATCGTATATTGCGCTTCTGGCGAGCTATTAGCTCTTAATGTCTCTTTG : 285
                CTTTCAGCTGCCACAAAGAACCAGATGCCATATCGTCTGATCGTATATTGCGCTTCTGGCGAGCTATTAGCTCTTAATGTCTCTTTG

      *      300      *      320      *      340      *      360      *      380
Ciclev10020814m : CGCAATCCTCCCGACGGCAAAGTTGAGAGGCTTTATGGCTTGCCCCCGTTTGTAAATTCCTACTAAAAATGAAGATGGTGTACACTTTCCGA : 380
CrOMT2          : CGCAATCCTCCCGACGGCAAAGTTGAGAGGCTTTATGGCTTGCCCCCGTTTGTAAATTCCTACTAAAAATGAAGATGGTGTACACTTTCCGA : 380
HM641694.1     : CGCAATCCTCCCGACGGCAAAGTTGAGAGGCTTTATGGCTTGCCCCCGTTTGTAAATTCCTACTAAAAATGAAGATGGTGTACACTTTCCGA : 380
                CGCAATCCTCCCGACGGCAAAGTTGAGAGGCTTTATGGCTTGCCCCCGTTTGTAAATTCCTACTAAAAATGAAGATGGTGTACACTTTCCGA

      *      400      *      420      *      440      *      460      *
Ciclev10020814m : TCTTTGTCTCATGAACCAAGACAAGTTCTCATGGAGAGCTGGTACTACTTAAAAGATGCAGTGTGAAGTGGCATTCCATTTACAAGGCC : 475
CrOMT2          : TCTTTGTCTCATGAACCAAGACAAGTTCTCATGGAGAGCTGGTACTACTTAAAAGATGCAGTGTGAAGTGGCATTCCATTTACAAGGCC : 475
HM641694.1     : TCTTTGTCTCATGAACCAAGACAAGTTCTCATGGAGAGCTGGTACTACTTAAAAGATGCAGTGTGAAGTGGCATTCCATTTACAAGGCC : 475
                TCTTTGTCTCATGAACCAAGACAAGTTCTCATGGAGAGCTGGTACTACTTAAAAGATGCAGTGTGAAGTGGCATTCCATTTACAAGGCCt

      480      *      500      *      520      *      540      *      560      *
Ciclev10020814m : ATGGGATGAATGCATTGATTACCATGGCAAAGATCTAAGATTCACAAGATTTTCAACAATGGAATGCTTCTCATTCTACCATTACCATGAAG : 570
CrOMT2          : ATGGGATGAATGCATTGATTACCATGGCAAAGATCTAAGATTCACAAGATTTTCAACAATGGAATGCTTCTCATTCTACCATTACCATGAAG : 570
HM641694.1     : ATGGGATGAATGCATTGATTACCATGGCAAAGATCTAAGATTCACAAGATTTTCAACAATGGAATGCTTCTCATTCTACCATTACCATGAAG : 570
                ATGGGATGAATGCATTGATTACCATGGCAAAGATCTAAGATTCACAAGATTTTCAACAATGGAATGCTTCTCATTCTACCATTACCATGAAG

      580      *      600      *      620      *      640      *      660
Ciclev10020814m : AAAATTCTGAAAATTACAAAGGGTTGAAGGCCTCAACTCAGTTGTCGACGTTGGTGGTGAATGGAGCCACACTTAACATGATTATCTCCAA : 665
CrOMT2          : AAAATTCTGAAAATTACAAAGGGTTGAAGGCCTCAACTCAGTTGTCGACGTTGGTGGTGAATGGAGCCACACTTAACATGATTATCTCCAA : 665
HM641694.1     : AAAATTCTGAAAATTACAAAGGGTTGAAGGCCTCAACTCAGTTGTCGACGTTGGTGGTGAATGGAGCCACACTTAACATGATTATCTCCAA : 665
                AAAATTCTGAAAATTACAAAGGGTTGAAGGCCTCAACTCAGTTGTCGACGTTGGTGGTGAATGGAGCCACACTTAACATGATTATCTCCAA

      *      680      *      700      *      720      *      740      *      760
Ciclev10020814m : GTATCCATCgATTAAGGCATcAACTTTGATTTGCCACATGTtGTCGAG-----CATGTTAGGGGAGACATGT : 733
CrOMT2          : GTATCCATCgATTAAGGCATcAACTTTGATTTGCCACATGTtATTcaggatgctccagcttttctGGTgTCGAGCATGtGGGGGAGACATGT : 760
HM641694.1     : GTATCCATCgATTAAGGCATcAACTTTGATTTGCCACATGTtATTcaggatgctccagcttttctGGTgTCGAGCATGtGGGGGAGACATGT : 760
                GTATCCATCgATTAAGGCATcAACTTTGATTTGCCACATGTtattcaggatgctccagcttttctGGTgTCGAGCATGtGGGGGAGACATGT

      *      780      *      800      *      820      *      840      *
Ciclev10020814m : TTGTTAGTGTTCAAAGGGAGATGCCATTTTATCAAGTGGATATGTCATGATTGGAGTGATGAGCACTGCGTGAAAATCTTGAAGAACTGCAT : 828
CrOMT2          : TTGTTAGTGTTCAAAGGGAGATGCCATTTTATCAAGTGGATATGTCATGATTGGAGTGATGAGCACTGCGTGAAAATCTTGAAGAACTGCAT : 855
HM641694.1     : TTGTTAGTGTTCAAAGGGAGATGCCATTTTATCAAGTGGATATGTCATGATTGGAGTGATGAGCACTGCGTGAAAATCTTGAAGAACTGCAT : 855
                TTGTTAGTGTTCAAAGGGAGATGCCATTTTATCAAGTGGATATGTCATGATTGGAGTGATGAGCACTGCGTGAAAATCTTGAAGAACTGCAT

      860      *      880      *      900      *      920      *      940      *

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Ciclev10020814m : GAAGCACTCCCAGTAAATGGGAAAGTCATTGTTGCTGAATCTATCCTCCCAGTAACCCCGGACACAAGCCTGGCATCCAAAGTAGTCATCCATGT : 923  
 CrOMT2 : GAAGCACTCCCAGTAAATGGGAAAGTCATTGTTGCTGAATCTATCCTCCCAGTAACCCCGGACACAAGCCTGGCATCCAAAGTAGTCATCCATGT : 950  
 HM641694.1 : GAAGCACTCCCAGTAAATGGGAAAGTCATTGTTGCTGAATCTATCCTCCCAGTAACCCCGGACACAAGCCTGGCATCCAAAGTAGTCATCCATGT : 950  
 GAAGCACTCCCAGTAAATGGGAAAGTCATTGTTGCTGAATCTATCCTCCCAGTAACCCCGGACACAAGCCTGGCATCCAAAGTAGTCATCCATGT

960 \* 980 \* 1000 \* 1020 \* 1040

Ciclev10020814m : CGACTGCATCATGTTGGCTCATAACCCGGGTGGCAAAGAGAGGACTGAACAAGAGTTCAGAGCATTGGCTAAGGCTGCTGGATTCCAAGGTTTCC : 1018  
 CrOMT2 : CGACTGCATCATGTTGGCTCATAACCCGGGTGGCAAAGAGAGGACTGAACAAGAGTTCAGAGCATTGGCTAAGGCTGCTGGATTCCAAGGTTTCC : 1045  
 HM641694.1 : CGACTGCATCATGTTGGCTCATAACCCGGGTGGCAAAGAGAGGACTGAACAAGAGTTCAGAGCATTGGCTAAGGCTGCTGGATTCCAAGGTTTCC : 1045  
 CGACTGCATCATGTTGGCTCATAACCCGGGTGGCAAAGAGAGGACTGAACAAGAGTTCAGAGCATTGGCTAAGGCTGCTGGATTCCAAGGTTTCC

\* 1060 \* 1080 \* 1100

Ciclev10020814m : AAGTGTGAGCTCTGCTTTAATACTTACATTATGGAATTCTCAAGAGTGCTTGA : 1074  
 CrOMT2 : AAGTGTGAGCTCTGCTTTAATACTTACATTATGGAATTCTCAAGAGTGCTTGA : 1101  
 HM641694.1 : AAGTGTGAGCTCTGCTTTAATACTTACATTATGGAATTCTCAAGAGTGCTTGA : 1101  
 AAGTGTGAGCTCTGCTTTAATACTTACATTATGGAATTCTCAAGAGTGCTTGA

**B**

\* 20 \* 40 \* 60 \* 80 \*

Ciclev10020814m : MGSTSSETQISPAQGSDEEANLLAMQLTSASVLPMLVKSATIELDLLEI IAKAGPDAFMSPKDIASQLPTKNPDAHIVLDRILRLLLASVYLNCSL : 95  
 CrOMT2 : MGSTSSETQISPAQGSDEEANLLAMQLTSASVLPMLVKSATIELDLLEI IAKAGPDAFMSPKDIASQLPTKNPDAHIVLDRILRLLLASVYLNCSL : 95  
 ADK97702.1 : MGSTSSETQISPAQGSDEEANLLAMQLTSASVLPMLVKSATIELDLLEI IAKAGPDAFMSPKDIASQLPTKNPDAHIVLDRILRLLLASVYLNCSL : 95  
 MGSTSSETQISPAQGSDEEANLLAMQLTSASVLPMLVKSATIELDLLEI IAKAGPDAFMSPKDIASQLPTKNPDAHIVLDRILRLLLASVYLNCSL

100 \* 120 \* 140 \* 160 \* 180 \*

Ciclev10020814m : RNLPDGKVERLYGLAPVCKFLTKNEDGVTLSDLCMLNQDKVLMESWYLLKDAVLEGGIPFNKAHGMNAFDYHGKDLRFNKIFNNGMSSHSTITMK : 190  
 CrOMT2 : RNLPDGKVERLYGLAPVCKFLTKNEDGVTLSDLCMLNQDKVLMESWYLLKDAVLEGGIPFNKAHGMNAFDYHGKDLRFNKIFNNGMSSHSTITMK : 190  
 ADK97702.1 : RNLPDGKVERLYGLAPVCKFLTKNEDGVTLSDLCMLNQDKVLMESWYLLKDAVLEGGIPFNKAHGMNAFDYHGKDLRFNKIFNNGMSSHSTITMK : 190  
 RNLPDGKVERLYGLAPVCKFLTKNEDGVTLSDLCMLNQDKVLMESWYLLKDAVLEGGIPFNKAHGMNAFDYHGKDLRFNKIFNNGMSSHSTITMK

200 \* 220 \* 240 \* 260 \* 280

Ciclev10020814m : KILENYKGFEGLSVVDVGGGIGATLNMIISKYPSIKGINFDLPHV S-----SMLGGDMFVSVPKGDAIFIKWICHDWSEHCVKFLKNCY : 276  
 CrOMT2 : KILENYKGFEGLSVVDVGGGIGATLNMIISKYPSIKGINFDLPHV IQDAPAFPVGEHVGGMDFVSVPKGDAIFIKWICHDWSEHCVKFLKNCY : 285  
 ADK97702.1 : KILENYKGFEGLSVVDVGGGIGATLNMIISKYPSIKGINFDLPHV IQDAPAFPVGEHVGGMDFVSVPKGDAIFIKWICHDWSEHCVKFLKNCY : 285  
 KILENYKGFEGLSVVDVGGGIGATLNMIISKYPSIKGINFDLPHV IQDAPAFPVGEHVGGMDFVSVPKGDAIFIKWICHDWSEHCVKFLKNCY

\* 300 \* 320 \* 340 \* 360

Ciclev10020814m : EALPVNGKVI AIESILPVPDTS LASKVVIHVDCIMLAHNPGGKERTEQEFRALAKAAGFQGFQVVSAPNTYIMEFLKSA : 357  
 CrOMT2 : EALPVNGKVI AIESILPVPDTS LASKVVIHVDCIMLAHNPGGKERTEQEFRALAKAAGFQGFQVVSAPNTYIMEFLKSA : 366  
 ADK97702.1 : EALPVNGKVI AIESILPVPDTS LASKVVIHVDCIMLAHNPGGKERTEQEFRALAKAAGFQGFQVVSAPNTYIMEFLKSA : 366  
 EALPVNGKVI AIESILPVPDTS LASKVVIHVDCIMLAHNPGGKERTEQEFRALAKAAGFQGFQVVSAPNTYIMEFLKSA

**C**

Percent identity matrix for DNA

	<i>Ciclev10020814m</i>	<i>CrOMT2</i>	<i>HM641694.1</i>
<i>Ciclev10020814m</i>	100.00	98.79	98.42
<i>CrOMT2</i>		100.00	99.64
<i>HM641694.1</i>			100.00

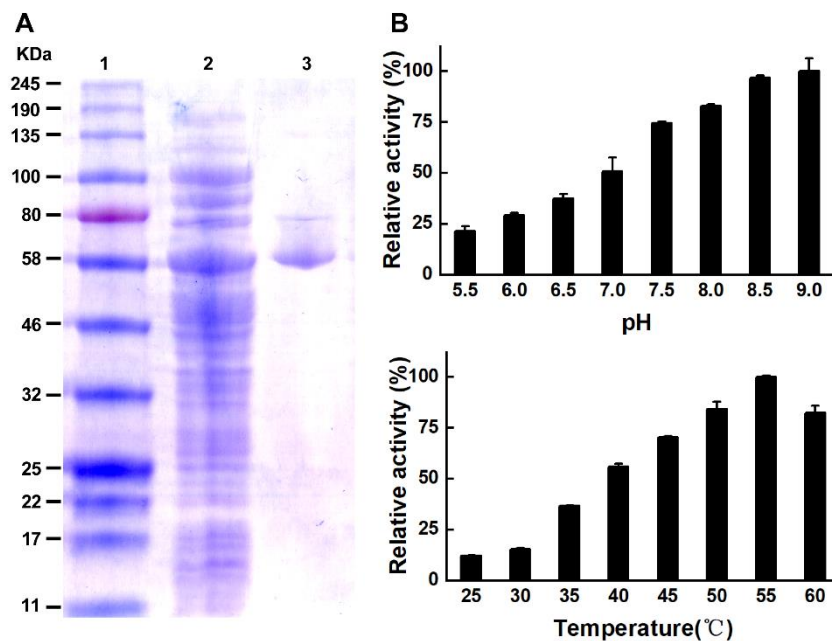
Percent identity matrix for protein

	<i>Ciclev10020814m</i>	<i>CrOMT2</i>	<i>ADK97702.1</i>
<i>Ciclev10020814m</i>	100.00	98.60	98.60
<i>CrOMT2</i>		100.00	100.00
<i>ADK97702.1</i>			100.00

**Figure S1** Sequences alignment of *Citrus reticulata* O-methyltransferase 2 (CrOMT2) and two paralogous genes from different citrus species at DNA and protein levels.

Complete CDs (A) and the deduced amino acid sequences (B) of *CrOMT2* and the two paralogous genes were aligned using Clustal2.1 and analyzed by GeneDoc, including *Ciclev10020814m* from *Citrus clementina*, *CrOMT2* from *Citrus reticulata*, and a putative caffeic acid *OMT* from *Citrus aurantium* (GenBank accession: HM641694.1 for complete CDs and ADK97702.1 for the deduced protein). The percent identity matrixes of the aligned sequences created by Clustal2.1 are shown (C).

**Figure S2**



**Figure S2** Biochemical characterization of the recombinant CrOMT2.

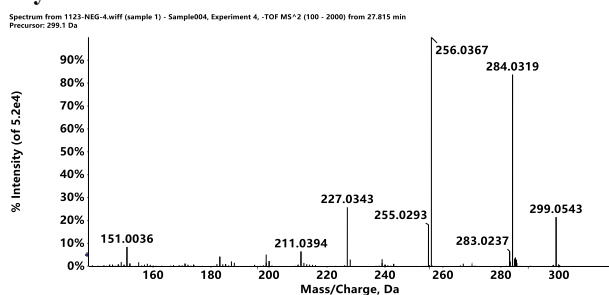
(A) SDS-PAGE profiles of the recombinant CrOMT2. Lanes: 1, the molecular weight of standard proteins; 2, unpurified fractions after induction; 3, purified enzyme.

(B) The dependency of the enzyme on pH and temperature.

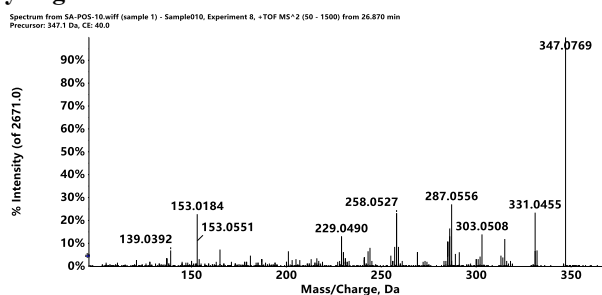
Enzyme activity was measured with luteolin as the substrate, and the corresponding product catalyzed by CrOMT2 was analyzed using HPLC. The data are shown as means  $\pm$  SE ( $n = 3$ ).

**Figure S3**

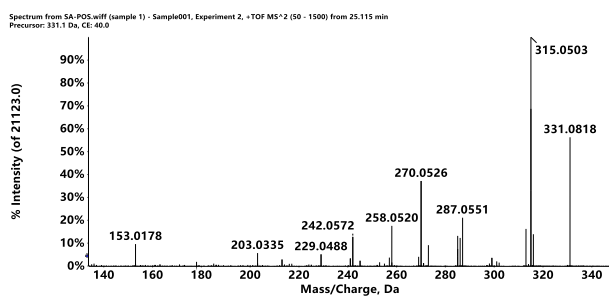
**A chrysoeriol standard**



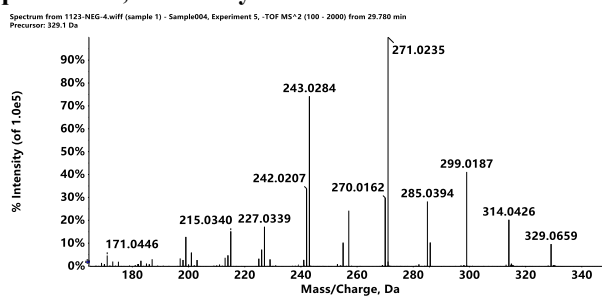
**E syringetin standard**



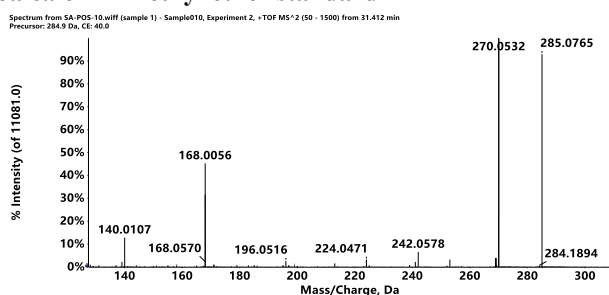
**B tricrin standard**



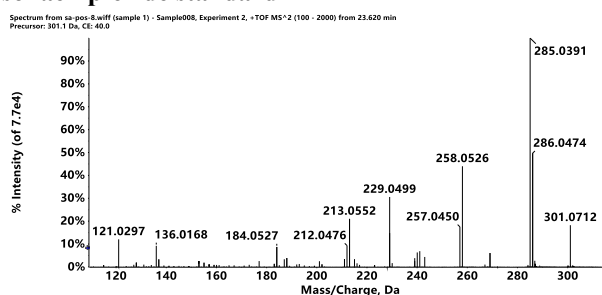
**F quercetin 3,3'-dimethyl ether standard**



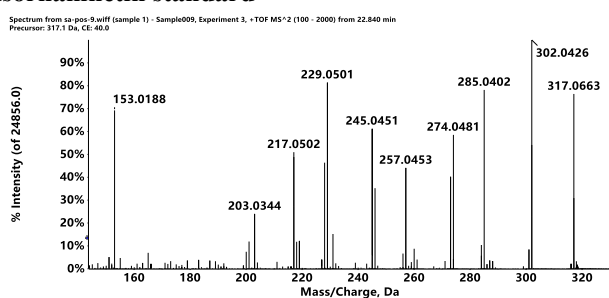
**C baicalein 7-methyl ether standard**



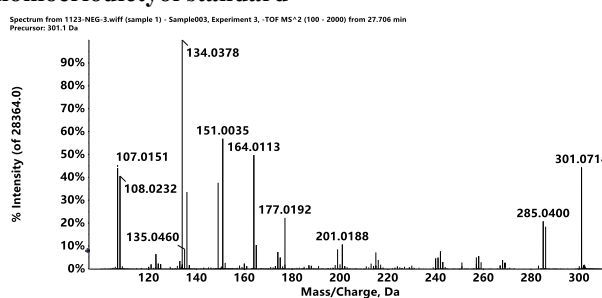
**G isokaempferide standard**



**D isorhamnetin standard**

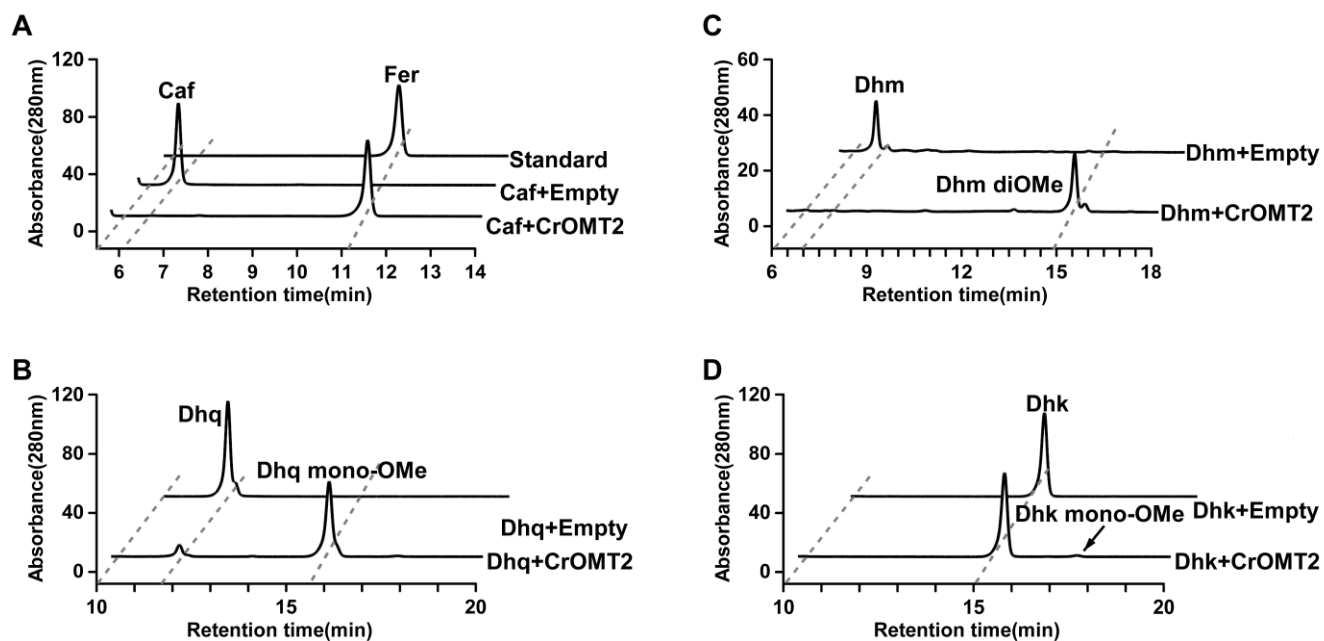


**H homoeriodictyol standard**



**Figure S3 MS/MS spectra of the authentic standards corresponding to the methylated products catalyzed by CrOMT2. Chrysoeriol (A), tricrin (B), baicalein 7-methyl ether (C), isorhamnetin (D), syringetin (E), quercetin 3,3'-dimethyl ether (F), isokaempferide (G), homoeriodictyol (H). (A, F, H) were operated in negative ions mode and the rest were in positive ions mode.**

**Figure S4**



**Figure S4** HPLC analysis of dihydroflavonols and caffeic acid methylation by recombinant CrOMT2.

HPLC chromatograms of enzyme reactions using caffeic acid (A), dihydroquercetin (B), dihydromyricetin (C) and dihydrokaempferol (D) are shown. The methylated product of caffeic acid produced by the recombinant CrOMT2 were inferred by comparison of the retention times with corresponding standards. For each dihydroflavonols substrate, a single peak generated by CrOMT2 was indicated. Caf, caffeic acid; Fer, ferulic acid; Dhq, dihydroquercetin; Dhm, dihydromyricetin; Dhk, dihydrokaempferol.

Figure S5

CaOMT1 1 M...L...FAMQLASASVLPMLVKSAIEEDLEITR
AtOMT1 1 MGSTAETQL T.P.VQ...V.T...DDE...AAL...FAMQLASASVLPMLVKSAIEEDLEIMA
ShMOMT1 1 MALSMNDI...V...I.S...NEE...EICMM...KAMHLE...CGLYLNMVVKSAIEDLDFEITA
ShMOMT2 1 MASNNC...AYELIE...EA...QSWDYLSYLRPSCKKCAIQGLGDFDILH
ShMOMT3 1 MALSMNDI...V...I.S...NEE...EYMM...KAMHLE...CGLYLNMVVKSAIEDLDFEITA
ShMOMT4 1 MALSMNDI...V...I.S...NEE...EYMM...KAMHLE...CGLYLNMVVKSAIEDLDFEITA
TaOMT1 1 MGSIA...A...G.A...DED...ACM...YALQLVSSSLPMLTKNAIEEDLLETLM
TaOMT2 1 MGSTAADMA...A...S.A...DEE...ACM...YALQLVSSSLPMLTKNAIEEDLLETLM
OsOMT1 1 MGSTAADMA...A...A.A...DEE...ACM...YALQLVSSSLPMLTKNAIEEDLLETLM
CrOMT2\* 1 MELQSS...EIRN...AQ...HFTQVFSFTSMSLKKAVQLGLGDFDAIH
CrCOMT1 1 MGSANPDNK N...S...M.T...KEEEE...ACL...SAMRLASASVLPMLVKSAIEDLDELTK
CrOMT6 1 MDLQTA...EFRE...AQ...KIWSQAFSANCALKKAVKLGADDAID
ObfOMT1 1 MRDEEA...A...AQ...FANNHGFGFKTSVVKTAIEEDLLETLM
ObfOMT2 1 MRDEEA...A...ARA...FANNHGFGFKTSVVKTAIEEDLLETLM
ObfOMT3 1 MVDKVEV...Q...LHA...QAWEHALSYINSTRALSAAVEEDLLETLM
ObfOMT4 1 MVDKVEV...Q...LHA...QAWDHALSYITPALSAAVEEDLLETLM
ObfOMT5 1 MVADEEA...Q...LHA...QAWDHALSYIKPTALSAAVEEDLLETLM
ObfOMT6 1 MVDKVEV...Q...LHA...QAWDHALSYIKPTALDAVEEDLLETLM
Obf8OMT-1 1 MPSSSGV...DSTQELLD...AQ...HIWNAIFNHNSMLKVAWGLGDFDIH
MpOMT3 1 MEASFENGR K.RSSS...S.S.S.EEE...SAS...FAMELAAGSVPMLVKSAIDLNLELTK
MpOMT1A 1 MAPEEDS...L...ALA...FANNHGFGFKTSVVKTAIEEDLLETLM
MpOMT1B 1 MAPKEDS...L...ALA...FANNHGFGFKTSVVKTAIEEDLLETLM
MpOMT4 1 MVADEV...R...VRA...FANNNAFGYIKPTAVATAVEEDLLETLM
MpOMT2 1 MALPNGI...SSKQELLE...AQ...HVWNHYSYINSMKLCALQGLGDFDAIH
CdfOMT5 1 MGSIVD...GER...DOSFA...YASQLVMGTVLPMAIQAVGLGDFEILD
ZmOMT1 1 MGSTAGDVA...V.V...DEE...ACM...YAMQSLPMLTKNAIEEDLLEVLQ
Hv7OMT 1 MQDTSSTQH KSL.PNNIEMDMVMTSMPLAENSNGQILQ...AEA...ELFCHSFGYKSMALQSVVKTRFEDVLH
HvOMT1 1 MGSIA...A...G.A...DED...ACM...YALQLVSSSLPMLTKNAIEEDLLETLM
MsCOMT1 1 MGSTGTEQI T.P.TH...I.S...DEE...ANL...FAMQLASASVLPMLVKSAIEDLLEITA
CrOMT2 1 MGSTSETQI T.P.AQ...G.S...DEE...ANL...LAMQLASASVLPMLVKSAIEDLLEITA
SaDMPM 1 MAPTEATR G.G.PADP...A.P...APEARRGGHT...EADPAEHAHQFGAQR...LTLVWGVYSSSELDLLETRD...PDLMG
consensus>70 M...e...a.q...i...lk.aieL...#...

CaOMT1 31 GQ...DT.CMSPTEIAASHLPTT.NPDAP.A.MVDRLRRLRSCYSVVTICSVRSVD...D...QRV...YGLTAPVCKRYLTKN
AtOMT1 50 KNG...S.PMSPTEIASKLPTK.NPEAP.V.MLDRRLRLRSLSYSLVLTCSNRKLS...GDG.VERI...YGLTAPVCKRYLTKN
ShMOMT1 48 KST...TQ.KLSSYEIASQIPTK.NPNASSLVLEIRLRLRFLASQSLTLCNITKND...DGNVHTT...YGLTAPVCKRYLTKN
ShMOMT2 45 KNA...D.PI...MSLSLDLIAALPNL.NPSKT.T.FPLRMLRVLVDFGLFNHYHQ...QQDGD...YSLTAPVCKRYLTKN
ShMOMT3 48 KST...TQ.KLSSYEIASQIPTK.NPNASSLVLEIRLRLRFLASQSLTLCNITKND...DGNVHTS...YGLTAPVCKRYLTKN
ShMOMT4 48 KST...TQ.KLSSYEIASQIPTK.NPNASSLVLEIRLRLRFLASQSLTLCNITKND...DGNVHTS...YGLTAPVCKRYLTKN
TaOMT2 43 AAG...G.KF.LTPAEVAAKLPST.A.NPEAP.D.MVDRMLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
TaOMT1 47 AAG...G.KL.LTPAEVAAKLPST.A.NPEAP.D.MVDRMLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
OsOMT1 47 SAAVAGGGG KAALLTPAEVADKLPST.A.NPEAA.D.MVDRMLRRLASVYNVVSCTMEEGA...DGRLSRR...YRAAPVCKRYLTKN
CrOMT2\* 42 SHG...K.P...MALSDLTNSLPI.NPSKA.P.YIYRMLRLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
CrCOMT1 50 KSG...P.GA.YVSPSELAALPTQ.NPDAP.V.MLDRRLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
CrOMT6 42 NHD...K.KA...LTLSELTEELSI.KPKSK.P.FLQRLMRRLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
ObfOMT1 40 NQG...G.P...LSLSALSSAVGV.P.P.D.RLHRIMRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
ObfOMT2 40 NHG...A.P...LSLSALSSAVGV.P.P.D.RLHRIMRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
ObfOMT3 40 DHG...G.L...MSLSSELSSAAGC.P.R.E.PLYRMLRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
ObfOMT4 40 DHG...G.L...MSLSSELSSAAGC.P.R.E.PLYRMLRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
ObfOMT5 40 NHG...G.P...MTLSSELSSAAGC.P.R.E.PLYRMLRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
ObfOMT6 40 DHG...G.P...MTLSSELSSAAGC.P.R.E.PLYRMLRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
Obf8OMT-1 47 KHD...K.P...MNTLSQIADAPI.NRAKS.D.ALHRIMRRLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
MpOMT3 53 RGG...E.E...GASAYELAAQINAE.NPKAA.AEMDIRLOLAAHSVLTCTRVETPP...SRR.RR...YSLTAPVCKRYLTKN
MpOMT1A 40 SRG...A.P...VSIPELATAVDC.S.A.D.RIYRVMRFLAYHGIFKRTKPPPLS...T.EGGSVY...YALQTVSRRLLTRD
MpOMT1B 40 SRG...A.P...VSIPELATAVDC.S.A.D.RIYRVMRFLAYHGIFKRTKPPPLS...T.EGGSVY...YALQTVSRRLLTRD
MpOMT4 40 NHD...G.P...MSLELSAATDC.P.A.E.PLHRMLRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
MpOMT2 47 KHG...N.P...ITLSQIADAPI.NRAKS.H.GLDIRMLRRLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
CdfOMT5 43 KVG...P.GAK.LCASDIAAQLLTK.NKAP.M.MLDRRLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
ZmOMT1 47 K...EAGGKAA.LAPEEVARMPAAGPDPAAAA.MVDRMLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
Hv7OMT 69 RY...G...ASLPELLSTVPI.HPNKL.P.YLRLRMLRFLVAVAGYVNSE...EKNV...YSLTAPVCKRYLTKN
HvOMT1 43 SAG...G.KF.LTPAEVAAKLPST.A.NPEAP.D.MVDRMLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
MsCOMT1 50 KAG...P.GA...QISPIEIASQIPTK.NPDAP.V.MLDRRLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
CrOMT2 51 KAG...P.DA...FMSPKDIASQIPTK.NPDAP.V.MLDRRLRRLASVYNVVSCTMEEGK...DGRLSRR...YRAAPVCKRYLTKN
SaDMPM 71 TEE...R.A...ALELAASLDT...D.P.V.A...R...r.\$r.l...v...EETGAGR...l.n
consensus>70 ...e...r.\$r.l...v...EETGAGR...l.n

CaOMT1 95 QD...GVSIAALCLMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
AtOMT1 117 ED...GVSIAALCLMNDQKVLME.S.W.YHLKDAI...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
ShMOMT1 107 KD...GVSIAALCLMNDQKVLME.S.W.YHLKDAI...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
ShMOMT2 107 HH...F.GNRSFFLEAQAHPVVLNT.A.ASVGDWL...KDDLRTA.F.ETADGKSHWDYCGADPE...F.NGVENDMAGDSRLM.SNL
ShMOMT3 117 KD...GVSIAALCLMNDQKVLME.S.W.YHLKDAI...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
ShMOMT4 117 KD...GSSIAALCLMNDQKVLME.S.W.YHLKDAI...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
TaOMT2 112 ED...GVSIAALCLMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
TaOMT1 116 ED...GVSMAALALMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
OsOMT1 123 ED...GVSMAALALMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
CrOMT2\* 100 DP...L.NSISMVLGVNQAELKA.W.NAMSEWF...QNEDLTA.F.ETAHGKNFWDFGAEADK...Y.GKNFEDGVMAADSVLV.SKM
CrCOMT1 119 ED...GVSMAALALMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
CrOMT6 112 EQWN...L.GI.VLTMLDPAELKA.W.SVLNDWF...KNDPTA.F.OTAHEKKNYDYTAENT...H.CQIFEDAMANDSVLV.SKL
ObfOMT1 101 N...L.GPFVLLQGA.Q.RGP.SACITAQGL...KSRERPG.V.EELGSDPLY...EDPI.FTEKVERDAMTCHARV.TSA
ObfOMT2 101 N...L.GAFVLLQGA.Q.RGP.SACITAQGL...KSRERPG.V.EELGSDPLY...EDPI.FTEKVERDAMTCHARV.TSA
ObfOMT3 94 N...L.GPYMMLQATPVTRSP.A.GLSGEAL...KTGTSLY.L.KSIRGEDSW...SDPAYGHMKFAETNAMIAHARLT.AAA
ObfOMT4 94 N...L.GPYMMLQATPVTRSP.A.GLSGEAL...KTGTSLY.L.KSIRGEDSW...SDPAYGHMKFAETNAMIAHARLT.AAA
ObfOMT5 94 N...L.GPYMMLQATPVTRSP.A.GLSGEAL...KTGTSLY.L.KSIRGEDSW...SDPAYGHMKFAETNAMIAHARLT.AAA
ObfOMT6 94 N...L.GPYMMLQATPVTRSP.A.GLSGEAL...KTGTSLY.L.KSIRGEDSW...SDPAYGHMKFAETNAMIAHARLT.AAA
Obf8OMT-1 110 EP...L.SLTPFALA.VLDEDLVDMGT.F.HCVPDEF...GNECPSP.L.EFKHFKSIRREFAEENNOR...W.SILENEGGMANDARLV.GSI
MpOMT3 120 ED...GASLAPLSLVQDRVFMFEP.W.YHLKDAV...V.EGGV.A.F.ERAYGVAHFYHAKDPK...F.NKVENRGMSDHSSTIT.MKK
MpOMT1A 104 N...L.GPFVLLQGT.M.REP.SGCVTAETL...RTSKRPG.VVNNENSDHLY...EDPV.FSMKVERDAMASHARLT.TAA
MpOMT1B 104 N...L.GPFVLLQGT.M.REP.SGCVTAETL...RTSKRPG.VVNNENSDHLY...EDPV.FSMKVERDAMASHARLT.TAA
MpOMT4 102 E...L.GDFFMLLQGTGLPSQHP.A.GLTAASL...RTGKQPF.I.RSVNGEDSW...TDPVNGYHMKFAETNAMIAHARLT.TAA
MpOMT2 118 EP...L.SVAPPFALASDPVYVET.W.HLHSEWF...RNDAVA.F.DTKYGMTFEYAVADD...L.NVLENEGGMANDAGV.NSI
CdfOMT5 109 ED...L.GVLLGGLLQGTGLPSQHP.A.GLTAASL...RTGKQPF.I.RSVNGEDSW...TDPVNGYHMKFAETNAMIAHARLT.TAA
ZmOMT1 120 ED...GVSMAALALMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
Hv7OMT 137 ASVNGGASMSPCVLLGTVPVLF.LA.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
HvOMT1 112 ED...GVSMAALALMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
MsCOMT1 119 ED...GVSIAALCLMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
CrOMT2 120 ED...GVTLSDDLCLMNDQKVLME.S.W.YHLKDAV...L.DGGI.P.F.NKAYGMSSEFYHGTDP...F.NKVENRGMSDHSSTIT.MKK
SaDMPM 122 TD...VPSLHAELVJ.RQCMGVFRQA.WSHF...I.RTGE.PAF.DVQVGTDFEYSYLSEPE...L.SGTEFSMREATR...STA
consensus>70 e...l.m...d...n...g...d...f...F.d.m...

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CaOMT1      167 VEQAA.Y..QGFQGLTSLVDVGGGTGATLTMILSKYBIRRCINFDLHVIEDAPEY.PGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
AtOMT1      189 ILET.Y..KFEGLTSLVDVGGGTGATLKMIVSKYBIRKGINFDLHVIEDAPSH.PGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ShMOMT1     189 IVEC.Y..NGFQGLTSLVDVGGGTGATLIIISKYBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ShMOMT2     179 LISD.CCAGVEGLTSLVDVGGGTGAVAMAIAGAFBIRKGINFDLHVIADRRKGS.GNLE.....HVGCDFMFSVPEK.GDAIFMKWIC
ShMOMT3     189 IVEC.Y..NGFQGLTSLVDVGGGTGATLIIISKYBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ShMOMT4     189 IVEC.Y..NGFQGLTSLVDVGGGTGATLIIISKYBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
TaOMT2      184 LLES.Y..KFEGLTSLVDVGGGTGATVAITTAHYBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
TaOMT1      188 LLEV.Y..KFEGLTSLVDVGGGTGATVAITTAHYBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
OsOMT1      195 LLDL.Y..TFEGLTSLVDVGGGTGATVAIVSRHBIKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
CrOMT2*     171 LITE.FN.YLFEGLTSLVDVGGGTGATIAKAIKAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
CrCOMT1     191 LLEI.Y..QGFQGLTSLVDVGGGTGATLNMIVSKYBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
CrOMT6      184 LITE.YK.FLFEGLTSLVDVGGGTGATIAKAIKAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObFOMT1     166 VIEN.YG.EEGRGVSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObFOMT2     166 VIEN.YG.EEGRGVSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObFOMT3     162 IVSN.YP.AAFDGLRSLVDVGGGTGATIGRLVEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObFOMT4     162 IVTN.YP.TAFNGVRSVVDVGGRRGMAIGRLVEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObFOMT5     162 IVRN.YP.AAFDGVSVVDVGGRRGMAIGRLVEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObFOMT6     162 IVTN.YP.TAFDGVRSVVDVGGRRGMAIGRLVEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ObF8OMT-1   182 LAKE.SR.KVFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
MpOMT3      192 LLEI.Y..KFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
MpOMT1A     170 VIEN.YG.EEGRGVSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
MpOMT1B     170 VIEN.YG.EEGRGVSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
MpOMT4      170 IVRY.CP.AAFEGITSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
MpOMT2      190 LITE.CP.EEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
CdFOMT5     181 LLES.Y..KFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
ZmOMT1      192 LLDL.Y..TFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
Hv7OMT      217 AVRE.CP.DVFEAGITSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
HvOMT1      184 LLES.Y..KFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
MsCOMT1     191 LLET.Y..TFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
CrOMT2      192 LLEN.Y..KFEGLTSLVDVGGGTGATLGMVLEAFBIRKGINFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
SaDMPM      194 LAKEE.Y..YDFESSYTVVDLGGADGSLLAVALSAHVEGVVFDLHVIKDAPTY.EGIE.....HVGCDFMFSVPEK.GDAIFMKWIC
consensus>70 .....y....Feg....!Dvgg..G.....fp.i.gi.fDIP.vi.da....gve.....vgDmf.svP...#ai.lk.!lH

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CaOMT1      246 DWSDEHCLKLLKNCYDALPN....NGKVIIEC.LLPEVPE.D.SSLA.TKGVVHIDVITVAHNPVGKERTKKEFEALAKAAAGFGFQ.V
AtOMT1      268 DWSDEHCVKFLKNCYESLPE....DGKVIIEC.LLPEVPE.D.SSLA.TKGVVHIDVITVAHNPVGKERTKKEFEALAKAAAGFGKIK.V
ShMOMT1     268 SLDDDEOCVKLLKNCWRALPN....DGKVVVIEC.QIOPKYP.E.NLL.SKRSFSFDISMMIMFHGKERTKQOFEFLAKQAAGFYIK.V
ShMOMT2     260 NWDDEOCVKLLKNCRESISSR..ENGGKVVIIIDM.IMEDNYP.N.NQL.VQSQHMLDLMRIT.YASKERTKKEWKLFLLEAAGFGYK.I
ShMOMT3     268 NWDDEOCVKLLKNCWRALPN....DGKVVVIEC.QIOPKYP.E.NLL.SKNSSSVDMMLMTMLDGGKERTKQOFEFLAKQAAGFYIK.I
ShMOMT4     268 NWDDEOCVKLLKNCWRALPN....DGKVVVIEC.QIOPKYP.E.NLL.SKNSSSVDMMLMTMLDGGKERTKQOFEFLAKQAAGFYIK.I
TaOMT2      263 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
TaOMT1      267 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
OsOMT1      275 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
CrOMT2*     211 DWKDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
CrCOMT1     270 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
CrOMT6      246 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObFOMT1     264 NWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObFOMT2     246 NWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObFOMT3     242 DWSDDKCIIEFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObFOMT4     242 DWSDDKCIIEFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObFOMT5     242 DWSDDKCIIEFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObFOMT6     242 DWSDDKCIIEFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ObF8OMT-1   262 NWSDDKCIIEFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
MpOMT3      271 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
MpOMT1A     250 NWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
MpOMT1B     250 NWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
MpOMT4      250 NWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
MpOMT2      270 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
CdFOMT5     260 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
ZmOMT1      271 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
Hv7OMT      297 NWSDDKCIIEFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
HvOMT1      263 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
MsCOMT1     270 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
CrOMT2      271 DWSDEHCVKFLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
SaDMPM      282 DWSDAHCLKLLKNCYDALPN....HGKVVVIEC.LLPEVPE.D.ATPK.AQGVFVDMITVAHNPVGKERTKKEFEALAKAAAGFAAMK.T
consensus>70 dwsDe.c...$k.c.ea.p.....gkviiv#.i.....#.D.ml....gkeR...#.l...aGF....v

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CaOMT1      326 FCNAFN.T..YIEFSSKQICN
AtOMT1      348 VCDAPG.V..NLIELKLLK..
ShMOMT1     348 VARAY.Y.S..WLIELYKY..
ShMOMT2     342 ITSLGL.R..SLIEIYP...
ShMOMT3     348 VARAY.Y.C..WVIEFYKY..
ShMOMT4     348 MARAY.Y.Y..WVIEFYKY..
TaOMT2      343 TYIYAN.A..WAIEFTK...
TaOMT1      347 TYIYAN.A..FAIEFTK...
OsOMT1      355 TYIYAN.A..WAIEFTK...
CrOMT2*     335 FPMIDF.R..SPIEVYP...
CrCOMT1     351 .CCAYN.S..WIMEFLK...
CrOMT6      346 FPMYDF.R..SIEVYYP...
ObFOMT1     327 NNIKAL.E..SLIEAYP...
ObFOMT2     327 NNIKAL.E..SLIEAYP...
ObFOMT3     323 KNIKSI.E..SVIEAYP...
ObFOMT4     323 KNIKTI.E..FVIEAYP...
ObFOMT5     323 KNIKAM.E..FVIEAYP...
ObFOMT6     323 KNIKTI.E..FVIDAYP...
ObF8OMT-1   346 YPLLGL.R..SLIEVFP...
MpOMT3      352 .CAAFH.T..CIMECHK...
MpOMT1A     331 KNIKTL.E..SVIEAYP...
MpOMT1B     331 KNIKTL.E..SVIEAYP...
MpOMT4      330 KNINTV.E..FVIEAYP...
MpOMT2      353 TRVLGL.R..SVIEVFP...
CdFOMT5     340 EL.AIGSL.WVMEFYK...
ZmOMT1      351 TYIYAN.A..WAIEFIK...
Hv7OMT      377 HNVLGM.R..SLIEVQP...
HvOMT1      343 TYIYAN.A..WAIEFTK...
MsCOMT1     350 HCNAFN.T..YIMEFLKVV..
CrOMT2      351 VSSAFN.T..YIMEFLKSA..
SaDMPM      360 RTPPGL.TPFS.LIEAAPV..
consensus>70 .....i#.....

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Annotation according to Zubieta et al. (2002)

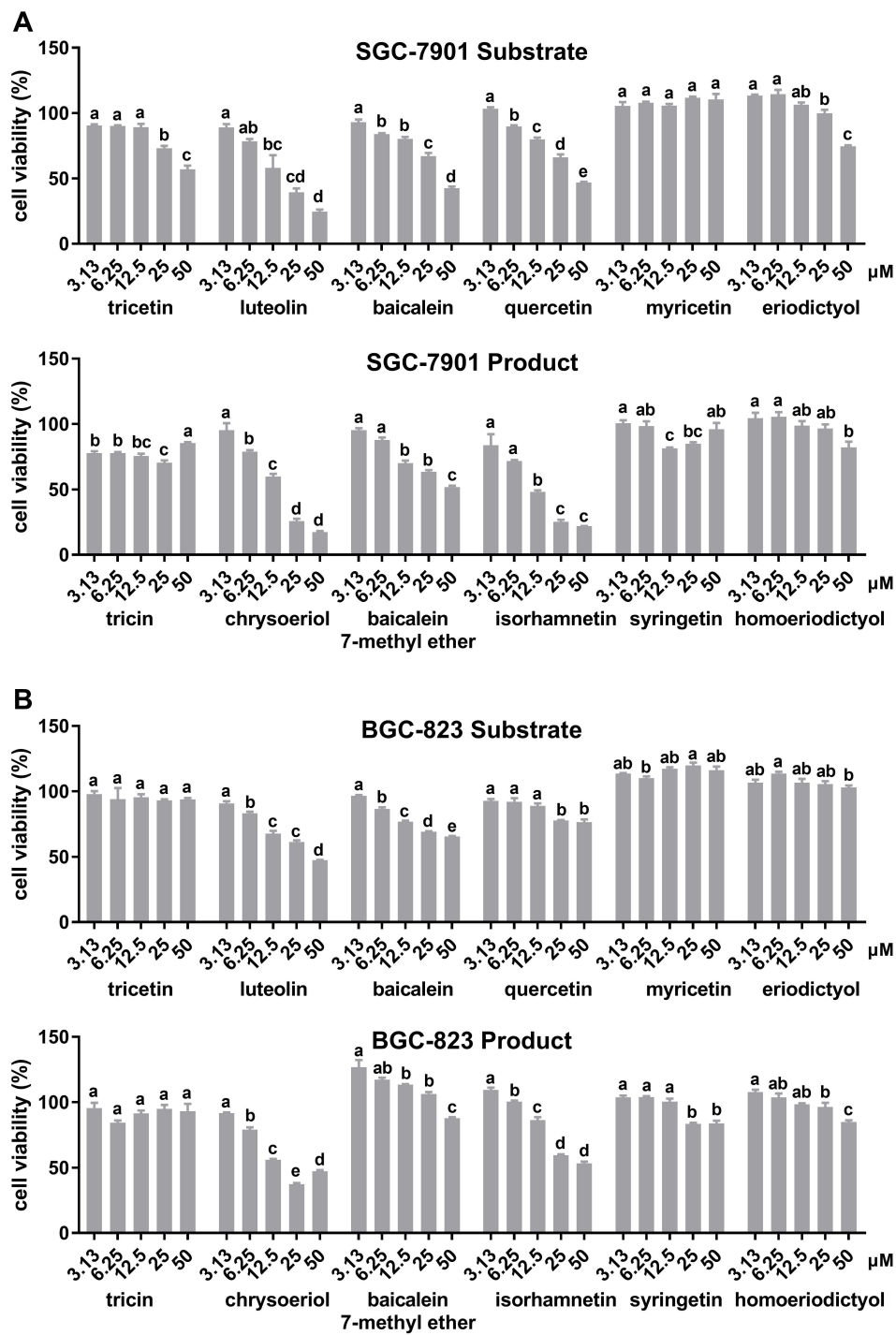
- \* Active site dimmer
- \* Active site substrate binding/positioning residues
- \* Conserved residues and motifs for SAM binding
- \* Catalytic residues



**Figure S5** Sequence alignment of CrOMT2 and other caffeic acid *O*-methyltransferases (COMTs) from plants.

Protein sequences were aligned via T-Coffee (Expresso) using structural information and analyzed using ESript 3.0. Residues that are important for dimer formation, substrate specificity, SAM binding and catalysis are shown [29], and are indicated with asterisks in green, blue, red and black, respectively. To avoid ambiguity, CrOMT2 from *Catharanthus roseus* was marked with a triangle.

Figure S6



**Figure S6** Cell viability after treated with flavonoids substrates or methylated products of CrOMT2 *in vitro*. For each cell line, bars marked by different letters within each index are significantly different ( $p < 0.05$ ) following Tukey's test.

**Table S1** Percent identity of AtOMT1 against OMTs in *Citrus clementina*.

<b>Query accession.version</b>	<b>Subject accession.version</b>	<b>Percentage of identical matches</b>	<b>Expect value</b>
AtOMT1	Ciclev10020814m	73.35	0
AtOMT1	Ciclev10024037m	72.53	0
AtOMT1	Ciclev10005230m	70.67	0
AtOMT1	Ciclev10020761m	70.20	0
AtOMT1	Ciclev10001661m	59.34	1.25E-147
AtOMT1	Ciclev10031952m	57.40	6.45E-141
AtOMT1	Ciclev10018226m	56.79	2.81E-142
AtOMT1	Ciclev10031953m	56.50	6.40E-138
AtOMT1	Ciclev10017683m	56.39	1.41E-142
AtOMT1	Ciclev10031951m	56.19	5.49E-138
AtOMT1	Ciclev10015685m	56.11	3.10E-142
AtOMT1	Ciclev10020875m	56.03	1.97E-142
AtOMT1	Ciclev10031949m	55.89	5.32E-137
AtOMT1	Ciclev10021145m	55.51	7.62E-94
AtOMT1	Ciclev10001555m	55.14	5.37E-154
AtOMT1	Ciclev10032454m	55.07	1.45E-85
AtOMT1	Ciclev10026361m	54.74	9.03E-81
AtOMT1	Ciclev10013542m	54.60	1.06E-127
AtOMT1	Ciclev10020880m	54.60	1.80E-140
AtOMT1	Ciclev10021670m	54.58	9.74E-90
AtOMT1	Ciclev10026359m	54.31	1.45E-80
AtOMT1	Ciclev10017649m	54.10	2.49E-131
AtOMT1	Ciclev10021888m	54.01	9.69E-86
AtOMT1	Ciclev10021678m	53.79	2.35E-90
AtOMT1	Ciclev10032453m	53.74	1.15E-82
AtOMT1	Ciclev10020874m	53.74	1.53E-138
AtOMT1	Ciclev10032027m	53.47	1.03E-124
AtOMT1	Ciclev10012042m	53.43	2.42E-137
AtOMT1	Ciclev10021321m	53.25	2.98E-79
AtOMT1	Ciclev10021326m	53.25	2.98E-79
AtOMT1	Ciclev10023568m	52.87	9.58E-137
AtOMT1	Ciclev10020870m	52.87	7.54E-136
AtOMT1	Ciclev10020873m	52.87	7.54E-136
AtOMT1	Ciclev10032452m	52.86	3.64E-82
AtOMT1	Ciclev10023994m	52.59	2.50E-128
AtOMT1	Ciclev10032460m	52.42	1.19E-80
AtOMT1	Ciclev10020782m	51.62	3.91E-130
AtOMT1	Ciclev10010860m	51.29	3.91E-81
AtOMT1	Ciclev10020818m	50.82	1.05E-130
AtOMT1	Ciclev10020821m	50.29	5.51E-120
AtOMT1	Ciclev10020377m	50.14	6.29E-122
AtOMT1	Ciclev10020820m	50.00	9.12E-121

<b>Query accession.version</b>	<b>Subject accession.version</b>	<b>Percentage of identical matches</b>	<b>Expect value</b>
AtOMT1	Ciclev10005251m	49.45	8.43E-127
AtOMT1	Ciclev10020828m	49.13	1.75E-119
AtOMT1	Ciclev10023965m	46.49	5.23E-114
AtOMT1	Ciclev10003737m	46.24	2.02E-81
AtOMT1	Ciclev10003323m	43.15	1.69E-87
AtOMT1	Ciclev10012087m	42.07	4.53E-89
AtOMT1	Ciclev10005309m	40.85	2.85E-84
AtOMT1	Ciclev10006704m	39.94	4.03E-78

**Table S2** Primers used for amplification.

<b>Gene</b>	<b>Forward primer (5' to 3')</b>	<b>Reverse primer (5' to 3')</b>
<i>CrOMT2</i> -CDs	ATGGGTTCAACCAGTTCAGAAAC	TCAAGCACTCTTGAGAAATTCC
<i>CrOMT2</i> -PET	ATAGGATCCATGGGTTCAACCAG TTCAGAAAC	GAAGGACTCGAGAGCACTCTTG AGAAATTCC

Underlined sequences represent restriction enzyme sites

**Table S3** UniProt entries of COMT proteins used in the phylogenetic tree.

<b>Protein names</b>	<b>UniProt entry</b>	<b>Organism</b>
AtOMT1	Q9FK25	<i>Arabidopsis thaliana</i> (Mouse-ear cress)
CrOMT2	Q8GSN1	<i>Catharanthus roseus</i> ( <i>Madagascar periwinkle</i> ) ( <i>Vinca rosea</i> )
CrCOMT1	Q8W013	<i>Catharanthus roseus</i> ( <i>Madagascar periwinkle</i> ) ( <i>Vinca rosea</i> )
CrOMT6	Q6VCW3	<i>Catharanthus roseus</i> ( <i>Madagascar periwinkle</i> ) ( <i>Vinca rosea</i> )
CaOMT1	P59049	<i>Chrysosplenium americanum</i> (Golden saxifrage)
CdFOMT5	A0A125T1T5	<i>Citrus depressa</i>
HvOMT1	Q43771	<i>Hordeum vulgare</i> (Barley)
Hv7OMT	A5YTR4	<i>Hordeum vulgare</i> subsp. <i>vulgare</i> (Domesticated barley)
MsCOMT1	P28002	<i>Medicago sativa</i> (Alfalfa)
MpOMT3	Q6VMV9	<i>Mentha piperita</i> (Peppermint) ( <i>Mentha aquatica</i> x <i>Mentha spicata</i> )
MpOMT1A	Q6VMW2	<i>Mentha piperita</i> (Peppermint) ( <i>Mentha aquatica</i> x <i>Mentha spicata</i> )
MpOMT1B	Q6VMW1	<i>Mentha piperita</i> (Peppermint) ( <i>Mentha aquatica</i> x <i>Mentha spicata</i> )
MpOMT4	Q6VMV8	<i>Mentha piperita</i> (Peppermint) ( <i>Mentha aquatica</i> x <i>Mentha spicata</i> )
MpOMT2	Q6VMW0	<i>Mentha piperita</i> (Peppermint) ( <i>Mentha aquatica</i> x <i>Mentha spicata</i> )
ObFOMT1	K0I977	<i>Ocimum basilicum</i> (Sweet basil)
ObFOMT2	K0II72	<i>Ocimum basilicum</i> (Sweet basil)
ObFOMT3	K0I7Q2	<i>Ocimum basilicum</i> (Sweet basil)
ObFOMT4	K0I210	<i>Ocimum basilicum</i> (Sweet basil)
ObFOMT5	K0ICR0	<i>Ocimum basilicum</i> (Sweet basil)
ObFOMT6	K0I986	<i>Ocimum basilicum</i> (Sweet basil)
ObF8OMT-1	S5DWK8	<i>Ocimum basilicum</i> (Sweet basil)
OsOMT1	Q6ZD89	<i>Oryza sativa</i> subsp. <i>japonica</i> (Rice)
ShMOMT1	F2YTN4	<i>Solanum habrochaites</i> (Wild tomato) ( <i>Lycopersicon hirsutum</i> )
ShMOMT2	F2YTN5	<i>Solanum habrochaites</i> (Wild tomato) ( <i>Lycopersicon hirsutum</i> )
ShMOMT3	M9Z1G5	<i>Solanum habrochaites</i> (Wild tomato) ( <i>Lycopersicon hirsutum</i> )
SIMOMT4	A0A088MF62	<i>Solanum lycopersicum</i> (Tomato) ( <i>Lycopersicon esculentum</i> )
TaOMT2	Q38J50	<i>Triticum aestivum</i> (Wheat)
TaOMT1	Q84N28	<i>Triticum aestivum</i> (Wheat)
ZmOMT1	Q6VWG3	<i>Zea mays</i> (Maize)
SaDMPM	P42712	<i>Streptomyces alboniger</i>