

SUPPLEMENTAL MATERIALS

Figure S1. Multiple sequence alignment of PMT. Amino acid sequences of the PMT from *A. thaliana* (AtPMT1, Q9FR44.1; AtPMT2, Q944H0.2; AtPMT3, Q9C6B9.2), *S. oleracea* (SoPMT, AAF61950.1), *T. aestivum* (TaPMT, AAL40895.1), *C. elegans* (CePMT1, AAA81102.1; CePMT2, AAB04824.1), *H. contortus* (HcPMT1, CDJ81011.1; HcPMT2, CDJ96940.1), and *P. falciparum* (PfPMT, AAR08195.1), was performed using MultAlign. Residues in orange highlight invariant and highly conserved amino acids with variations shown in white. Residues in the MT1 and MT2 SAM/SAH binding sites are colored blue and purple, respectively. Residues in the MT1 and MT2 phosphobase binding sites are colored green and red, respectively. The box corresponds to residues of the linker helix.

AtPMT1 MAAS YEEERD IQKNWIEHSADLTVEAMMLDSRASLDKEERPEVLSLLPPYEGKS VLELGAGIGRT
 AtPMT2 MATPYKEERD IQKSXWMEHSSDLTVEAMMLDSKASLDKEERPEVLSLPPYEGKS VLELGAGIGRT
 AtPMT3 MASYGEEREI QKNWIEHSVGLSVEAMMLDSKASLDKEERPEVLAFLPPPIEGTTVLE . GAGIGRT
 SoPMT MAASAMGVLOQEREVFKKWIEHSVDLTVEAMMLDSQASLDKVERPEVLSMLPPYEGKS VLELGAGIGRT
 TaPMT MDITIVVENVFGEVERVKVQKSXWEESKDLTVEAMMLDSRAKLDKEERPEVLAIPSYAGKT VLELGAGIGRT
 CePMT1 MCPLSPPPPYPYPRHSVSGVNMSDQQSSVEDQTAVMVNRANFKS WDKYSDKPDT SMML HSAE LSSDRADILASLPLLHNKD VDI GAGIGRT
 HcPMT1 MTAEVRRDSFKT WDKYSDKPDT SMML QTAQDL ASDRADILSSLPHLTNKD VDI GAGIGRT
 CePMT2 MSSLS PRQSLV V MPA ERQLIECL
 HcPMT2
 PfPMT

AtPMT1 GELAQKAGE LIALDFIDVIKKNESINGH . YKNVKFMCA DVTSPDLK TTDGSDL IFSNWLLM YLS DKE . VELLAER MVGW KVGGYIFFF RESCFHQ SGD
 AtPMT2 GELAQKAGE LIALDFIESAIQKNESINGH . YKNVKFMCA DVTSPDLK TTDGSDL IFSNWLLM YLS DKE . VELMAERMIGW KPGGYIFFF RESCFHQ SGD
 AtPMT3 TELAQKAGQVIAVDFIESVIKKNESINGH . YKNVKFMCA DVTSPSLNISPNSVD IFSNWLLM YLS DKE . VERLVERML KWLKPGGYIFFF RESCFHQ SGD
 SoPMT GELAEKAQS QVIALDFIESVIKKNESINGH . YKNVKFMCA DVTSPSLNISPNSVD IFSNWLLM YLS DKE . VERLVERML KWLKPGGYIFFF RESCFHQ SGD
 TaPMT GELAKEAGH VIALDFISVIKKNESINGH . YKNVKFMCA DVTSPSLNISPNSVD IFSNWLLM YLS DKE . VEKLRI VWKLPFGGHIFIRES CFHQ SGD
 CePMT1 TVLAETARWV STDFIDSFVKKERN A HLNIN YQVG D V . . GLKME SNSV D F NWL MYLS DEETVE . FIFNCMRWL SHGIVHLRESCSEPS G
 HcPMT1 TVLAETARWV STDFIESPIEK NERNAHMGNIS YQIG D V . . HLQMD EKVSDLV F NWL MYLS DREV E . FLLNAMRWL ADGYIHLRESCSEPS G
 CePMT2 NK T . EGRSVSNQV SPCOKQO TYVTAFTPLTSNVQVHTS L EQLSTIRNADVLFVN NALSOI IT A DL TDFLKNA TNATAI GGT V II RDL . LKDCSD
 HcPMT2 HH I . KGAEPQOVGICPQDDQRK ALTEQFGSKAT . SFC KEVDSL KNLNSNL DALIVN ALDEE INSEK D KFITAALRSL TDGV LILR D . LSKVK
 PfPMT

AtPMT1 SKRK SNPTHYREPRFYSKVFOQECQTRDAAGNSFELSMIGCKCIGAYVKNKKNQNQICW WQKVSS . ND RG FQRFLDNVQYKSSGILR
 AtPMT2 SKRK SNPTHYREPRFYT KVFQECQTRDASGNSFELSMVGCKCIGAYVKNKKNQNQICW WQKVSV . ND KD FQRFLDNVQYKSSGILR
 AtPMT3 NKKR YNPTHYREPRFYT KFKECHMMDGNSV ELSLVSCKCIGAYVKNKKNQNQICWLWQKVSSD . ND RG FQRFLDNVQYKSSGILR
 SoPMT HKRK SNPTHYREPRFYT KFKECHMMDGNSV ELSLVSCKCIGAYVKSNNQNQICWLWQKVSSD . DDKG FQRFLDNVQYKSSGILR
 TaPMT SKRK VNPTHYREPRFYT KVFKECHSYDQEGNSFELSLVTSKCIGAYVKSNNQNQICWLWKEVKCT . EDKG FQRFLDNVQYKSTGILR
 CePMT1 RS AKSMHD TANANP THYRFSSLYIN LRAIRYR DVL KLRPN QWS CPTY KRSNNWROVH LAEKVPAEDGAR GTSF NELVELIKNT QNEQEW
 HcPMT1 RL TATMHSADVANP THYRFSSLYIK LRAIRYR DSGKM KFD QWS CPTY RCRNNWROVH LT KKVPAV GDEETSVD LLLNFSQI PAEQKTW
 CePMT2 K QV AR LTDY FDVRFTT DSDGNT GLDLYTVDQ EHSN VYE QNFL F IF FRKKVFA PTT DATITFRDFLDK TQY TNGIDA
 HcPMT2 MK M AMLTDY FDVFRL E GNGN . VGQFYAVNE L DS VV H QWL F INTL IKKPF K DINGVVSFRDFLDRTQY TDTGIFA
 PfPMT

AtPMT1 YERVFCQG VSTGGLETTKEFVEKMLKPGQ . . KVL DVCG GIGGGDFYMAEKFDVH VVG IDLSVN M ISF ALERA IGL CS VEF EVADCTTK HY
 AtPMT2 YERVFGEG VSTGGLETTKEFVAKM DLKPGQ . . KVL DVCG GIGGGDFYMAENFDVH VVG IDLSVN M ISF ALERA IGL CS VEF EVADCTTK TY
 AtPMT3 YERVFGEG VSTGGLETTKEFVDM DLKPGQ . . KVL DVCG GIGGGDFYMAENFDVH VVG IDLSVN M ISF ALERA IGL CS VEF EVADCTTK BY
 SoPMT YERVFGEG VSTGGLETTKEFVSKM DLKPGQ . . KVL DVCG GIGGGDFYMAEN . DVE VVG IDLSIN M ISF ALERA IGL CS VEF EVADCTTK DY
 TaPMT YERVFGEG VSTGGLETTKEFV DKL DLK GQ . . KVL DVCG GIGGGDFYMAET DVH VLG IDLSIN M ISF ALERA IGL CS VEF EVADCTTK BY
 CePMT1 DA LDDEK YVW TDKV F SALT S . . LPSNSTF LYPT PRTVSPYCHINA HLT AET FNAN VNTTE IPE YSLT KSNL K DQ RVF GWQS TDSV TY WQO
 HcPMT1 DE LDNEK YS WT DKF I . . NAIDDEV VPKN STAY VFT P RQSPFLHV NSHLLA EKFT CNV VNVET KEYL RTLSL T KANN QD Q RVF GWNES SSS IDY WNO
 CePMT2 YEW FG VNF SPGGYDEN LK I KRFG D KPGQ . . TMLD GVGIGGGARQVA EFGVH VH GIDLS NM AIALER LHEE KDS RVK Y STD LVY Q
 HcPMT2 YEW FG VNF SPGGWQN LAI KRFG PMK GQ . . RMLD GVGIGGGARQ A SE F GLQV HG VDL STN M AVALER VHEE K D A R V T Y AVCD CEY E
 PfPMT YEF FG E NY SSGGLEAT KKI S DIEL NENS . . KVLD GSG GGGCMY IN E GA HT H GID IC SN VN MANER VSG . . NNK IF END LTK E

AtPMT1 PDNSFDV IY SRTD ILH I . . QDKPAL FRT F KWLPGG KV L ISD YCRSPKTP . SA EFSE YIK QRG YD LHD V QAY GQML K DAG F TDV IA E DRT DQ FM QV LKR
 AtPMT2 PDNSFDV IY SRTD ILH I . . QDKPAL FRT F KWLPGG KV L IDT YCRSPKTP . S PFEA EYIK QRG YD LHD V QAY GQML K DAG F DD V IA E DRT DQ FM QV LKR
 AtPMT3 PDNSFDV IY SRTD ILH I . . QDKPAL FRT F KWLPGG KV L IDT YCRSPKTP . S PDAI YIK RGYD LHD V QAY GQML K DAG F E V IA E DRT DQ FM QV LKR
 SoPMT P NSFDV IY SRTD ILH I . . QDKPAL FRSF KWLPGG KV L IDT YCRSPGTP . SE FF AA YIR QRG YD LHD V KAY G RML K DAG F V B V IA E RTD QF IO VL QK
 TaPMT A NTFD V IY SRTD ILH I . . QDKPAL FRSF KWLPGG KV L IDT YCRSPGTP . SE FF AA YIK QRG YD LHD V KTY G KML D DAG F HDV V A E DRT DQ FL R V L E R
 CePMT1 KDA LF DV F VATE F STV . . DDET . . IRQLPNVMSD GAK I D L . . PV D E V N . EA EM K Q R I O E L G Y TL K S . . TD V TD Q C I E A Q . E Q Y F K O H E Q L R D E K V I R K
 HcPMT1 RDAS F DC I VATE ATC . . DDES . . IKSIA S I K P E A K V I L . . P VSE V D . . ETS VR Q R T T C G F K N I T . . V D V T O E S L N A E . . TS F I K O H N L . . D V E L S C C
 CePMT2 EDNSFDV V S R D C I Q H I . . P D T K L F S R I Y K A L K P G G K V L I T M Y G K G Y G E Q . . S D K F K T V A Q R A Y F L K N . . K E A D I A N K T G F V V Q T E . . M T P R F K E I L L E
 HcPMT2 E N S F D Y V S R D C I Q H I . . K D T D K L F S R I Y K A L K P G G K V L I T M Y G V G H G T L . . S E S F K E Y V S Q R O Y Y L K N . . E Q I E E I A K K T G F I D I E V E . . M T P R F K E I L L E
 PfPMT P NNF D L I Y S R D A I L H . . S L E N K N K L F Q K C Y K W L K P T G T L I T D Y C A T E K E N W D D F K E V K Q R K Y T L I T V E E Y A D I L T A C N F K V V S K D L D Y . . N Q L E V

AtPMT1 ELD R EKEKEKF I SDFS KED Y D DIV G G W K S K L E R C A S D E Q K W G L F I A N K N . .
 AtPMT2 ELEK V EKEKEEF I SDFS SEEDY DIV G G W S A K L E R T A S G E Q K W G L F I A D K K . .
 AtPMT3 ELD A V EKEKEEF I SDFS KEDY D I G G W K S K L L R S S G E Q K W G L F I A K R N . .
 SoPMT ELD A L E Q E K D F I D D F S E E D Y D I V D G W K A K L V R T T G E Q Q K W G L F I A K K M . .
 TaPMT E L G E E K K E A F A D F Q E D Y D D I V N G W S A K L K R S S A G E Q K W G L F I A T K . .
 CePMT1 N V L L E L T H
 HcPMT1 N Y L L E K A S L
 CePMT2 E R G H L E Q N E A E F S K F I Q R E R D S S G W T D K L G Y I E K D J H N N N F L A Q K P P K . .
 HcPMT2 E R E R D E Q K E T F F I A K F S Q N A Y D G V S G W K S K L Q Y I A D D J H N N N F A A V K P Q . .
 PfPMT E H K Y L H E R K E E F L K L F S E K K I S D D G W S R K K D S K R K M Q R W G Y F K A T K N . .

Figure S2. Protein expression and purification of AtPMT. Size-exclusion chromatograms are shown for AtPMT1 (**A**), AtPMT2 (**B**), and AtPMT3 (**C**). The inset in each panel shows SDS-PAGE analysis of protein purification for each protein. Samples were stained for total protein using Coomassie Blue. Triangles correspond to the indicated molecular mass markers. In each inset, the lanes are as follows: lane 1, 12.5 μ g of sonicate; lane 2, 5 μ g of affinity-purified AtPMT; lane 3, 5 μ g of size-exclusion purified AtPMT. (**D**) Molecular weight determination of AtPMT. The molecular weight calibration curve of the size-exclusion column is shown. The following standards were used: ferritin (440 kDa), aldolase (158 kDa), conalbumin (75 kDa), ovalbumin (43 kDa), carbonic anhydrase (27 kDa), ribonuclease A (13.7 kDa), and aprotinin (6.5 kDa). An arrow indicates the elution volume for each AtPMT.

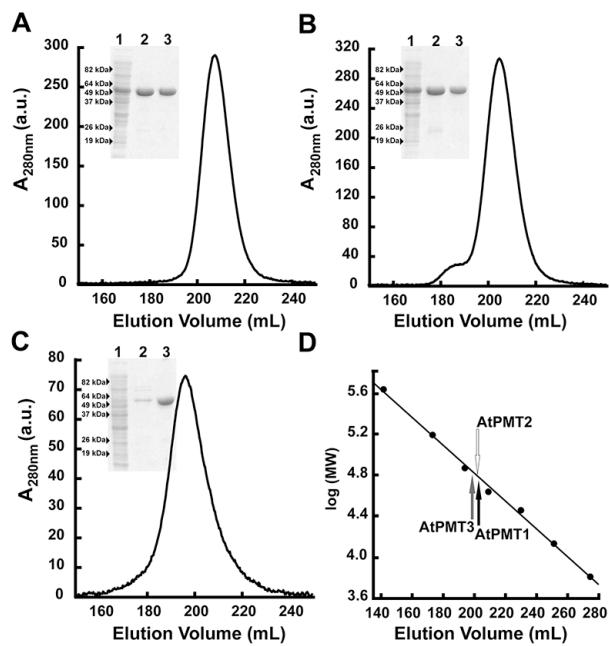


Figure S3. Isothermal titration calorimetry of SAH binding to AtPMT2. (A) Titration of AtPMT2 with SAH. ITC data are plotted as heat signal ($\mu\text{cal sec}^{-1}$) versus time (min). The experiment consisted of 30 injections of SAH into a solution containing AtPMT2 at 20 °C. (B) Integrated heat response per injection from (A) is plotted as normalized heat per mol of injectant. The solid line represents the fit to the data.

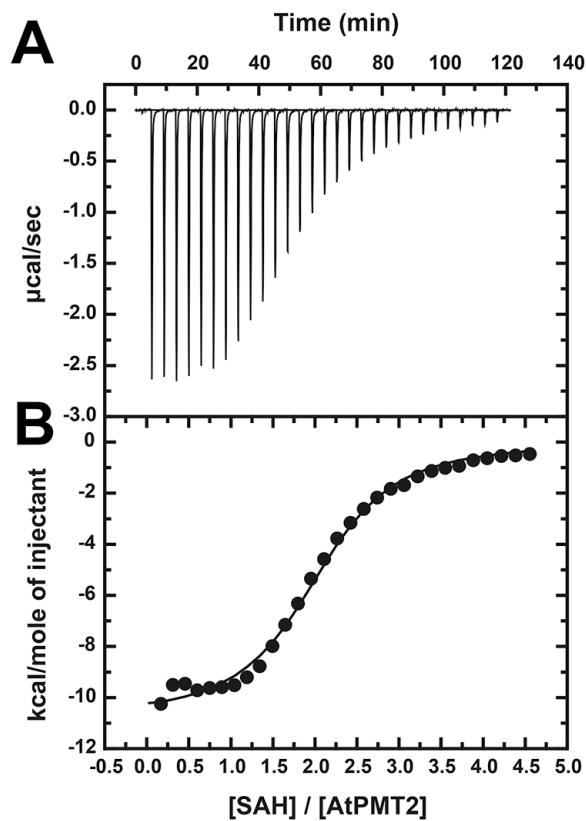


Figure S4. Polar lipid profiling of wild-type and *atpm13* T-DNA knockout line.

(A) Total polar lipid levels for wild-type (white) and *atpm13* (grey) plants are shown as nmol per mg dry weight (DW). Analysis of polar lipid content was performed as described in the experimental methods. **(B)** Comparison of total polar lipid digalactosyldiacylglycerol (DGDG), monogalactosyldiacylglycerol (MGDG), phosphatidylglycerol (PG), phosphatidylcholine (PC), phosphatidylethanolamine (PE), phosphatidylinositol (PI), phosphatidylserine (PS), and phosphatidic acid (PA) species in wild-type (white) and *atpm13* knockout (grey) plants. The inset is a close-up of the changes in phosphatidic acid (PA). All values in panels A and B are shown as mean \pm standard deviation ($n = 6-8$).

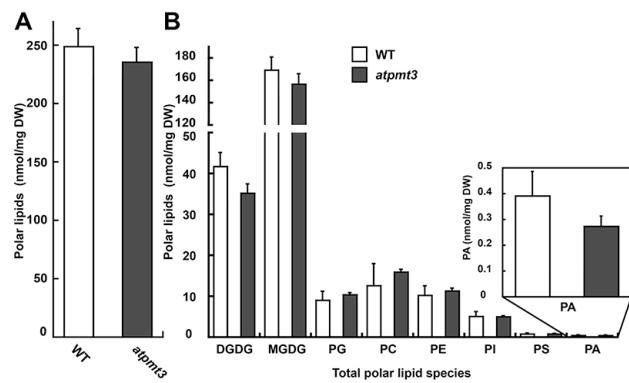


Figure S5. Electron density for active site ligands in AtPMT1 and AtPMT2.

(A) Electron density for pCho (top) and SAH (bottom) in the AtPMT1 MT1 domain active site is shown as a $2F_o - F_c$ omit map (1.5σ). **(B)** Electron density for pCho (top) and SAH (bottom) in the AtPMT1 MT2 domain active site is shown as a $2F_o - F_c$ omit map (1.5σ). **(C)** Electron density for SAH in the AtPMT2 MT 1 domain active site is shown as a $2F_o - F_c$ omit map (1.25σ). **(D)** Electron density for SAH in the AtPMT2 MT2 domain active site is shown as a $2F_o - F_c$ omit map (1.25σ).

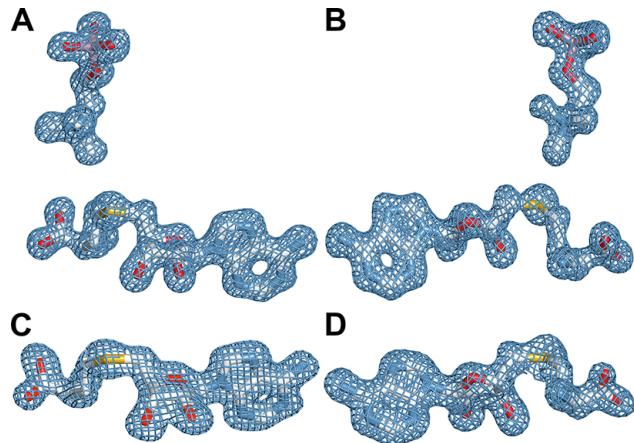


Table S1. Summary of sequences used to generate phylogenetic tree. The AtPMT1 sequence was used as a BLAST query to identify 153 sequences encoding putative PMT (see Fig. 8).

Type	Species	Accession	Phylogenetic Type	Reference Species	Accession	Source	
I	<i>Gossypium arboreum</i>	KHG16117.1	[eudicot]	Type I	<i>Xenopus laevis</i>	NP_001087172.1	[frogs & toads]
I	<i>Gossypium hirsutum</i>	XP_016666825.1	[eudicot]	Type I	<i>Strongylocentrotus purpuratus</i>	XP_794381.2	[sea urchins]
I	<i>Gossypium raimondii</i>	KJB30122.1	[eudicot]	Type I	<i>Branchiostoma florid</i>	XP_002594089.1	[lancelets]
I	<i>Halostachys caspica</i>	AHX22003.1	[eudicot]	Type II	<i>Eimeria acervulina</i>	CDI77742.1	[apicomplexans]
I	<i>Ipomoea nil</i>	XP_019169742.1	[eudicot]	Type II	<i>Eimeria maxima</i>	CDJ58552.1	[apicomplexans]
I	<i>Jatropha curcas</i>	KDP23922.1	[eudicot]	Type II	<i>Eimeria mitis</i>	CDJ34460.1	[apicomplexans]
I	<i>Juglans regia</i>	XP_018857980.1	[eudicot]	Type II	<i>Eimeria necatrix</i>	CDJ67597.1	[apicomplexans]
I	<i>Lupinus angustifolius</i>	OIV94185.1	[eudicot]	Type II	<i>Eimeria tenella</i>	CDJ43178.1	[apicomplexans]
I	<i>Lycium barbarum</i>	AGI56231.1	[eudicot]	Type II	<i>Plasmodium cynomolgi</i>	PCYB_122070	[apicomplexans]
I	<i>Malus domestica</i>	XP_008360927.1	[eudicot]	Type II	<i>Plasmodium falciparum</i>	PF3D7_1343000	[apicomplexans]
I	<i>Manihot esculenta</i>	OAY46532.1	[eudicot]	Type II	<i>Plasmodium knowlesi</i>	PKH_121150	[apicomplexans]
I	<i>Medicago truncatula</i>	AES76054.1	[eudicot]	Type II	<i>Plasmodium vivax</i>	PVX_083045	[apicomplexans]
I	<i>Morus notabilis</i>	EXB69095.1	[eudicot]	Type II (MT1)	<i>Ascaris suum</i>	ERG79882.1	[nematodes]
I	<i>Musa acuminata</i>	XP_009385384.1	[eudicot]	Type II (MT1)	<i>Bursephelenchus xylophilus</i>	BUX.s01513.225	[nematodes]
I	<i>Nelumbo nucifera</i>	XP_010274723.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis brenneri</i>	CBN10892	[nematodes]
I	<i>Nicotiana attenuata</i>	OIT04993.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis briggsae</i>	CBG02363	[nematodes]
I	<i>Nicotiana sylvestris</i>	XP_009782224.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis elegans</i>	NP_494990.2	[nematodes]
I	<i>Nicotiana tabacum</i>	XP_016437407.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis japonica</i>	CJA07932	[nematodes]
I	<i>Nozzea caerulescens</i>	JAU57851.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis remanei</i>	CRE11930	[nematodes]
I	<i>Phaseolus vulgaris</i>	ESW24678.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis sp.11</i>	Csp11.Scaffold630.g214.23.1	[nematodes]
I	<i>Phoenix dactylifera</i>	XP_008799221.1	[eudicot]	Type II (MT1)	<i>Caenorhabditis sp.5</i>	Csp5_scaffold_01891.g2373.1	[nematodes]
I	<i>Populus euphratica</i>	XP_011039130.1	[eudicot]	Type II (MT1)	<i>Haemonchus contortus</i>	CDJ81011.1	[nematodes]
I	<i>Populus tomentosa</i>	APR64075.1	[eudicot]	Type II (MT1)	<i>Necator americanus</i>	ETN83758.1	[nematodes]
I	<i>Populus trichocarpa</i>	EEF06229.2	[eudicot]	Type II (MT1)	<i>Pristionchus pacificus</i>	PPA22786	[nematodes]
I	<i>Prunus mume</i>	XP_008240152.1	[eudicot]	Type II (MT1)	<i>Strongyloides stercoralis</i>	US 2007/0009981 A1 ID no: 10	[nematodes]
I	<i>Prunus persica</i>	XP_007209941.1	[eudicot]	Type II (MT2)	<i>Ascaris suum</i>	GS_23928	[nematodes]
I	<i>Pyrus betulifolia</i>	AER10513.1	[eudicot]	Type II (MT2)	<i>Bursephelenchus xylophilus</i>	BUX.s01143.358	[nematodes]
I	<i>Pyrus × bretschneideri</i>	XP_009360079.1	[eudicot]	Type II (MT2)	<i>Caenorhabditis brenneri</i>	CBN22056	[nematodes]
I	<i>Raphanus sativus</i>	XP_018432929.1	[eudicot]	Type II (MT2)	<i>Caenorhabditis briggsae</i>	CBG08775	[nematodes]
I	<i>Ricinus communis</i>	XP_002532097.1	[eudicot]	Type II (MT2)	<i>Caenorhabditis elegans</i>	NP_504248.1	[nematodes]

Type I	<i>Salicornia europaea</i>	ABG57185.1	[eudicot]	Type II (MT2)	<i>Caenorhabditis japonica</i>	CJA04052	[nematodes]
Type I	<i>Sesamum indicum</i>	XP_0110729 95.1	[eudicot]	Type II (MT2)	<i>Caenorhabditis remanei</i>	CRE18566	[nematodes]
Type I	<i>Solanum lycopersicum</i>	XP_0042416 42.1	[eudicot]	Type II (MT2)	<i>Haemonchus contortus</i>	CDJ96940.1	[nematodes]
Type I	<i>Solanum pennellii</i>	XP_0150801 67.1	[eudicot]	Type II (MT2)	<i>Meloidogyne hapla</i>	MhA1_Contig1162.frz3. gene5	[nematodes]
Type I	<i>Solanum tuberosum</i>	XP_0063466 42.1	[eudicot]	Type II (MT2)	<i>Meloidogyne javanica</i>	US 2007/0009981 A1 ID no: 12	[nematodes]
Type I	<i>Spinacia oleracea</i>	Q9M571.1	[eudicot]	Type II (MT2)	<i>Necator americanus</i>	ETN82894.1	[nematodes]
Type I	<i>Suaeda japonica</i>	BAC57432.1	[eudicot]	Type II (MT2)	<i>Pristionchus pacificus</i>	PPA16775	[nematodes]
Type I	<i>Suaeda liaotungensis</i>	ABK42071.1	[eudicot]				