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.

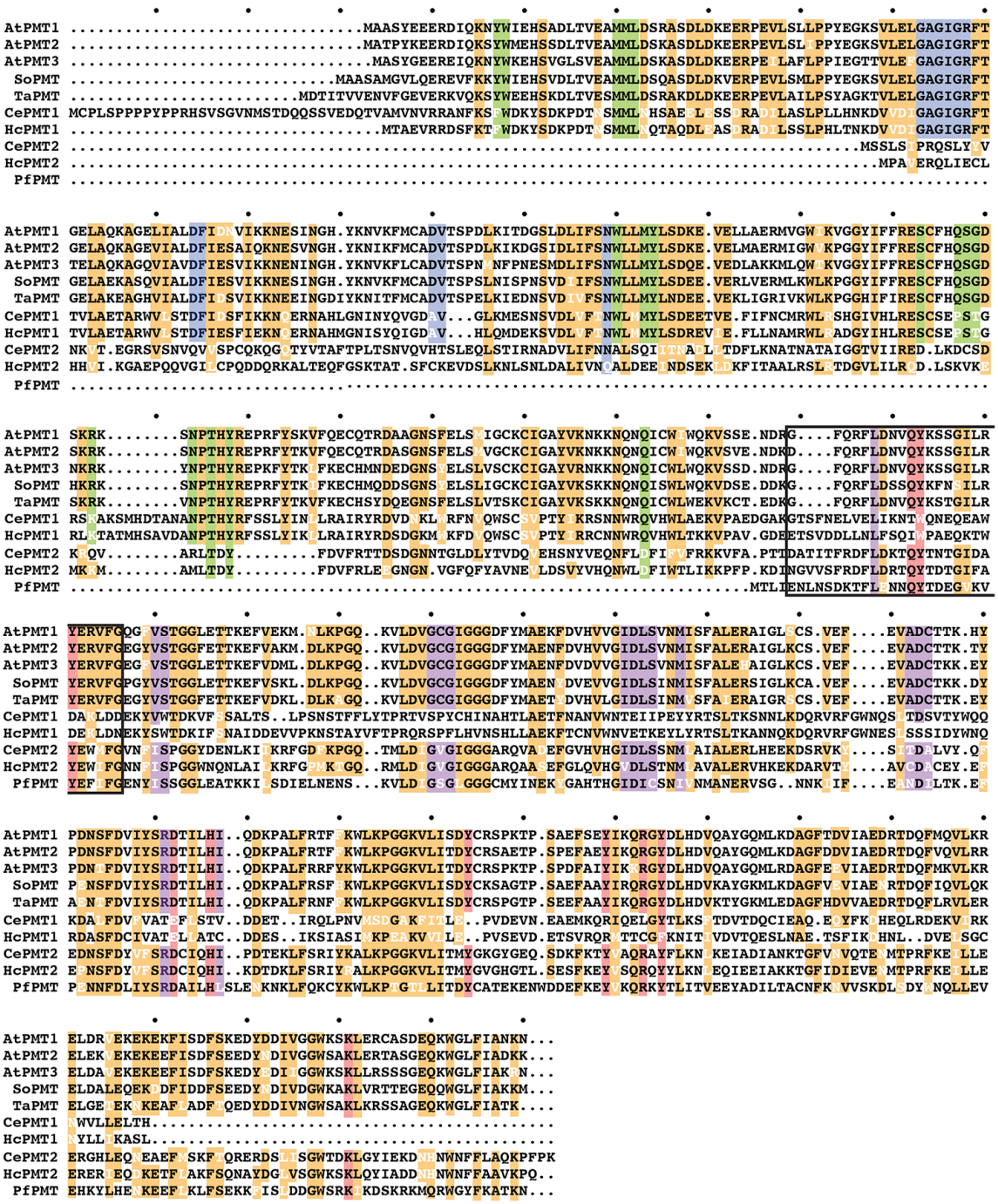
AtPMT1
AtPMT2
AtPMT3
SoPMT
TaPMT
CePMT1
HcPMT1
CePMT2
HcPMT2
PfPMT

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 μg of sonicate; lane 2, 5 μg of affinity-purified AtPMT; lane 3, 5 μg 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.

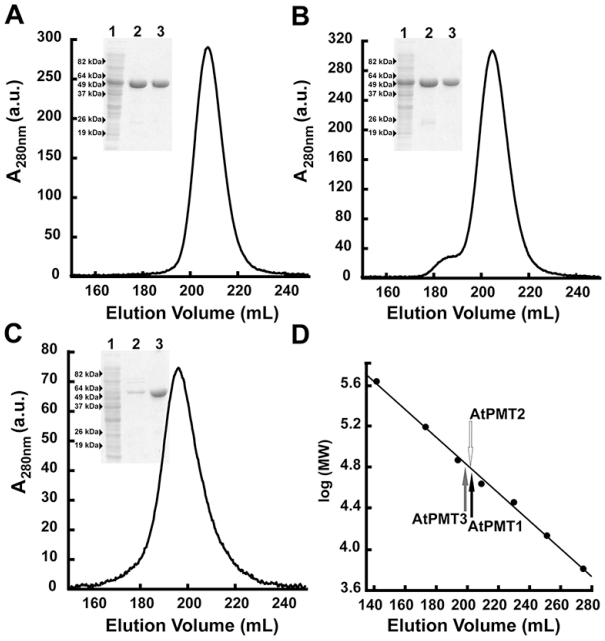

Figure S3. Isothermal titration calorimetry of SAH binding to AtPMT2. (A) Titration of AtPMT2 with SAH. ITC data are plotted as heat signal (μcal sec^{-1}) versus time (min). The experiment consisted of 30 injections of SAH into a solution containing AtPMT2 at 20 °C. **(B)** Integrated heat response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

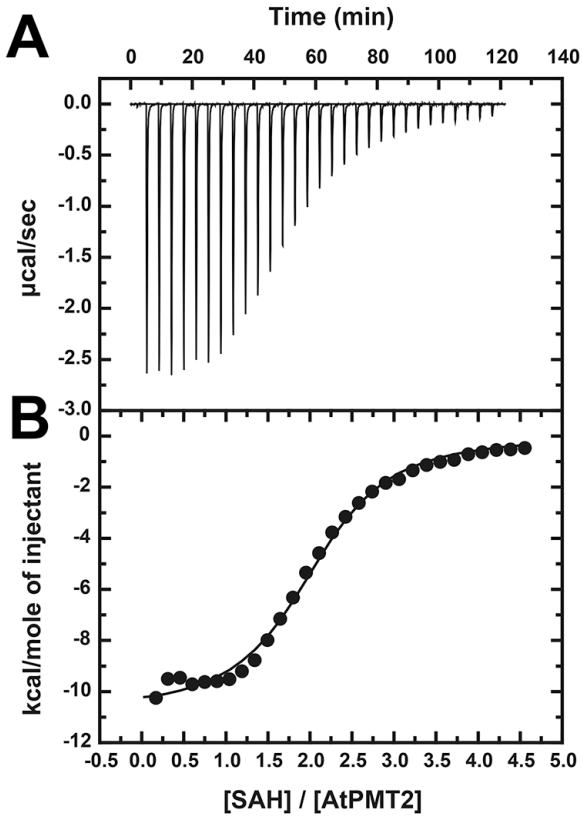

Figure S4. Polar lipid profiling of wild-type and *atpmt3* T-DNA knockout line.
(A) Total polar lipid levels for wild-type (white) and *atpmt3* (grey) plants are shown as nmol per mg dry weight (DW). Analysis of polar lipid content was performed as described in the experimental methods. **(B)** Comparison 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 *atpmt3* 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 ± standard deviation (n = 6-8).

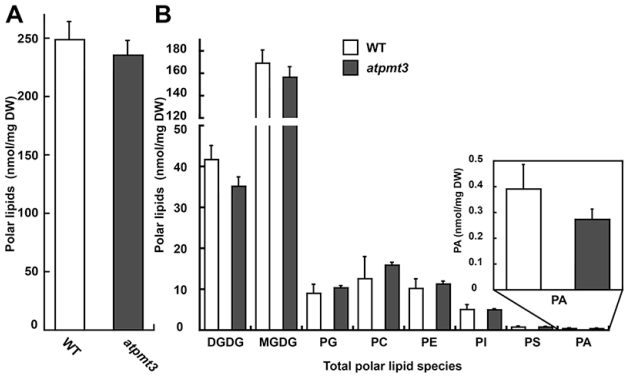

Figure S5. Electron density for active site ligands in AtPMT1 and AtPMT2.
(A) Electron density for pCho (top) and SAH (bottom) in the AtPMT1 MT1 domain active site is shown as a $2F_o$-F_c omit map (1.5 σ). **(B)** Electron density for pCho (top) and SAH (bottom) in the AtPMT1 MT2 domain active site is shown as a $2F_o$-F_c omit map (1.5 σ). **(C)** Electron density for SAH in the AtPMT2 MT 1 domain active site is shown as a $2F_o$-F_c omit map (1.25 σ). **(D)** Electron density for SAH in the AtPMT2 MT2 domain active site is shown as a $2F_o$-F_c omit map (1.25 σ).

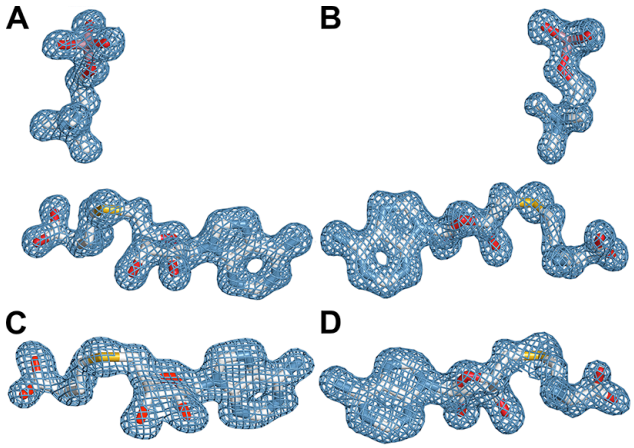

Table S1. Summary of sequences used to generate phylogenetic tree. The AtPMT1 sequence was used as a BLAST query to identify 153 sequences encoding putative PMT (see Fig. 8).

Type I	*Gossypium arboreum*	KHG16117.1	[eudicot]	Type I	*Xenopus laevis*	NP_001087172.1	[frogs & toads]
Type I	*Gossypium hirsutum*	XP_016666825.1	[eudicot]	Type I	*Strongylocentrotus purpuratus*	XP_794381.2	[sea urchins]
Type I	*Gossypium raimondii*	KJB30122.1	[eudicot]	Type I	*Branchiostoma florid*	XP_002594089.1	[lancelets]
Type I	*Halostachys caspica*	AHX22003.1	[eudicot]	Type II	*Eimeria acervulina*	CDI77742.1	[apicomplexans]
Type I	*Ipomoea nil*	XP_019169742.1	[eudicot]	Type II	*Eimeria maxima*	CDJ58552.1	[apicomplexans]
Type I	*Jatropha curcas*	KDP23922.1	[eudicot]	Type II	*Eimeria mitis*	CDJ34460.1	[apicomplexans]
Type I	*Juglans regia*	XP_018857980.1	[eudicot]	Type II	*Eimeria necatrix*	CDJ67597.1	[apicomplexans]
Type I	*Lupinus angustifolius*	OIV94185.1	[eudicot]	Type II	*Eimeria tenella*	CDJ43178.1	[apicomplexans]
Type I	*Lycium barbarum*	AGI56231.1	[eudicot]	Type II	*Plasmodium cynomolgi*	PCYB_122070	[apicomplexans]
Type I	*Malus domestica*	XP_008360927.1	[eudicot]	Type II	*Plasmodium falciparum*	PF3D7_1343000	[apicomplexans]
Type I	*Manihot esculenta*	OAY46532.1	[eudicot]	Type II	*Plasmodium knowlesi*	PKH_121150	[apicomplexans]
Type I	*Medicago truncatula*	AES76054.1	[eudicot]	Type II	*Plasmodium vivax*	PVX_083045	[apicomplexans]
Type I	*Morus notabilis*	EXB69095.1	[eudicot]	Type II (MT1)	*Ascaris suum*	ERG79882.1	[nematodes]
Type I	*Musa acuminata*	XP_009385384.1	[eudicot]	Type II (MT1)	*Bursephelenchus xylophilus*	BUX.s01513.225	[nematodes]
Type I	*Nelumbo nucifera*	XP_010274723.1	[eudicot]	Type II (MT1)	*Caenorhabditis brenneri*	CBN10892	[nematodes]
Type I	*Nicotiana attenuata*	OIT04993.1	[eudicot]	Type II (MT1)	*Caenorhabditis briggsae*	CBG02363	[nematodes]
Type I	*Nicotiana sylvestris*	XP_009782224.1	[eudicot]	Type II (MT1)	*Caenorhabditis elegans*	NP_494990.2	[nematodes]
Type I	*Nicotiana tabacum*	XP_016437407.1	[eudicot]	Type II (MT1)	*Caenorhabditis japonica*	CJA07932	[nematodes]
Type I	*Noccaea caerulescens*	JAU57851.1	[eudicot]	Type II (MT1)	*Caenorhabditis remanei*	CRE11930	[nematodes]
Type I	*Phaseolus vulgaris*	ESW24678.1	[eudicot]	Type II (MT1)	*Caenorhabditis sp.11*	Csp11.Scaffold630.*g21423.t1*	[nematodes]
Type I	*Phoenix dactylifera*	XP_008799221.1	[eudicot]	Type II (MT1)	*Caenorhabditis sp.5*	Csp5_scaffold_01891.*g23737.t1*	[nematodes]
Type I	*Populus euphratica*	XP_011039130.1	[eudicot]	Type II (MT1)	*Haemonchus contortus*	CDJ81011.1	[nematodes]
Type I	*Populus tomentosa*	APR64075.1	[eudicot]	Type II (MT1)	*Necator americanus*	ETN83758.1	[nematodes]
Type I	*Populus trichocarpa*	EEF06229.2	[eudicot]	Type II (MT1)	*Pristionchus pacificus*	PPA22786	[nematodes]
Type I	*Prunus mume*	XP_008240152.1	[eudicot]	Type II (MT1)	*Strongyloides stercoralis*	US 2007/0009981 A1 ID no: 10	[nematodes]
Type I	*Prunus persica*	XP_007209941.1	[eudicot]	Type II (MT2)	*Ascaris suum*	GS_23928	[nematodes]
Type I	*Pyrus betulifolia*	AER10513.1	[eudicot]	Type II (MT2)	*Bursephelenchus xylophilus*	BUX.s01143.358	[nematodes]
Type I	*Pyrus x bretschneideri*	XP_009360079.1	[eudicot]	Type II (MT2)	*Caenorhabditis brenneri*	CBN22056	[nematodes]
Type I	*Raphanus sativus*	XP_018432929.1	[eudicot]	Type II (MT2)	*Caenorhabditis briggsae*	CBG08775	[nematodes]
Type I	*Ricinus communis*	XP_002532097.1	[eudicot]	Type II (MT2)	*Caenorhabditis elegans*	NP_504248.1	[nematodes]

Type I	*Salicornia europaea*	ABG57185.1	[eudicot]	Type II (MT2)	*Caenorhabditis japonica*	CJA04052	[nematodes]
Type I	*Sesamum indicum*	XP_011072995.1	[eudicot]	Type II (MT2)	*Caenorhabditis remanei*	CRE18566	[nematodes]
Type I	*Solanum lycopersicum*	XP_004241642.1	[eudicot]	Type II (MT2)	*Haemonchus contortus*	CDJ96940.1	[nematodes]
Type I	*Solanum pennellii*	XP_015080167.1	[eudicot]	Type II (MT2)	*Meloidogyne hapla*	MhA1_Contig1162.frz3.gene5	[nematodes]
Type I	*Solanum tuberosum*	XP_006346642.1	[eudicot]	Type II (MT2)	*Meloidogyne javanica*	US 2007/0009981 A1 ID no: 12	[nematodes]
Type I	*Spinacia oleracea*	Q9M571.1	[eudicot]	Type II (MT2)	*Necator americanus*	ETN82894.1	[nematodes]
Type I	*Suaeda japonica*	BAC57432.1	[eudicot]	Type II (MT2)	*Pristionchus pacificus*	PPA16775	[nematodes]
Type I	*Suaeda liaotungensis*	ABK42071.1	[eudicot]				