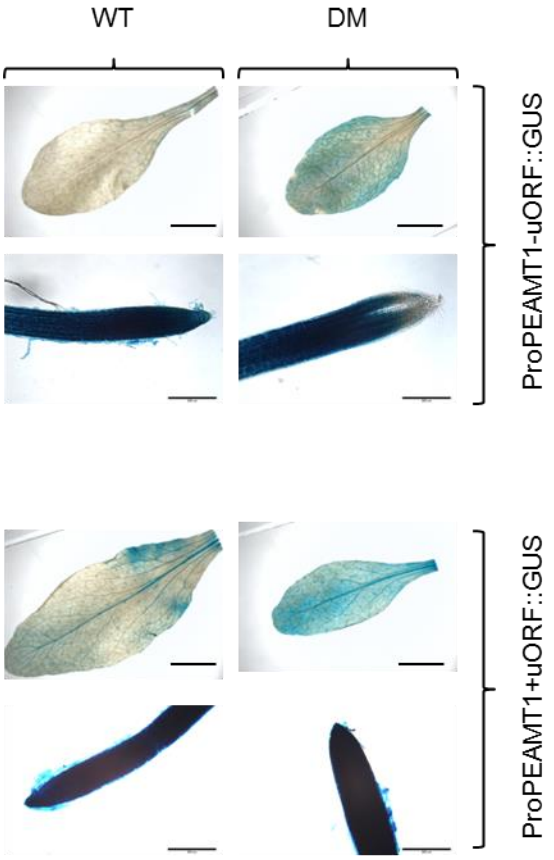

Supplemental Figure 1. ProPEAMT1:GUS expression in roots and leaves of WT and *pah1 pah2* plants.

Histochemical staining for GUS activity was performed on four-week-old roots and leaves of WT and DM (*pah1 pah2*) plants containing a ProPEAMT1:GUS construct without or with a functional uORF in the 5' UTR. Single insertion site transgenic lines were first created by transforming WT and the T-DNAs were then introduced into the *pah1 pah2* background by crossing. Scale bars = 0.5 cm for leaves and 0.2 mm for roots.

Supplemental Table 1. Analysis of gene expression for genes associated with phospholipid synthesis in *pah1 pah2* roots.

Enzyme	Name	AGI	Fold change
Phosphoethanolamine *N*-methyltransferase	*PEAMT1*	At3g18000	1.2 ±0.3
	PEAMT2	At1g48600	1.4 ±0.4
	PEAMT3	At1g73600	0.9 ±0.2
Choline kinase	*CKI*	At1g71697	1.2 ±0.3
	CKI-L1	At4g09760	0.7 ±0.3
	CKI-L2	At1g74320	0.9 ±0.5
CTP-phosphocholine cytidylyltransferase	*CCT1*	At2g32260	1.3 ±0.4
	CCT2	At4g15130	1.0 ±0.2
Aminoalcoholphosphotransferase	*AAPT1*	At1g13560	0.9 ±0.2
	AAPT2	At3g25585	1.4 ±0.3
Phospholipid *N*-methyltransferase	*PLMT*	At1g80860	1.1 ±0.4
Ethanolamine kinase	*EKI-L*	At2g26830	1.5 ±0.3
CTP-phosphoethanolamine cytidylyltransferase	*ECT*	At2g38670	1.4 ±0.5

Real-time PCR analysis of transcript abundance for genes associated with phospholipid synthesis in *pah1 pah2* double mutant roots. Values are the mean ± SE (n = 4) of measurements on roots of three-week-old plants grown on agar plates. Values are normalized using the level of *ACT2*/*ACT8* expression as a constitutive control.

Supplemental Table 2. Kinetic parameters for recombinant CCT1 activity in the presence and absence of lipids vesicles containing a 1:1 ratio of PC to either oleic acid or PA.

Condition	V_{max}	K_m P-Cho	K_m CTP
No lipid	3.9 ±0.3	0.61 ±0.07	0.19 ±0.03
PC:OE	24.2 ±1.8*	0.57 ±0.12	0.23 ±0.06
PC:PA	18.1 ±1.0*	0.59 ±0.11	0.22 ±0.04

Kinetic parameters were determined by regression analysis of the Michaelis-Menten hyperbola using Hyper32 freeware. Values are the mean ± SE of three separate experiments, each using five different concentration of substrate. Asterisk denotes a significant difference from the no lipid control ($P < 0.05$).

Supplemental Table 3. Primers used for cloning.

Primer	Sequence
AttB1-PAH1S	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGAGTTTGGTTG GAAGAGTTGGGAG
AttB2-PAH1A (minus stop codon)	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTCAACCTCTTC TATTGGCAGTTTCC
AttB2-PAH1A (plus stop codon)	GGGGACCACTTTGTACAAGAAAGCTGGGTTCATTCAACCTCT TCTATTGGCAGTTTCC
$PAH1^{\Delta cat}S$ (mutagenesis)	CACCAAGATAGTGATTTCAGAGGTTGAGGGAACTATAACTAA ATCTG
$PAH1^{\Delta cat}A$ (mutagenesis)	CAGATTTAGTTATAGTTCCCTCAACCTCTGAAATCACTATCTT GGTG
AttB1-CCT1S	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGAGCAACGTTA TCGGCGATCGC
AttB2-CCT1A (plus stop codon)	GGGGACCACTTTGTACAAGAAAGCTGGGTTTACTTGTTGTCT TTAGCATCCGTC
$AttB2\text{-}CCT1^{-211}A$ (plus stop codon)	GGGGACCACTTTGTACAAGAAAGCTGGGTTTACTGGAGTTTC TTTAGCCTCATA