

Supplementary Table S1. Primers used in this study.

Primer name	Primer sequence (5'→3')	Primer Specification
FP	TTATAGGTGCCCCAAAACCC	<i>lpat2</i> mutant identification
RP	TTACAGTTTCGCGCAGTGAC	<i>lpat2</i> mutant identification
T-border primer	ATTCCAGATCCCCCGAATTA	<i>lpat2</i> mutant identification
COMF	GAATTCGCGAAAAACGCACCGTATAG	Promoter for LPAT2 COM
COMR	GGTACCATCTTTCTTGACACGGTTC	Promoter for LPAT2 COM
LPAT2 FK	GGTACCATGGCGGTCCCACTCGTGC	CDS for <i>LPAT2</i> COM
LPAT2 Rb	GGATCCATCTTTCTTGACACGGTTC	CDS for <i>LPAT2</i> COM
Pcambia-F	TAGCCAATACGCAAACCGC	COM identification
OsLp2	CTTCAGTAACCCTTGGGCATAG	COM identification
LPAT2-ProF	GAATTCATGGCGGTCCCACTCGTGC	LPAT2 protein expression
LPAT2-ProR	CTCGAGATCTTTCTTGACACGGTTCC	LPAT2 protein expression
LPAT2-GFPF	GGGGTACCATGGCGGTCCCACTCGTGC	LPAT2-GFP localization
LPAT2-GFPR	GCTCTAGAATCTTTCTTGACACGGTTCC	LPAT2-GFP localization
LPAT2-RTF	AGTGAGATGCCAAAGTCA	Real time PCR
LPAT2-RTR	ACAGGAGTTGAGTCCATAGG	Real time PCR
β-actin F	TGCTATGTACGTCGCCATCCAG	Real time PCR
β-actin R	AATGAGTAACCACGCTCCGTCA	Real time PCR

ScLPAT0231	: MSVIGR-----	: 6
AtLPAT1	: MDVASARSISSHPSYGKPICSSQSSLRIRSRDKVCCFGRISNGMTSFTTSLHAVPSEKFMGETRRTGIQWSNRSRLRHPYRFLDKKSPR	: 90
AtLPAT2	: M-----	: 1
AtLPAT3	: M-----	: 1
AtLPAT4	: M-----	: 1
AtLPAT5	: M-----	: 1
OsLPAT1	: MGTLLRPRPLAHAAGADATPSTAHAVV-----VSGG-----RGRGVCEQPHRVRRRPGPQ	: 51
OsLPAT2	: M-----	: 1
OsLPAT3	: MDTV-----	: 4
OsLPAT4	: M-----	: 1
OsLPAT5	: M-----	: 1

ScLPAT0231	: -----FLYYLRSVLVVALAGCGFYGVIAS-----TL-----CTLIGKQHLAQWITAR	: 49
AtLPAT1	: -----SSQLARDITVRADLS--GAAT-PDSSFPEPEIKLSSRLRGFFCCVVAGISATFLVLM-----TLGHPPVL-----LFDPPYRRK	: 161
AtLPAT2	: -----VIAAAVIVPLGLFFISGLAVNLFOAVCY-----VLRPL-----SKNTYRKI	: 44
AtLPAT3	: -----KIPAAVIFIPVGLFLISGLIVNIIQVFF-----TVRPF-----SRSLYRKI	: 45
AtLPAT4	: -----EVCGLKSDNLKNRPLTPRILRGIMLLVFLSTAFMFILYFAPIAAGLR-L-----LSVQQRK	: 61
AtLPAT5	: -----EKKSVPNSDKLSLRVLRLGICLMVLVSTAFMMILFWGFLSAVLR-L-----FSIRYSRK	: 56
OsLPAT1	: VAVATASWRRRRRETIVRSDFAAAGGAATMGDSPQALSDIDVSRVRGCFYAVTAVAAIFLVAM-----VVVHPLVL-----LFDRYRRR	: 131
OsLPAT2	: -----AVVVVSGGIINAAVSI-----RKSRYRKI	: 26
OsLPAT3	: VAAATTGSRRLWPARRQAAAYLAAAGGGDDGWAACAASAVRIV--VCFVSMATTAAWAVML-----LLPWPCARIRQGNLYGHVTGR	: 88
OsLPAT4	: --MNGSNGSQGYHVG--KQVQSVVPSIQNNGPRHRPLTLRRCRGLCLVIMPLTAEMMVYLSPTVTFILIR-L-----FSVHYSRK	: 79
OsLPAT5	: ---NGSSGSQGHNVNGGQKVKQHASPLTLNNGSKHRPLTPRRCRGACVVIILSTAFTLVFIAPITTFILVR-L-----VSVHYSRK	: 80

ScLPAT0231	: CFYHVMKLMIGI-----DVK-----VGEEN-----AKKPYIMIANHOSLIDIFMLGRIFPP-----GCTVTAKKSLKYVEFLGWFMAIS	: 120
AtLPAT1	: FHHFIKWLASI--SIYF-YKIN-----EGLENLPS-SDTPAVVSNHOSLIDITLLSLGK-----SPKFTSKTGIFVPIIGWAMSM	: 239
AtLPAT2	: NRVVAETLWLEVMIVDWAGVKIQVFADNETFNRMGKEHAIIVCNHRSIDIDLVGWILAQRSGLGSALA-MKKSSKFLPVIIGWSMWF	: 134
AtLPAT3	: NKNVAELLWLQIWLFDWACIKINLYVDAETELIGKEHAIIVSNHRSIDIDLIGWVMAQRVGLGSSLA-MKKEAKYLPVIIGWSMWF	: 135
AtLPAT4	: VVSLIFGLWLA--WPYLEETVNGTTVFSGDIIPV--EKRVLLTANHRTVDWMYLWDLALRKGCLGYIKYIKSSIMKLPPIFGWGFHVL	: 148
AtLPAT5	: CVSFFFGSWLA--WPFLFEKINKTKVFSGDKVPC--EDRVLLTANHRTVDWMYFWDALRKGQIGNIKYIKSSIMKLPPIFGWAFHLF	: 143
OsLPAT1	: AQHYIAKIWATL--TISM-YKLD-----EGMENLPP-NSSPAVYANHOSLIDITLLTGR-----CFKFTSKTSIFMFPPIIGWAMYLL	: 209
OsLPAT2	: NRAWV-----W-VDWAGVK--HADDTYKA--MGNHAIIVSNHRSIDIDW-IGWI--ARSGC--GSTAMKSSK--VIGWSMW--	: 92
OsLPAT3	: MLMWILG-----NPIK-----EGMEN-----NTRGELFCNHASLIDIFLVMWAPT-----GTVGAKKEIIWYPIFCQLYVLA	: 154
OsLPAT4	: STCFLFGMWLA--WPFLFEKINKTKVFSGETVPP--KERVLLFANHRTVDWMYLWDLALRKGRLQCIKYIKSSIMKLPPIFNFAFHII	: 166
OsLPAT5	: ATSVLFGMWLSI--WPFLFEKINKTNVFSGESVLP--KKRVLLFANHRTVDWMYLWDLALRKGYLGYIKYIKSSIMKLPPIFNFAFHIF	: 167

ScLPAT0231	: GTYFDRSKRQEAIDTNKGLENVKKNKRALW--VPECTRSYSELTMLPFKKGAFLAQGKIPIVEVVSNTSTLVSPKYGVFN--	: 205
AtLPAT1	: GVVPIKRM DPRSQVDCIKRCMELLKKGASVF--EPECTRSKDG-LG--SFKKGAFVAKTGAVVPIITLMTGTGIMPTGSEGILN--	: 322
AtLPAT2	: EYLFERNWAKDE-STKSGLQRLSDFFRPFWLALVECTRFTEAL--KAAQEYASSELPIPRNVILPRTGFVSAVSNMRSFV	: 217
AtLPAT3	: DYLFERNWAKDE-NTKAGFKRLEDFFMTFWLALVECTRFTEAL--EAAQEYASIRSLSPRNVLIPRTGFVSAVSEIRSFV	: 218
AtLPAT4	: EFIPVERKREVDE-PVQLQLSSFKDPQEPFLALVECTDFTEEC--KRSQKFAEVGLEALSNVLIPKTGFVGVCEVLHNSL	: 231
AtLPAT5	: EFIPVERREWEVDE-ANRQIVSSFKDPRDALWALVECTDYTEAC--QRSKKFAENGLEILNNVLIPRTGFVSVCLQELSCSL	: 226
OsLPAT1	: GVVPIRMRDSRSQLDCKRCVDLVKKGASVF--EPECTRSKDG-LG--AFKRGAFSVAKTGAVIPITLGTGLMPSGMEGILN--	: 292
OsLPAT2	: ---AYRSWAKDK-----TKWGRKDRWAV-----GTRTAKAAY-----ASGARNVIT--RTG-VSAVTIMRDV--	: 144
OsLPAT3	: NHRIRHRSNPAAAIESKEVARAVTKNNLSLI--LPPDTRSKTG-LL--PFKKGFVHTALQTRPIVEMVVTGTHLAWRKNSLRVR--	: 237
OsLPAT4	: EFIPVERKWEVDE-PLRSRLSELKNPKDPLWALVECTDYTEKC--IKSQEYAKEHGLEILNNVLIPKTGFHCCLOELRDSM	: 249
OsLPAT5	: EFIPVERKWEIDE-AIQNKLSAFKDPDRPLWALVECTDYTEKC--IKSQEYASEHGLEILNNVLIPKTGFHCCLOELKSSL	: 250

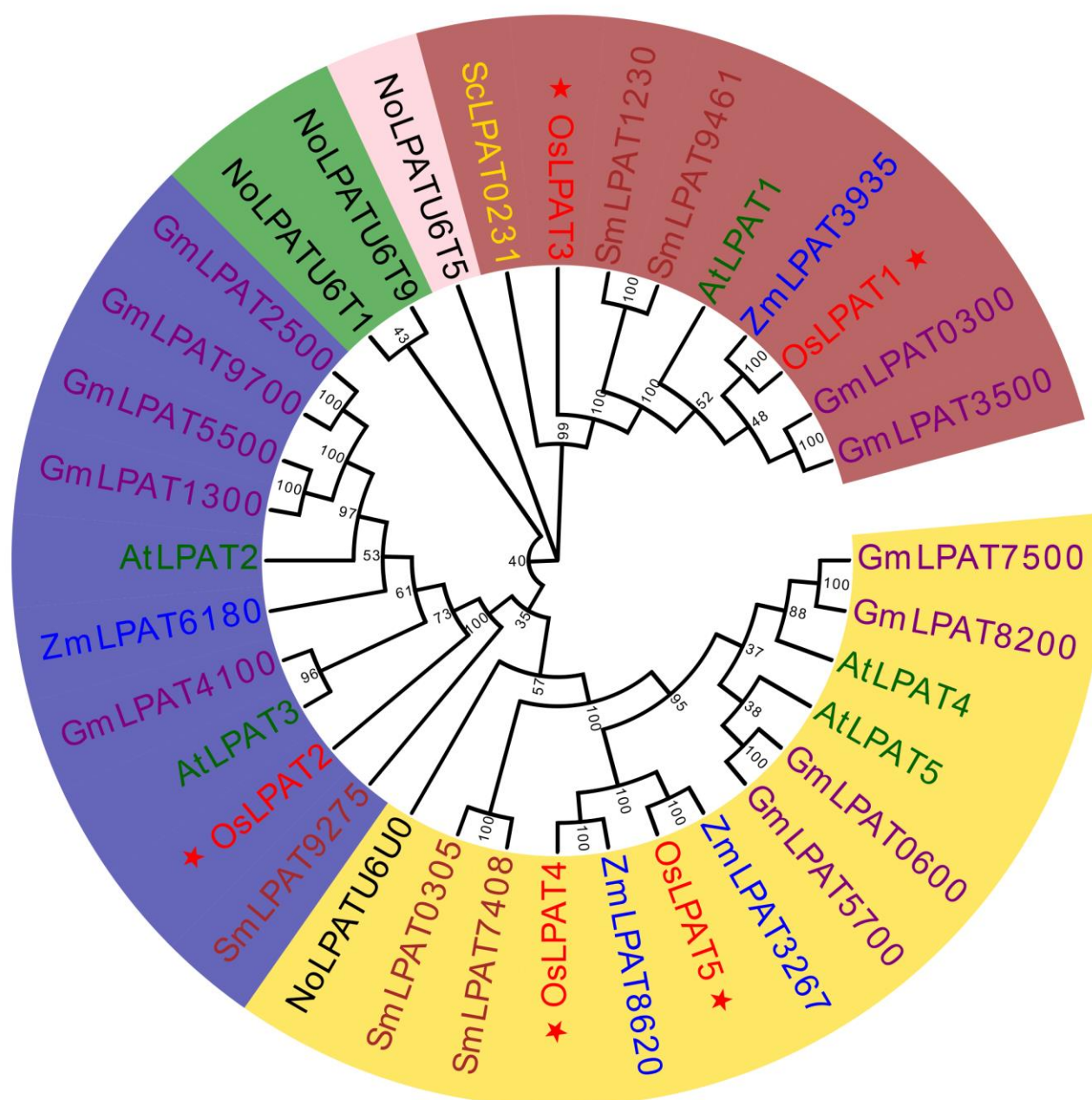
ScLPAT0231	: -----RGCMIVRILK-----LISTENLTCKDIGEFAEKVDMQVDTLKEIGYSPAINDTTLPPQAIIEY	: 263
AtLPAT1	: -----HGNVRVLIHK-----BIHGSKA-----DVLCEASAKIAESMDL-----	: 356
AtLPAT2	: PAIYDMTIVTIKTPSPPTMLRLFKGQPSVVMVHIKCHSKMDLESDDAIAQWCRDQF--VADALLDKHIAADTFPG-----	: 292
AtLPAT3	: PAIYDCTLTVHNNQPTPTLLRMFSGQSSEINLQMRHKMSELDETDDGIAQWCQDLF--ITDAQLEKYFTKDVFS-----	: 293
AtLPAT4	: DAVYDLTIAYKPRCPS-FMDNVFGTDPSEVHHVRRVLLKEIANEAESSAWLMDSF--KLQKLLSDFNAQGFKN--	: 305
AtLPAT5	: DAVYDVTIGYKTRCPS-FLDNVYGIEPSEVHHIRRLNLTQINQEKDINAWLMNTE--QLDQLLNDFYSGHGFN-----	: 300
OsLPAT1	: -----SGSVKLIHH-----IEGND-----EKLCEASAKVIADTLILNGYGVH-----	: 332
OsLPAT2	: -AIYDTTVIKDKST-----MRIKGSVVHVRMKRHAMS--MKSDDVSKWCKDI--VADA--DKHATG-----	: 200
OsLPAT3	: -----PAPLVKVLV-----IETDGWVEERIDEYVEMVHSLYADSLPD-----S-----	: 277
OsLPAT4	: DSVCDITIAKHPPT-FMDNVYGIDPSEVHHVHIIQVSDITSEDEVADWLIERF--KLQKLLSDFSALGHGFN-----	: 323
OsLPAT5	: DAVYDVTIAKHLPD-FLDIYGTDPSEVHHIRTVKLCDIITSEDEVTDWMIERF--RQDQLLSDFFMQGHFPD-----	: 324

ScLPAT0231	: AALQHDKKVNKKIKN-----EPVPSVISNDVN	: 291
AtLPAT1	: -----	: -
AtLPAT2	: ---QQEQNIGRPIKSLAVLSWACVLTLAGKFLH-WAQLFSSWKGITISALGLGIITLCMQILIRSSQSERSTPAKVVPAPKPKDNHHP	: 378
AtLPAT3	: ---LEVHQINRPIKPLIVVLIWLGLVFGGFKLLQ-WLSIVASWKIILLVFVFLVIATITMQILIQSSSESQRSTPAKRPLQEQLISA---	: 376
AtLPAT4	: QRPEEELSVLKCIATFAGVISLTVFYLYTLYSHS-CFKVYACLSGTYLT----FATYKQFQSP-GCFREDSCKVKNH-----	: 378
AtLPAT5	: EGTEKEFNTKKYLINCLAVIAFTTICTHLTFSSMIWFRIYVSLACVYLT----SATHFNLSRVPLVETAKNSLKLVNK-----	: 375
OsLPAT1	: -----	: -
OsLPAT2	: ---TDIRIGR-----VKSVTWSCYGAVKWT-----TWKGVGTGAVTAVMHVIMSSRSSAKAARNRVKDK-----	: 259
OsLPAT3	: QKPLEPVNTGK-----	: 288
OsLPAT4	: EGTEDDLSTLKCIAFVAVISTTTVLTLYTLFSSV-WFKIFVAFSSAFLT----FATLYSIHLPLQLICSPEAGTHAKKS-----	: 397
OsLPAT5	: EGTEGDEVSTPECLANFIAIVSSGTFFLYLSLFSSV-WFKVYVLLSCAYLT----FVTFYSIQPQLICSSEGGTHAKKVL-----	: 399

ScLPAT0231	: THNEGSSVKKMH	: 303
AtLPAT1	: -----	: -
AtLPAT2	: SSSQTETEKEK-	: 389
AtLPAT3	: -----	: -
AtLPAT4	: -----	: -
AtLPAT5	: -----	: -
OsLPAT1	: -----	: -
OsLPAT2	: -----	: -
OsLPAT3	: -----KKMS	: 292
OsLPAT4	: -----	: -
OsLPAT5	: -----	: -

Supplementary Figure S1. Sequence alignment and domain structures of LPATs.

Alignment of amino acid sequences of LPATs were analyzed using MAFFT. The identical and similar residues are shaded in black and gray, respectively. The conserved motifs including I, II, III and IV related to acyltransferases are indicated in boxes. Sc, *Saccharomyces cerevisiae*; At, *Arabidopsis thaliana*; Os, *Oryza sativa*.



Supplementary Figure S2. Phylogenetic analysis of LPAT family in various species.

The amino acid sequences of LPAT orthologous proteins were aligned using the MAFFT software and The phylogenetic tree was constructed through MEGA11 software using neighbor-joining and bootstrap (1000) as default setting. At, *Arabidopsis thaliana*; Gm, *Glycine max*; Os, *Oryza sativa*; Zm, *Zea mays*; Sm, *Selaginella moellendorffii*; No, *Nannochloropsis oceanica*; Sc, *Saccharomyces cerevisiae*. OsLPAT1, Os10g0497100; OsLPAT2, Os11g0637800; OsLPAT3, Os04g0625200; OsLPAT4, Os05g0502200; OsLPAT5, Os01g0782500; AtLPAT1, At4g30580; AtLPAT2, At3g57650; AtLPAT3, At1g51260; AtLPAT4, At1g5020; LPAT5, At4g18850.