Supplemental Figure S1. Sequence Comparisons Between AtGPAT9 and Other Plant and Mammalian Proteins.

The amino acid sequence of AtGPAT9 was aligned and compared individually to that of mouse GPAT3 (A), AtLPEAT1 (B), and AtLPEAT2 (C), and AtGPAT7 (D) using the ClustalX algorithm (Thompson et al., 1997). Identical amino acid residues are marked with asterisks, highly similar residues with two dots, and similar residues with one dot.

(A) mouse GPAT3

```
CLUSTAL X (1.81) multiple sequence alignment


AtGPAT9         -------------------------------MSSTAGRLVTSKSELDLDHPNIEDYLPSG
mGPAT3          MEGADLAVKLLSTWLTLVGGLILLPSAFGLSLGISEIYMKILVKTLEWATLRIQKGAPKE
                                               :. :   :    . *:    .*:.  *.

AtGPAT9         SSINE--------------PRGKLSLR----DLLDISPTLTEAAGAIVDDSFTRCFKSNP
mGPAT3          SALKNSASVGIIQRDESPMEKGLSGLRGRDFELSDVFYFSKKGLEAIVEDEVTQRFSSEE
                *::::               :*  .**    :* *:    .:.  ***:*..*: *.*:

AtGPAT9         PEPWNWN-------IYLFP----LYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNA
mGPAT3          LVSWNLLTRTNVNFQYISPRLTMVWVLGVLVRYCFLLPLR-VTLAFIGISLLIIGTTLVG
                  .**          *: *    :: :**:****:*:*** .****  * :* :  .: .

AtGPAT9         LLKGQDRLRKKIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVL
mGPAT3          QLP-DSSLKNWLSELVHLTCCRICVRSLSGTIHYHNKQYRPQKGGICVANHTSPIDVLIL
                 *  :. *:: :..::    * : * * :*.::**. :   :   : ****** **.::*

AtGPAT9         EQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDHVQGADSNPL
mGPAT3          ATDGCYAMVGQVHGGLMGIIQRAMVKACPHVWFERSEIKDRHLVTKRLKEHIADKKKLPI
                    .:*:: * * * :*::* :::::   :**:*** ***.:*:*:*::*: . .. *:

AtGPAT9         LIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMT
mGPAT3          LIFPEGTCINNTSVMMFKKGSFEIGGTIYPVAIKYNPQFGDAFWNSSKYNLVSYLLRIMT
                ********:**. .:*****:**:. *: *:*****  * ****** * .:. :**::**

AtGPAT9         SWAVVCEVWYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSER
mGPAT3          SWAIVCDVWYMPPMTREEGEDAVQFANRVKSAIAVQGGLTELPWDGGLKRAKVKDTFKEE
                ***:**:***: * * . ** .::**:**:. *:::.**.::**** ** :: . ...*.

AtGPAT9         KQQSFAESILARLEEK----
mGPAT3          QQKNYSKMIVGNGSPNLARD
                :*:.::: *:.. . :

136 residues identical (based on 376 aa in AtGPAT9:  36% identical)
90 residues highly similar (60% identical + highly similar)
44 residues similar (72% identical + similar)
```

(B) AtLPEAT1

```
CLUSTAL X (1.81) multiple sequence alignment


AtGPAT9         MSSTAGRLVTSKS--ELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAI
AtLPEAT1        MESELKDLNSNSNPPSSKEDRPLLKSESDLAAAIEELDKKFAPYARTDLYGTMGLGPFPM
                *.*    * :...  . . *:* ::.    .::*:*   *::     *:  *:  .. .:

AtGPAT9         VDDS-FTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLR--CFTLAFGWIIFLSLF
AtLPEAT1        TENIKLAVALVTLVPLRFLLSMSILLLYYLICRVFTLFSAPYRGPEEEEDEGGVVFQEDY
                .::  :: .: :  *  :  .: :: ** :   *   :  * *        * ::* . :

AtGPAT9         IPVNALLK-GQDRLRKKIERVLVEMICSFFVAS---------------WTGVVKYHGPRP
AtLPEAT1        AHMEGWKRTVIVRSGRFLSRVLLFVFGFYWIHESCPDRDSDMDSNPKTTSTEINQKGEAA
                  ::.  :    *  : :.***: ::  ::: .                :  :: :*  .

AtGPAT9         SIRPKQ--VYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSE
AtLPEAT1        TEEPERPGAIVSNHVSYLDILYHMSASFPSFVAKRSVGKLPLVG-LISKCLGCVYVQREA
                : .*::  . *:**.* :*::   . :  :.: ::  * : *:   * :.:**::.:*.

AtGPAT9         -AKDREIVAKKLRDHVQGADSN----PLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIA
AtLPEAT1        KSPDFKGVSGTVNERVREAHSNKSAPTIMLFPEGTTTNGDYLLTFKTGAFLAGTPVLPVI
                 : * : *: .:.::*: *.**    .:::***** .*.:* : **.***  . .* *:

AtGPAT9         IKYNKIFVDAFWNSRK--QSFTMHLLQLMTSWAVVCEVWYLEPQTIRPGETGIEFAERVR
AtLPEAT1        LKYPYERFSVAWDTISGARHILFLLCQVVNHLEVIRLPVYYPSQEEKDDPK--LYASNVR
                :**    ... *:: .  : : : * *::.   *:    *  .*  : . .   :*..**

AtGPAT9         DMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILARLEEK
AtLPEAT1        KLMATEGNLILSELG----LSDKRIYHATLNGNLSQTRDFHQKEE-
                .::: ...*     .     *     *:  : :      : : **

71 residues identical (19% identical)
93 residues highly similar (44% identical + highly similar)
51 residues similar (57% identical + similar)
```

(C) AtLPEAT2

```
CLUSTAL X (1.81) multiple sequence alignment


AtGPAT9         -------------MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDI
AtLPEAT2        MADPDLSSPLIHHQSSDQPEVVISIADDDDDESGLN-LLPAVVDPRVSRG--FEFDHLNP
                              **   .:* * :: * *...::  **:  . . .**     * *:

AtGPAT9         SPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTLAFG
AtLPEAT2        YGFLSESEPPVLGPTTVDPFRNNTPGVSGLYEAIKLVICLPIALIRLVLFAA---SLAVG
                   *:*:  .::. : .  *:.*.*   .    :  : *: :.:   :**.    :**.*

AtGPAT9         WIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVY
AtLPEAT2        YLATKLALAGWKDKENPMPLWRCRIMWITRICTRCILFSFGYQWIRRKGKPARREIAPIV
                ::     :   :   :     * :*  :      .::.:     :: :*  .  .   :

AtGPAT9         VANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKK
AtLPEAT2        VSNHVSYIEPIFYFYELSPTIVASESHDSLPFVG-TIIRAMQVIYVNRFSQTSRKNAVHE
                *:**.* *: *.     : ::: .:  . : ::  **:.::  *:.** . ..*: ..::

AtGPAT9         LRDHVQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWN--
AtLPEAT2        IKRKASCDRFPRLLLFPEGTTTNGKVLISFQLGAFIPGYPIQPVVVRYPHVHFDQSWGNI
                :: :..      **:***** .*.:  : *: ***  . .: *:.::* ::..*  *.

AtGPAT9         ---------------------------SRKQSFTMHLLQLMTSWAVVCEVWYLEP-----
AtLPEAT2        SLLTLMFRMFTQFHNFMEVEYLPVIYPSEKQKQNAVRLSQKTSHAIATSLNVVQTSHSFA
                                           *.**. .   *.  ** *:. .:  ::.

AtGPAT9         --------------------------------------------QTIRPGETG-------
AtLPEAT2        DLMLLNKATELKLENPSNYMVEMARVESLFHVSSLEATRFLDTFVSMIPDSSGRVRLHDF
                                                             :: *..:*

AtGPAT9         --------IEFAERVRDMISLRAG----------------------------LKKVPWDG
AtLPEAT2        LRGLKLKPCPLSKRIFEFIDVEKVGSITFKQFLFASGHVLTQPLFKQTCELAFSHCDADG
                          :::*: ::*.:.                              :.:   **

AtGPAT9         -----------YLKYSRPSPKHSERK-----------QQSFAESILARLEEK--------
AtLPEAT2        DGYITIQELGEALKNTIPNLNKDEIRGMYHLLDDDQDQRISQNDLLSCLRRNPLLIAIFA
                            ** : *. ::.* :           *:   :.:*: *..:

AtGPAT9         ------
AtLPEAT2        PDLAPT
```

74 residues identical (20% identical)
89 residues highly similar (43% identical + highly similar)
58 residues similar (59% identical + similar)

(D) AtGPAT7

```
CLUSTAL X (1.81) multiple sequence alignment


AtGPAT9         MSSTAGRLVTSKSELD---LDHPNIEDYLP----SGSSINEPRGKLSLRDLLDISPTLTE
AtGPAT7         MESSTTTSYSVVSELEGTLLKNPKPFAYFMLVAFEASGLIRFATLLFLWPIIALLDVLGY
                *.*::    :  ***:   *.:*:   *:     ..*.: .    * *  :: :  .*

AtGPAT9         AAG-----------AIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFG------VVVRYCIL
AtGPAT7         RNGSLKLMIFVATAGLHESEIESVARAVLPKFFMDDISMDAWRAFGSCDKRVVVTRMPRV
                  *           .: :..:    ::  *: :  :* : .  .**      **.*   :

AtGPAT9         FPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKK-IERVLVEMICSFFVASWTGV----
AtGPAT7         MVERFAKDHLSADEVIGTEIVVNRFGYATGLIQETNVDQSVFNSVANLFVDRRPQLGLGR
                :  *  .  :.   .:.  * ** :  . . :::. ::: :.: :..:**   . :

AtGPAT9         --------------VKYHGPRPS----------IRPKQVYVAN-----HTSMIDFIVLEQ
AtGPAT7         HIISDSPTFLSLCEEQVHAPVPSNYNGHNQRLHVQPLPVIFHDGRLVKLPTPATALIILL
                               : *.* **          ::*  * . :      .:    :::

AtGPAT9         MTAFAVIMQKHPGWVG-LLQSTILESVGCIWFNRSEAK-------------------DRE
AtGPAT7         WIPFGIILAMIRIFVGFLLPLWAIPYVSRIFNTRFIVKGKPPAQATTGNPGVLFVCTHRT
                  .*.:*:     :** **    :  *. *: .*  .*                   .*

AtGPAT9         IVAKKLRDHVQG---------------------------------------ADSNPLLIF
AtGPAT7         LMDPVVLSYVLGRSIPAVTYSISRLSEILSPIPTFRLTRIRDVDAEMIKKELSNGDLVVY
                ::   : .:* *                                        ... *:::

AtGPAT9         PEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNS--RKQSFTMHLLQLMTS
AtGPAT7         PEGTTCREPFLLRFSALFAELTDNIVPVAMNYRVGFFHATTARGWKGLDPIFFFMNPRPV
                ****  .: : : *.    **  .: *:*::*.  *..*      :  .  :.:::  .

AtGPAT9         WAVVCEVWYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERK
AtGPAT7         YEVTFLNQLEVEATCSSGKSPYDVANYVQRILAATLGFECTNFTRKDKYRVLAGNDGTVS
                : *.         *  .*::  :.*: *: :::   *:: . :    **   : :..  .

AtGPAT9         QQSFAESILARLEEK-----
AtGPAT7         YLSFLDQVKKVVTTFKPFLH
                  ** :.:   :

 68 residues identical (18% identical)
 85 residues highly similar (41% identical + highly similar)
 54 residues similar (55% identical + similar)
```

Supplemental Figure S2. Sequence Comparison of Selected GPAT9 Enzymes from Plants.

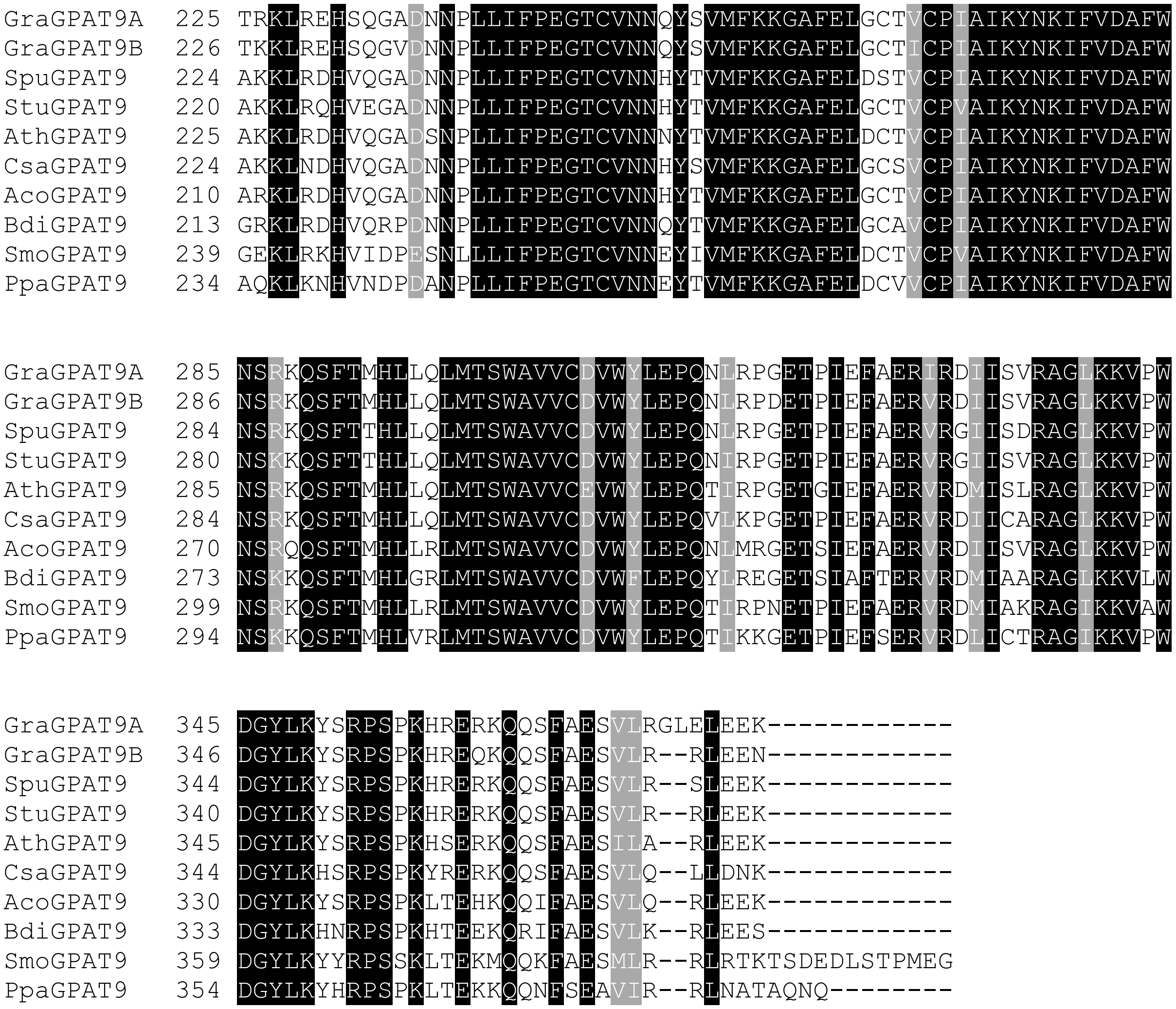
Amino acid sequences from *Aquilegia coerulea, Arabidopsis thaliana*, *Brachypodium distachyon*, *Cucumis sativus, Gossypium raimondii, Physcomitrella patens*, *Salix purpurea, Selaginella moellendorffii*, and *Solanum tuberosum* were aligned using the ClustalX algorithm as described in Figure S1 above. Amino acids identical in all ten proteins are shaded in black, similar residues are shaded in grey. Name abbreviations indicate the first letter of the genus, and the first two letters of the species.

```
GraGPAT9A    1 -----------MNSSEG-KLKSSSSELDLDRPNIEDYLPSGSSIQEP----HGKLRLRDL
GraGPAT9B    1 -----------MSSGKGGELIPSSSELDLDRPNIEDYLPSGSSIHEP----LGKLRLCDL
SpuGPAT9     1 ------------MDTPG-NLKTSISELDLDRPNIEDYLPSGTSIQEP----LDKLSLRDL
StuGPAT9     1 ---------------MS-NLKSSSSELDFDRPNLEDYLPTG-SIQEP----HGKLRLRDL
AthGPAT9     1 -----------MSSTAG-RLVTSKSELDLDHPNIEDYLPSGSSINEP----RGKLSLRDL
CsaGPAT9     1 ------------MSGAA-LLKSSASELDLDRPNIEDYLPSGSSIQQP----TAKLRLRDL
AcoGPAT9     1 --------------------------MDIDRPNIEEYLTTD-SIHKP----QEKLLLRDL
BdiGPAT9     1 -------------------MASS-----LDAPNLDDYLPTDSLPQEP----PRSLNLRDL
SmoGPAT9     1 MGIQRTGVKDSNQLRDSSLFRPSQSEVDLYQHDMEDFLLDSAAEPAAPH--QNKLLLCDL
PpaGPAT9     1 -------MEGDQFKGSADGINAGEAGRGICNEVVADFLNTNVEEDSSEAYLDNKMQLRDL


GraGPAT9A   45 LDISPALTEAAGAIVDDSFTRCFKSNPPEPWNWNVYLFPLWCCGVVFRYLILFPMRALVL
GraGPAT9B   46 LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNVYLFPLWCCGVVIRYLILFPVRVIVL
SpuGPAT9    44 LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNVYLFPLWCCGVVIRYGILFPVRVLVL
StuGPAT9    40 LDISPTLTEAAGAIIDDSFTRCFKSNPPEPWNWNIYLFPLWCLGVVVRYGILFPIRVIVL
AthGPAT9    45 LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTL
CsaGPAT9    44 LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLWCCGVVIRYLFLFPARVLIL
AcoGPAT9    30 LDISPALTEAAGAIIDDSFTRCFKSNPPEPWNWNVYLFPLWCFGVVIRYGILYPVRVLVL
BdiGPAT9    33 LDISPVLTEAAGAIVDDSFTRCFKSNSPEPWNWNIYLFPLWCFGVVVRYGLLFPLRVLTL
SmoGPAT9    59 LDISGVLSEAASAIVDDSFTRCFKSNIPEPWNWNIYLLPLWCLGVIVRYCILFPVRVLLL
PpaGPAT9    54 LDISQVLSEAGSAIIDDSFTRCFKSNAPEPWNWNIYLFPLWVMGVAVRYLILFPIRVILL


GraGPAT9A  105 TIGWIIFLSCFIPVHFLLKGNDNLRKKMERALVELICSFFVASWTGVVKYHGPRPSMRPK
GraGPAT9B  106 TVGWIIFLSCFIPVHLLLKGHDKLQKNMERALVELICSFFVASWTGVINYHGPRPSMRPK
SpuGPAT9   104 AIGWIIFLSSYIPVHLLLKGHDKLRKKIERSLVEVICMFFVASWTGVVKYHGPRPSRRPK
StuGPAT9   100 TIGWIIFLSCYIPVHLLLKGHDKFRKKLERCLVELICSFFVASWTGVVKYHGPRPSIRPK
AthGPAT9   105 AFGWIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKYHGPRPSIRPK
CsaGPAT9   104 TIGWIIFLSTFIPVNLLLKGHPKLRAKLERFLVELICSFFVASWTGVVKYHGPRPSIRPK
AcoGPAT9    90 TIGWIIFLSSFTAVHFLLKGNDKWRRQMERYLVELICSFFVASWTGVVKYHGPRPSMRPK
BdiGPAT9    93 GLGWMVFFAAFFPVHFLLKGQNKLRSKIERKLVEMMCSVFVASWTGVIKYHGPRPSSRPY
SmoGPAT9   119 TVGWIIFLGAFIPVHFILRKHDHMRRKIERGLVEFICSVFVASWTGVVKYHGPRPSRRPR
PpaGPAT9   114 ALGWIIFLSLFFPLHFALKNHDQLRRQIERGLVEFMCSVFVASWTGVVKYHGPRPSRRTK


GraGPAT9A  165 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV
GraGPAT9B  166 QVFVANHTSMIDFIILEQMSSFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDRETV
SpuGPAT9   164 QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLLQSTILESVGCIWFHRSEAKDREIV
StuGPAT9   160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILEGVGCIWFNRSEAKDREIV
AthGPAT9   165 QVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV
CsaGPAT9   164 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRTELKDREIV
AcoGPAT9   150 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDREIV
BdiGPAT9   153 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV
SmoGPAT9   179 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQNTVLESLGCIWFNRTESKDRHVV
PpaGPAT9   174 QVFVANHTSMIDFVILEQMTGFSAIMQKHPGWVGFLQTTVLESLGCIWFNRTEANDRHAV
```

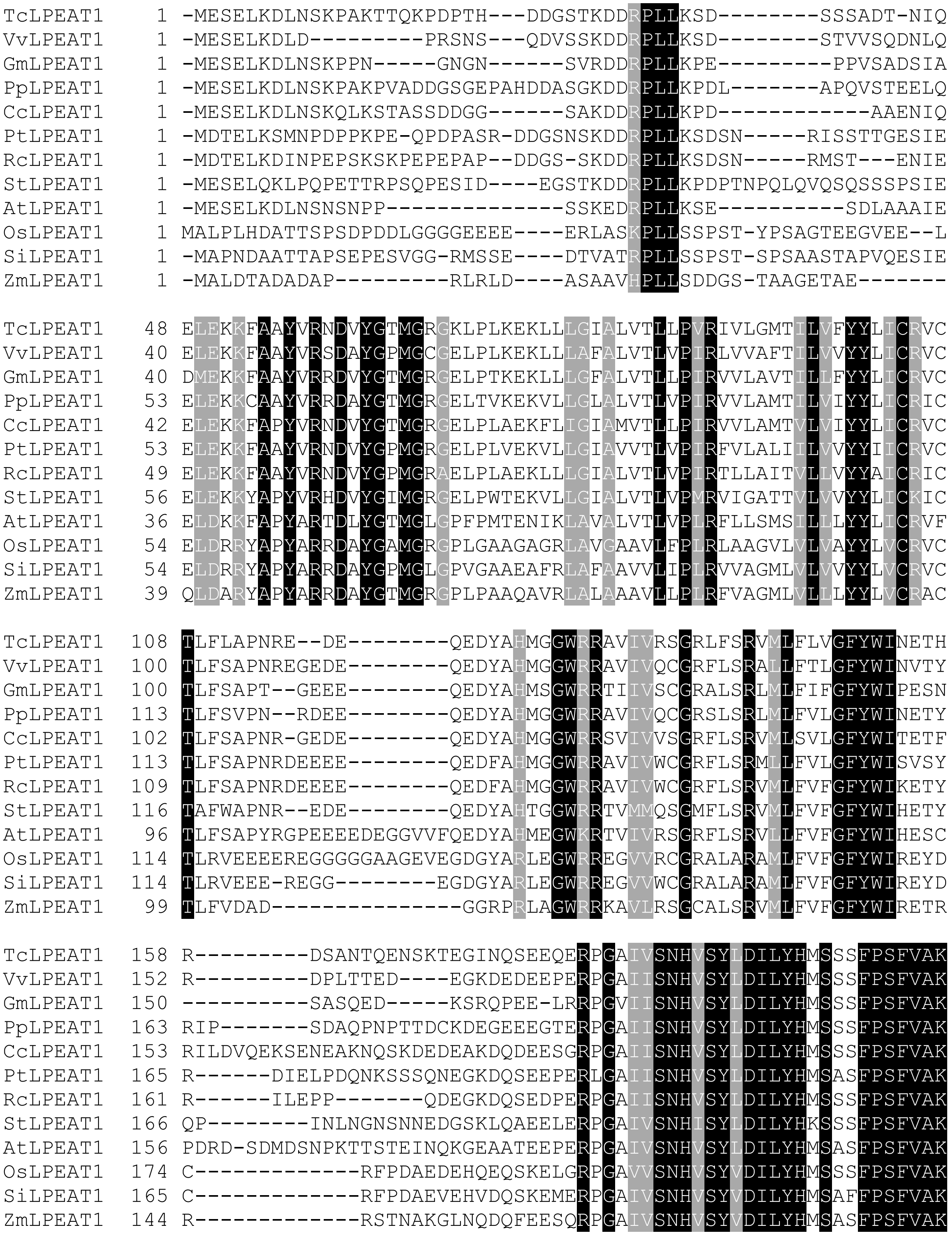


```
GraGPAT9A  225 TRKLREHSQGADNNPLLIFPEGTCVNNQYSVMFKKGAFELGCTVCPIAIKYNKIFVDAFW
GraGPAT9B  226 TKKLREHSQGVDNNPLLIFPEGTCVNNQYSVMFKKGAFELGCTICPIAIKYNKIFVDAFW
SpuGPAT9   224 AKKLRDHVQGADNNPLLIFPEGTCVNNHYTVMFKKGAFELDSTVCPIAIKYNKIFVDAFW
StuGPAT9   220 AKKLRQHVEGADNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPVAIKYNKIFVDAFW
AthGPAT9   225 AKKLRDHVQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFW
CsaGPAT9   224 AKKLNDHVQGADNNPLLIFPEGTCVNNHYSVMFKKGAFELGCSVCPIAIKYNKIFVDAFW
AcoGPAT9   210 ARKLRDHVQGADNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPIAIKYNKIFVDAFW
BdiGPAT9   213 GRKLRDHVQRPDNNPLLIFPEGTCVNNQYTVMFKKGAFELGCAVCPIAIKYNKIFVDAFW
SmoGPAT9   239 GEKLRKHVIDPESNLLLIFPEGTCVNNEYIVMFKKGAFELDCTVCPVAIKYNKIFVDAFW
PpaGPAT9   234 AQKLKNHVNDPDANPLLIFPEGTCVNNEYTVMFKKGAFELDCVVCPIAIKYNKIFVDAFW

GraGPAT9A  285 NSRKQSFTMHLLQLMTSWAVVCDVWYLEPQNLRPGETPIEFAERIRDIISVRAGLKKVPW
GraGPAT9B  286 NSRKQSFTMHLLQLMTSWAVVCDVWYLEPQNLRPDETPIEFAERVRDIISVRAGLKKVPW
SpuGPAT9   284 NSRKQSFTTHLLQLMTSWAVVCDVWYLEPQNLRPGETPIEFAERVRGIISDRAGLKKVPW
StuGPAT9   280 NSKKQSFTTHLLQLMTSWAVVCDVWYLEPQNIRPGETPIEFAERVRGIISVRAGLKKVPW
AthGPAT9   285 NSRKQSFTMHLLQLMTSWAVVCEVWYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPW
CsaGPAT9   284 NSRKQSFTMHLLQLMTSWAVVCDVWYLEPQVLKPGETPIEFAERVRDIICARAGLKKVPW
AcoGPAT9   270 NSRQQSFTMHLLRLMTSWAVVCDVWYLEPQNLMRGETSIEFAERVRDIISVRAGLKKVPW
BdiGPAT9   273 NSKKQSFTMHLGRLMTSWAVVCDVWFLEPQYLREGETSIAFTERVRDMIAARAGLKKVLW
SmoGPAT9   299 NSRKQSFTMHLLRLMTSWAVVCDVWYLEPQTIRPNETPIEFAERVRDMIAKRAGIKKVAW
PpaGPAT9   294 NSKKQSFTMHLVRLMTSWAVVCDVWYLEPQTIKKGETPIEFSERVRDLICTRAGIKKVPW

GraGPAT9A  345 DGYLKYSRPSPKHRERKQQSFAESVLRGLELEEK------------
GraGPAT9B  346 DGYLKYSRPSPKHREQKQQSFAESVLR--RLEEN------------
SpuGPAT9   344 DGYLKYSRPSPKHRERKQQSFAESVLR--SLEEK------------
StuGPAT9   340 DGYLKYSRPSPKHRERKQQSFAESVLR--RLEEK------------
AthGPAT9   345 DGYLKYSRPSPKHSERKQQSFAESILA--RLEEK------------
CsaGPAT9   344 DGYLKHSRPSPKYRERKQQSFAESVLQ--LLDNK------------
AcoGPAT9   330 DGYLKYSRPSPKLTEHKQQIFAESVLQ--RLEEK------------
BdiGPAT9   333 DGYLKHNRPSPKHTEEKQRIFAESVLK--RLEES------------
SmoGPAT9   359 DGYLKYYRPSSKLTEKMQQKFAESMLR--RLRTKTSDEDLSTPMEG
PpaGPAT9   354 DGYLKYHRPSPKLTEKKQQNFSEAVIR--RLNATAQNQ--------
```

Supplementary Figure S3. Sequence Alignment and Identity/Similarity Shading of Various Plant LPEAT1 Proteins.
Phylogenetic tree depiction of this alignment makes up part of Figure 1 in the main body of the text.



```
TcLPEAT1    1 -MESELKDLNSKPAKTTQKPDPTH---DDGSTKDDRPLLKSD--------SSSADT-NIQ
VvLPEAT1    1 -MESELKDLD---------PRSNS---QDVSSKDDRPLLKSD--------STVVSQDNLQ
GmLPEAT1    1 -MESELKDLNSKPPN-----GNGN------SVRDDRPLLKPE---------PPVSADSIA
PpLPEAT1    1 -MESELKDLNSKPAKPVADDGSGEPAHDDASGKDDRPLLKPDL-------APQVSTEELQ
CcLPEAT1    1 -MESELKDLNSKQLKSTASSDDGG------SAKDDRPLLKPD------------AAENIQ
PtLPEAT1    1 -MDTELKSMNPDPPKPE-QPDPASR-DDGSNSKDDRPLLKSDSN-----RISSTTGESIE
RcLPEAT1    1 -MDTELKDINPEPSKSKPEPEPAP--DDGS-SKDDRPLLKSDSN-----RMST---ENIE
StLPEAT1    1 -MESELQKLPQPETTRPSQPESID----EGSTKDDRPLLKPDPTNPQLQVQSQSSSPSIE
AtLPEAT1    1 -MESELKDLNSNSNPP--------------SSKEDRPLLKSE----------SDLAAAIE
OsLPEAT1    1 MALPLHDATTSPSDPDDLGGGGEEEE----ERLASKPLLSSPST-YPSAGTEEGVEE--L
SiLPEAT1    1 -MAPNDAATTAPSEPESVGG-RMSSE----DTVATRPLLSSPST-SPSAASTAPVQESIE
ZmLPEAT1    1 -MALDTADADAP---------RLRLD----ASAAVHPLLSDDGS-TAAGETAE-------

TcLPEAT1   48 ELEKKFAAYVRNDVYGTMGRGKLPLKEKLLLGIALVTLLPVRIVLGMTILVFYYLICRVC
VvLPEAT1   40 ELEKKFAAYVRSDAYGPMGCGELPLKEKLLLAFALVTLVPIRLVVAFTILVVYYLICRVC
GmLPEAT1   40 DMEKKFAAYVRRDVYGTMGRGELPTKEKLLLGFALVTLLPIRVVLAVTILLFYYLICRVC
PpLPEAT1   53 ELEKKCAAYVRRDAYGTMGRGELTVKEKVLLGLALVTLVPIRVVLAMTILVIYYLICRIC
CcLPEAT1   42 ELEKKFAPYVRNDVYGTMGRGELPLAEKFLIGIAMVTLLPIRVVLAMTVLVIYYLICRVC
PtLPEAT1   53 ELEKKFAAYVRNDVYGPMGRGELPLVEKVLLGIAVVTLVPIRFVLALIILVVYYIICRVC
RcLPEAT1   49 ELEKKFAAYVRNDVYGPMGRAELPLAEKLLLGIALVTLVPIRTLLAITVLLVYYAICRIC
StLPEAT1   56 ELEKKYAPYVRHDVYGIMGRGELPWTEKVLLGIALVTLVPMRVIGATTVLVVYYLICKIC
AtLPEAT1   36 ELDKKFAPYARTDLYGTMGLGPFPMTENIKLAVALVTLVPLRFLLSMSILLLYYLICRVF
OsLPEAT1   54 ELDRRYAPYARRDAYGAMGRGPLGAAGAGRLAVGAAVLFPLRLAAGVLVLVAYYLVCRVC
SiLPEAT1   54 ELDRRYAPYARRDAYGPMGLGPVGAAEAFRLAFAAVVLIPLRVVAGMLVLVVYYLVCRVC
ZmLPEAT1   39 QLDARYAPYARRDAYGTMGRGPLPAAQAVRLALAAAVLLPLRFVAGMLVLLLYYLVCRAC

TcLPEAT1  108 TLFLAPNRE--DE--------QEDYAHMGGWRRAVIVRSGRLFSRVMLFLVGFYWINETH
VvLPEAT1  100 TLFSAPNREGEDE--------QEDYAHMGGWRRAVIVQCGRFLSRALLFTLGFYWINVTY
GmLPEAT1  100 TLFSAPT--GEEE--------QEDYAHMSGWRRTIIVSCGRALSRLMLFIFGFYWIPESN
PpLPEAT1  113 TLFSVPN--RDEE--------QEDYAHMGGWRRAVIVQCGRSLSRLMLFVLGFYWINETY
CcLPEAT1  102 TLFSAPNR-GEDE--------QEDYAHMGGWRRSVIVVSGRFLSRVMLSVLGFYWITETF
PtLPEAT1  113 TLFSAPNRDEEEE--------QEDFAHMGGWRRAVIVWCGRFLSRMLLFVLGFYWISVSY
RcLPEAT1  109 TLFSAPNRDEEEE--------QEDFAHMGGWRRAVIVWCGRFLSRVMLFVFGFYWIKETY
StLPEAT1  116 TAFWAPNR--EDE--------QEDYAHTGGWRRTVMMQSGMFLSRVMLFVFGFYWIHETY
AtLPEAT1   96 TLFSAPYRGPEEEEDEGGVVFQEDYAHMEGWKRTVIVRSGRFLSRVLLFVFGFYWIHESC
OsLPEAT1  114 TLRVEEEEREGGGGGAAGEVEGDGYARLEGWRREGVVRCGRALARAMLFVFGFYWIREYD
SiLPEAT1  114 TLRVEEE-REGG--------EGDGYARLEGWRREGVVWCGRALARAMLFVFGFYWIREYD
ZmLPEAT1   99 TLFVDAD---------------GGRPRLAGWRRKAVLRSGCALSRVMLFVFGFYWIRETR

TcLPEAT1  158 R---------DSANTQENSKTEGINQSEEQERPGAIVSNHVSYLDILYHMSSSFPSFVAK
VvLPEAT1  152 R---------DPLTTED----EGKDEDEEPERPGAIISNHVSYLDILYHMSSSFPSFVAK
GmLPEAT1  150 ----------SASQED-----KSRQPEE-LRRPGVIISNHVSYLDILYHMSSSFPSFVAK
PpLPEAT1  163 RIP-------SDAQPNPTTDCKDEGEEEGTERPGAIISNHVSYLDILYHMSSSFPSFVAK
CcLPEAT1  153 RILDVQEKSENEAKNQSKDEDEAKDQDEESGRPGAIISNHVSYLDILYHMSSSFPSFVAK
PtLPEAT1  165 R------DIELPDQNKSSSQNEGKDQSEEPERLGAIISNHVSYLDILYHMSASFPSFVAK
RcLPEAT1  161 R------ILEPP-------QDEGKDQSEDPERPGAIISNHVSYLDILYHMSSSFPSFVAK
StLPEAT1  166 QP--------INLNGNSNNEDGSKLQAEELERPGAIVSNHISYLDILYHKSSSFPSFVAK
AtLPEAT1  156 PDRD-SDMDSNPKTTSTEINQKGEAATEEPERPGAIVSNHVSYLDILYHMSASFPSFVAK
OsLPEAT1  174 C-------------RFPDAEDEHQEQSKELGRPGAVVSNHVSYVDILYHMSSSFPSFVAK
SiLPEAT1  165 C-------------RFPDAEVEHVDQSKEMERPGAIVSNHVSYVDILYHMSAFFPSFVAK
ZmLPEAT1  144 R-------------RSTNAKGLNQDQFEESQRPGAIVSNHVSYVDILYHMSASFPSFVAK
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TcLPEAT1   209 RSVAKIPLVGLISKCLGCVYVQRESKSSDFKGVAGVVTERVCEAHQNESAPMMMLFPEGT
VvLPEAT1   199 RSVAKLPLIGLISKCLGCVYVQRESKSSDFKGVAGVVTERVCEAHQNKFAPMMMLFPEGT
GmLPEAT1   194 RSVAKLPLVGLISKCLGCVYVQRESRSSDFKGVSAVVTDRIREAHQNESAPLMMLFPEGT
PpLPEAT1   216 RSVAKLPLVGLISKCLGCVYVQRESKSSDFKGVSGVVTERVKEAHQNNSAPPMMLFPEGT
CcLPEAT1   213 RSVAKLPLVGLISKCLGCVYVQRESKSSDFKGVSGVVTERVREAHRDKSAPMMMLFPEGT
PtLPEAT1   219 RSVAKLPLVGLISKCLGCVYVQRESKSSDFKGVSGIVTERVKESHENSSAPMMMLFPEGT
RcLPEAT1   208 RSVAKLPLVGLISKCLGCVYVQRESKSSDFKGVAGVVTERVREAHQNKSAPIMMLFPEGT
StLPEAT1   218 RSVAKLPLVGLISKCLGCVYVQRESKSPDFKGVSGVVNERIREAHQNKSAPIMLLFPEGT
AtLPEAT1   215 RSVGKLPLVGLISKCLGCVYVQREAKSPDFKGVSGTVNERVREAHSNKSAPTIMLFPEGT
OsLPEAT1   221 RSVARLPMVGLISKCLGCIFVQRESKTSDFKGVSGAVTERIQRAHQQKNSPMMLLFPEGT
SiLPEAT1   212 RSVARLPLVGLISKCLGCIFVQRESKTSDFKGVSGAVTERIQRAHQQKNAPMMLLFPEGT
ZmLPEAT1   191 ESVSRLPLIGLISNCLGCIFVQRESKSSEAKGVSGAVTERIQDVCQDKNTPMMLLFPEGT

TcLPEAT1   269 TTNGDFLLPFKTGAFLARAPVVPVILRYPYQRFSVAWDSISGLRHVVFLLCQFVNRMEVT
VvLPEAT1   259 TTNGGFLLPFKTGAFLAKAPVLPVILRYPYQRFSPAWDSISGVRHVIFLFCQFVNHIEVT
GmLPEAT1   254 TTNGEFLLPFKTGGFLAKAPVLPVILQYHYQRFSPAWDSISGVRHVIFLLCQFVNYMEVI
PpLPEAT1   276 TTNGDFLLPFKTGAFLAKAPVLPVILRYPYERFSPAWDSISGVRHVIFLFCQFVNHIEVT
CcLPEAT1   273 TTNGDYLLPFKTGAFLARAPVLPVILRYPYQRFSPAWDSISGARHVFFLLCQFVNHIEVT
PtLPEAT1   279 TTNGDFLLPFKTGAFLATAPVRPVILRYPYQRFSPAWDSISGALHVFYLFCQFINHMEAV
RcLPEAT1   268 TTNGDFLLPFKTGAFLAGAPVLPVILRYPYQRFSPAWDSISGVRHVIFLLCQFVNCIEVT
StLPEAT1   278 TTNGDFLLPFKSGAFLSGAPVQPVILRYPYQRLSPAWDSISGARHVILLLCQFVNYLEAT
AtLPEAT1   275 TTNGDYLLTFKTGAFLAGTPVLPVILKYPYERFSVAWDTISGARHILFLLCQVVNHLEVI
OsLPEAT1   281 TTNGDYLLPFKTGAFLAKAPVKPVILRYPYKRFSPAWDSMSGARHVFLLLCQFVNNLEVI
SiLPEAT1   272 TTNGDYLLPFKTGAFLAKAPVQPVILRYPYKRFNPAWESMSGARHVFLLLCQFVNYVEVT
ZmLPEAT1   251 TTNGDYLLPFKTGAFLAGAPVQPVILKYPYRRFSPAWDSMDGARHVFLLLCQFVNHMEVV

TcLPEAT1   329 WLPVYYPSQQEKDDQKLYANNVRRLMANEGNLILSDIGLAEKRTYHAALNG------LFC
VvLPEAT1   319 RLPVYIPSQQEKDDPKLYANNVRKLMASEGNLIMSDIGLAEKRIYHAALNG------LFC
GmLPEAT1   314 RLPVYHPSQQEMDDPKLYANNVRRLMATEGNLILSDIGLAEKRIYHAALNGNNSLPSVLH
PpLPEAT1   336 RLPVYYPSQQEKDDPKLYATNVRRLMASEGKMTQSDIGLAEKRVYHAALNGNNSRPSVLH
CcLPEAT1   333 SLPVYHPSQQEKDDPKLYAENVRRLMASERNLTVSDIGLAEKRIYHAALNGNNSLPSVLH
PtLPEAT1   339 WLPVYYPSQEEKDDPKLYASNVRRLMAREGNLKMSDIGLAEKRIYHTALNGNISLPSVLH
RcLPEAT1   328 RLPVYYPSQEEKDDPKLYANNVRRLMAHEGNLLMSDIGLAEKRVYHAALNGLF-------
StLPEAT1   338 WLPVYYPSQQEKDDPRLYAENVRRLMAHEGNLLLSDIGLAEKRVYHAALNG------LFC
AtLPEAT1   335 RLPVYYPSQEEKDDPKLYASNVRKLMATEGNLILSELGLSDKRIYHATLNGNLSQTRDFH
OsLPEAT1   341 HLPVYYPSEQEKEDPKLYANNVRKLMAVEGNLILSDLGLAEKRVYHAALNGNNSLPRALH
SiLPEAT1   332 HLPVYYPSEQEKDDPKLYANNVRKLMAVEGNLILSDLGLAEKRVYHAALNGN-SLPRALH
ZmLPEAT1   311 RLPVYYPSQLEKEDPKLYANNVRKLIAMEGNLVLSNIGLAEKRVYHAALTGS-SLPGARH

TcLPEAT1   383 QS--
VvLPEAT1   373 QR--
GmLPEAT1   374 QKDE
PpLPEAT1   396 QKDD
CcLPEAT1   393 QKDD
PtLPEAT1   399 QKDD
RcLPEAT1       ----
StLPEAT1   392 QQ--
AtLPEAT1   395 QKEE
OsLPEAT1   401 QKDD
SiLPEAT1   391 QKDD
ZmLPEAT1   370 EKDD
```

Supplementary Figure S4. Sequence Alignment and Identity/Similarity Shading of Various Plant LPEAT2 Proteins. Phylogenetic tree depiction of this alignment makes up part of Figure 1 in the main body of the text.

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PpLPEAT2     1 MADN------DLASPLISSPPSDHP------------HLILTVQDDTDTD-HNNHNGNHG
VvLPEAT2     1 MAGTG----ADLITPLISSQPSDQP------------ELILTVDDRPGFESFSDHCSSNG
PtLPEAT2     1 MAN------HDLESPLLSSQPSDPP------------HIILNVHDSDS-------SIQQS
RcLPEAT2     1 MTD------DSLSSPLLQPQPSDHP------------PVILSIRDNHN-------HYYHR
CcLPEAT2     1 MADHHRDHDHDLSSPLLQSPRSDHS------------PVIISIEADGNDTVSDPATQDQL
TcLPEAT2     1 MAE------HDLTSPLLSPRSSDQP------------QTVLIVSDDEDSEPSDRPPSNQQ
AtLPEAT2     1 MADP------DLSSPLIHHQSSDQP------------EVVISIADDDDDESGLNLLPAVV
GmLPEAT2     1 MADD-----SDLTSPLLSSSSSSSSD-----------HVVVTVHPSAAP-----------
StLPEAT2     1 MSDH------SIFAPLLPSDHLPHKSNGDDQEHAPEPHVILTVEDDGVQH-----QLSNG
SiLPEAT2     1 MASTSPSP-ASLFTPLLSGSVAPAR----------------AANGHANNHR--HHGDSDG
ZmLPEAT2     1 MASTCLAP-ASLSTPLLSDSIARAP----------------AANGHATNHRHHHHDDSDG
OsLPEAT2     1 MASRNPSP-ASLSTPLLSDSISPTP----------------TTNGHAGHHN--HHDDDEE

PpLPEAT2    42 S-----------------NSTHHHFR--NPYAFLGSDG-----FTVPGSTTADPFRNHTL
VvLPEAT2    45 T-----------------KSDHTQPESDNPFEFLGSAG-----FSVPGTPTVDPFRNNTP
PtLPEAT2    36 N----------------NHKPNPNTSSRNPFEFIGSDG-----LSVPAPSTLDPFRNDTP
RcLPEAT2    36 H----------------NSNSSSHN-LRNPFEFLGSDF-----LSVPPPSTVDPFRNNTP
CcLPEAT2    49 N----------------NHDTRYHNNPGNPYWFIGSDG-----LSVPGPNTANPFLNDTP
TcLPEAT2    43 SSLQTGIPRQNHNQSYGNGNGNSQVSSRNPYEFLGSDG-----FSVPAPTTIDPFRNGTP
AtLPEAT2    43 DP---------------RVSRGFEFDHLNPYGFLSESE-----PPVLGPTTVDPFRNNTP
GmLPEAT2    34 --------------------------PRNPFRVLGTDDDDDDDLSVPPPSTLDPFRNRTP
StLPEAT2    50 D----------------HLGTHISEVDDNPYAFLGANR-----FDMPGSTTVDPFRNNTP
SiLPEAT2    42 AA---------------AVSVCDDGGG-DPFAFLSEDRPP----QDRGPSPADPFRNGTP
ZmLPEAT2    44 AA---------------AVSVCDDGGG-DPFAFLSEDRPP----RDRGPSPADPFRNGTP
OsLPEAT2    42 SP---------------TVCGGDGGGGGDPFAFLSEDRPAW--WSPRGVSPADPFRNGTP

PpLPEAT2    78 EIRG-LYEWLKIGICLPIALARLVLFGASLLIGFVATKLALQGWKDK--------KNPMP
VvLPEAT2    83 KIDG-FYEWFKILVCVPIAAIRLVLFGLCLLVGYLATKFALQGWKDK--------QNPMP
PtLPEAT2    75 DIEG-LYELIKIVICLPIAIVRLVLFGVCLATGYVATKIALLGWRDK--------HNPMP
RcLPEAT2    74 KIEG-VYEVLKSLICLPIALARLVLFGACLLVGYLATKLALGGWKDK--------NNPMP
CcLPEAT2    88 HVVG-VYEFVKIVVCFPIVLIRLVLFGFCLLVGYLATKLALEGWKDK--------QNPMP
TcLPEAT2    98 FVSG-VYEVIKILLCLPIALARLVLFGVCLAVGYIATRIALEGWKDK--------QNPMP
AtLPEAT2    83 GVSG-LYEAIKLVICLPIALIRLVLFAASLAVGYLATKLALAGWKDK--------ENPMP
GmLPEAT2    68 AIEG-LYEWAKTVLCLPLAALRLAIFGLCLALGYVATKVALQGWKDK--------ENPMP
StLPEAT2    89 RVEG-VYEWLKIVVCLPITLVRLVLFGLALMIGYVATRTALLGWKDR--------SSPMP
SiLPEAT2    82 AWGGGVYAWARTLLLAPVAAVRLVLFGLAIAIGYAATWVALRGWADVQDRP-REGAGPMP
ZmLPEAT2    84 AWGGGVYAWSRTLLLLPVALVRLALFGLSIAIGYAATWVALRGWADTHGRP-RVGGGPMP
OsLPEAT2    85 GWCG-AYELVRALVCAPVAAARLVLFGLSIAVGYAATWVALRGWVDVRERAAQEGAGPMP

PpLPEAT2   129 KWRCRIMWITRVCTRCILFSFGYHWIRRKGKPAPREIAPIVVSNHVSFIEPIFYFYELFP
VvLPEAT2   134 KWRCRVMWVTRICSRCILFSFGYHWIKRRGRPASRETAPIVVSNHVSYVEPIFFFYELFP
PtLPEAT2   126 KWRSRLMWLTRGCTRCILFSFGYHWIKRKGKLAPREIAPIVVSNHVSYIDPIFYFFEFFP
RcLPEAT2   125 KWRS-----------------SYHWIKRKGNPAPREIAPIVVSNHVSYIEPIFYFYELFP
CcLPEAT2   139 VWRSRLMWVTRVCSRCILFSFGYHWIRRKGKPAPRQIAPIVVSNHISYIEPIFFFYELFP
TcLPEAT2   149 KWRSRIMWVTRVCARFILFSFGYQWIRRKGKPAPRDVAPIVVSNHVSYIEPIFYFYELFP
AtLPEAT2   134 LWRCRIMWITRICTRCILFSFGYQWIRRKGKPARREIAPIVVSNHVSYIEPIFYFYELSP
GmLPEAT2   119 KWRCRVMWITRLCARCILFSFGYQWIKRKGKPAPREIAPIIVSNHVSYIEPIFYFYELFP
StLPEAT2   140 KWRSRLMWVTRMSARTILFSFGYQWIRRKGKPAPREIAPIVVSNHVSYIDPIFFFYELFP
SiLPEAT2   141 AWRRRLMWITRISARCILFSFGYHWIRKKGRPAPRELAPIVVSNHVSYIEPIFFFYELFP
ZmLPEAT2   143 AWRRRLMWITRISARCILFSFGYHWIRKKGRPARRELAPIVVSNHISYIEPIFFFYELFP
OsLPEAT2   144 AWRRRLMWITRISARCILFSFGYHWIRRKGKPAPRELAPIVVSNHVSYIEPIYFFYELFP
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PpLPEAT2  189 TIVASESHDSLPLVGTIIRAMQVIYVNRFSASSRKHAVSEIKRKASCDRFPRVLLFPEGT
VvLPEAT2  194 TIVASESHDSLPFVGTIIRAMQVIYVNRFSQSSRKQAVNEIKKKASCERYPRVLLFPEGT
PtLPEAT2  186 TIVAAESHDSMPFVGTIIRAMQVIYVNRFSPSSRKLAVNEIKRKASCGRFPRVLLFPEGT
RcLPEAT2  168 TIVAAESHDSIPFVGTIIRAMQVIYVNRFSQSSRKLAVNEIKRKASCDRFPRVLLFPEGT
CcLPEAT2  199 TIVASESHDSIPFVGTIIRAMQVIYVDRFSQSSRKNAVSEIKRKASCDRFPRVLLFPEGT
TcLPEAT2  209 TIVASESHDSIPFVGTIIRAMQVIYVNRFSQASRKNAVNEIKRRASCDTFPRLLLFPEGT
AtLPEAT2  194 TIVASESHDSLPFVGTIIRAMQVIYVNRFSQTSRKNAVHEIKRKASCDRFPRLLLFPEGT
GmLPEAT2  179 TIVAAESHDSIPFVGTIIRAMQVIYVNRFLPSSRKQAVREIKRRASCNRFPRVLLFPEGT
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SiLPEAT2  201 TIVASESHDALPFVGTIIRAMQVIYVDRFSPASRKAAVNEIKRKAACNSFPRVLLFPEGT
ZmLPEAT2  203 TIVSSESHDALPFVGTIIRAMQVIYVDRFSPASRKAAVNEIKRKAACNSFPRVLLFPEGT
OsLPEAT2  204 TIVSSDSHDSIPFVGTIIRAMQVIYVDRFSPASRKSAVNEIKRKAACNSFPRVLLFPEGT

PpLPEAT2  249 TTNGRFLISFELGAFIPGFPIQPVTVRYPHVHFDQSWGHISLAKLMFRMFTQFHNFMEVE
VvLPEAT2  254 TTNGRVIISFQLGAFIPGYPIQPVVVRYPHIHFDQSWGHISLGRLMFRMFTQFHNFMEVE
PtLPEAT2  246 TTNGKVLISFQLGAFIPGYAVQPVIVRYPHVHFDQSWGNVSLGMLMFRMFTQFHNFMEVE
RcLPEAT2  228 TTNGKVVISFQLGAFIPGYAIQPVIVRYPHVHFDQSWGYISLAKLMFRMFTQFHNFMEVE
CcLPEAT2  259 TTNGKFLISFQLGAFIPAYPIQPVIVRYPHVHFDQSWGDVSLGKLMFRMFTQFHNFMEVE
TcLPEAT2  269 TTNGKVLISFQLGAFIPGHPIQPVVVRYPHVHFDQSWGLISLAKLMLRMFTQFHNFMEVE
AtLPEAT2  254 TTNGKVLISFQLGAFIPGYPIQPVVVRYPHVHFDQSWGNISLLTLMFRMFTQFHNFMEVE
GmLPEAT2  239 TTNGRNLISFQLGAFIPGYPIQPVIVRYPHVHFDQSWGHVSLGKLMFRMFTQFHNFFEVE
StLPEAT2  260 TTNGRSIISFQLGAFIPGYPIQPVIVRYPHVHFDQSWGNVSLAMLMFRMFTQFHNFMEVE
SiLPEAT2  261 TTNGRFLISFQHGAFIPGYPVQPVVVRYPHVHFDQSWGNISLLKLMFKMFTQFHNFMEVE
ZmLPEAT2  263 TTNGRFLISFQHGAFIPGYPVQPVVVRYPHVHFDQSWGNISLLKLMFKMFTQFHNFMEVE
OsLPEAT2  264 TTNGRFLISFQHGAFIPGYPVQPVIVRYPHVHFDQSWGNISLGKLMFKMFTQFHNFMEVE

PpLPEAT2  309 YLPVVSPLDNKKESAVRFSERTCHAMATSLNVVQTSHSYGDLMLLMKATQSKSKLERPAS
VvLPEAT2  314 YLPVISPLENKKENAVHFAKRTSHAIATALNVVQTSHSYGDLMLLTRASQSKQ--EKPSS
PtLPEAT2  306 YLPIVSPLDNCKENPSHFAKRTSHAIASALNVVQTNHSYGDLMLLMKASELKQ--EKPSS
RcLPEAT2  288 YLPIVSPLDNCKENPVHFAKRTSHSIASALNVVQTFHSYGDLMLLMKASHSKQ--EKPSS
CcLPEAT2  319 YLPVVFPSDNQKENALRFAERTSHAMASALNAVQTSHAYGDLMLLMKASELKE--ENASS
TcLPEAT2  329 YLPTIMPPDHQKQNAVHFAERTGQAMASALNVVQTSHSYGDLMLLMKAAQLQK--EKPWS
AtLPEAT2  314 YLPVIYPSEKQKQNAVRLSQKTSHAIATSLNVVQTSHSFADLMLLNKATELKL--ENPSN
GmLPEAT2  299 YLPVIYPLDD-KETAVHFRERTSRDIATALNAVQTGHSYGDIMLHMKAQEAKQ--ENPSS
StLPEAT2  320 YLPVITPHENRKESAVRLSQRTGHAVASALNVVQTSHSYGDVLLLAKALEANQ--ENPSL
SiLPEAT2  321 YLPVVYPPEIKQENALHFAENTNYAMARALNVLPTSYSYGDSMIMARAVEAGK--ANCSN
ZmLPEAT2  323 YLPVVYPPEIKQENALHFAEDTSYAMARALNVLPTSYSYGDSMIMARAIEAGK--VNGSN
OsLPEAT2  324 YLPVVYPPEIKQENALHFAENTSYAMAHALNVIPTSYSYGDSMIMARAVEDGK--VNCSN

PpLPEAT2  369 YMVEMATVKSLLHISSMEAVDFLDKFLSMNPDPRGHVNYSGFLRVLRLKACTFSEEIFAF
VvLPEAT2  372 YMVEMARVESSFHLSTLEAVDFLDTFLSMNPDPSGCVKIHDFFRVLRLKPCYLSEKIFGF
PtLPEAT2  364 YMVEMAKVESLFHINSLEAVNFLDKFLSMNPDASGRVKFNDFLRAFRLRTCTLSEELFGF
RcLPEAT2  346 YMVEMAKVESLYHISSLEAVDFLDKFLSMNPDPSGRVKFHDFLRAMRLRTCSLLEEIFGF
CcLPEAT2  377 YMVEMARVGSIFHISSLEAVNFLEKFLSMNPDPSGCVKLLDFLSVLRLKTCPLSDEIFGF
TcLPEAT2  387 YMVEMARIESLYHISSLEAVDFLDKFLSMNPDTSGCVKLHDFLRVLRLKACTLSEEIFGF
AtLPEAT2  372 YMVEMARVESLFHVSSLEATRFLDTFVSMIPDSSGRVRLHDFLRGLKLKPCPLSKRIFEF
GmLPEAT2  356 FMVEMTKVESLFHISSMEAVDFLDKFLAMNPDSSGRVQYHDFLRVLRLKACPLSAKIFSF
StLPEAT2  378 YLVEMAGVEAEFHLSSLEAVDFLDVFLSMNPDSRGQVEIHHFLKVLRLKPSTLSEKIFGF
SiLPEAT2  379 YMVEMAWVKDMYGVSTAEAMELLEHFLAMNPDSDGRVKAQDFWAYFGLDCSPLCKKIFHY
ZmLPEAT2  381 YMVEMAWVKDIYGVSTAEAMDLLEHFLAMNPDNDGRVKAQDFWAHFGLDCSPLCKKIFHY
OsLPEAT2  382 YMVEMAWVKETYGVSTSEAMALLEDFLCMSPDKDGRVNAQDFWAHFGLNCTPLCKKIFQY

PpLPEAT2  429 IDVEKSGSITFKQFLFGSVHVLKQPLFRRACELVFSEYVSGENDYISEQEFGESVRPAIP
VvLPEAT2  432 IDVDKSGRVTFKQFLFGSAHVMKQPLFRQACELAFAECDSDGDLYISEQELGDSIRPVIP
PtLPEAT2  424 LDVEKNGSITFKQFLYGSAHVMKRPLFHQSCELAFAQCDTRGHNQISEQELGETIRHAIP
RcLPEAT2  406 VDVEKIGSITFKQFLYGSAHVMKQPLFRQTCELACTRCSGGEDNLISKEQLGDTIRLAIP
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CcLPEAT2  437 IDVDKNGSITFKQFLYASAHVMKLPLFWQACELAFAECDPDGNGFISENQLEVTIRPAIP
TcLPEAT2  447 LDVEKNGSITFKQFLFGSAHVLKQPLFRQACELAFAECDVEGENYFMEKDLADILRHAIP
AtLPEAT2  432 IDVEKVGSITFKQFLFASGHVLTQPLFKQTCELAFSHCDADGDGYITIQELGEALKNTIP
GmLPEAT2  416 IDVEKSGTITFRQFLYGSAHVMSQPGFHQACEEAFAGCGGAVKAYVVEQELRDFIQPVIL
StLPEAT2  438 IDVQKSGKITFKQFLVGSAHILKQPLFHQACESAFTACDGDGKNYIMEKEFGDSLMLSIP
SiLPEAT2  439 FDFSIKESITFRQFLVGCAHLRKQPLFQGACETAFEKCRDPETSEISRGQLADILRLSML
ZmLPEAT2  441 FDLGIKESITFRQFLVGCAHLRKQPLFQGACETAFEKCRDPETSEISRAQLADVLRLSML
OsLPEAT2  442 FDFEAKESITFRQFLIGCAHLRKQPSFQDACETAFERCRNPLTSHIGREQLADVLRSSML

PpLPEAT2  489 DLNED-EVHELFNLFDADGDGRISKDEFWTCLKRNPLLIALFSPCLLNKDISQDGNRLEE
VvLPEAT2  492 DLNED-EIQEMFNLFDTDKDGRVSKDDFSNCLRRHPLLIALFSPSLLHNA----------
PtLPEAT2  484 DFDED-EIHELFSIFDMDGDGSVSKDNFLYCLRQNPLLIALFKPCLVHKDSSQVGQGILE
RcLPEAT2  466 DLDDA-EIHELFKLFGGNDDGRASKETFMCCLKKNPLLIALFWPCLVYKDSLECGGRMLE
CcLPEAT2  497 DLNKY-EIDSLFRLFDSDGDGRVSRDDFICCLRKNPLLIAIFSPTLLHTDLSEARNRMPG
TcLPEAT2  507 ELNED-EIHGLFNLFDTDKDGRISRDDFFSCLRKNPLLISLFSPRLLHRDTSKAGDRMLE
AtLPEAT2  492 NLNKD-EIRGMYHLLDDDQDQRISQNDLLSCLRRNPLLIAIFAPDLAPT-----------
GmLPEAT2  476 NWSED-EVHELFMVFDNDNDGRIDKNDFLSCLRKTPLLIAFFTLQLQQKEFE--GNGVIE
StLPEAT2  498 GLSNN-EIRGLFTLFDIDRDGKMSKDDFIGCLRRYPLLIALFSPCVLQQICP--------
SiLPEAT2  499 LPSDD-GMQKLFKTFDVDGDEKISRDDFITCLGRFPFLIAFFAAPINGEVYIEIV-----
ZmLPEAT2  501 LPSGD-RMLDLFKTFDIDGDEKISKDDFMTCLGRFPFLIAFFAAPINGEVYIEIV-----
OsLPEAT2  502 ELMTDNGMMKLFKTLDVDDDDGISKDDLMASLRKLPFMIALFARRINGEVYIEIV-----

PpLPEAT2  548 IV-
VvLPEAT2      ---
PtLPEAT2  543 EIV
RcLPEAT2  525 ELV
CcLPEAT2  556 DVI
TcLPEAT2  566 EIV
AtLPEAT2      ---
GmLPEAT2  533 IV-
StLPEAT2      ---
SiLPEAT2      ---
ZmLPEAT2      ---
OsLPEAT2      ---
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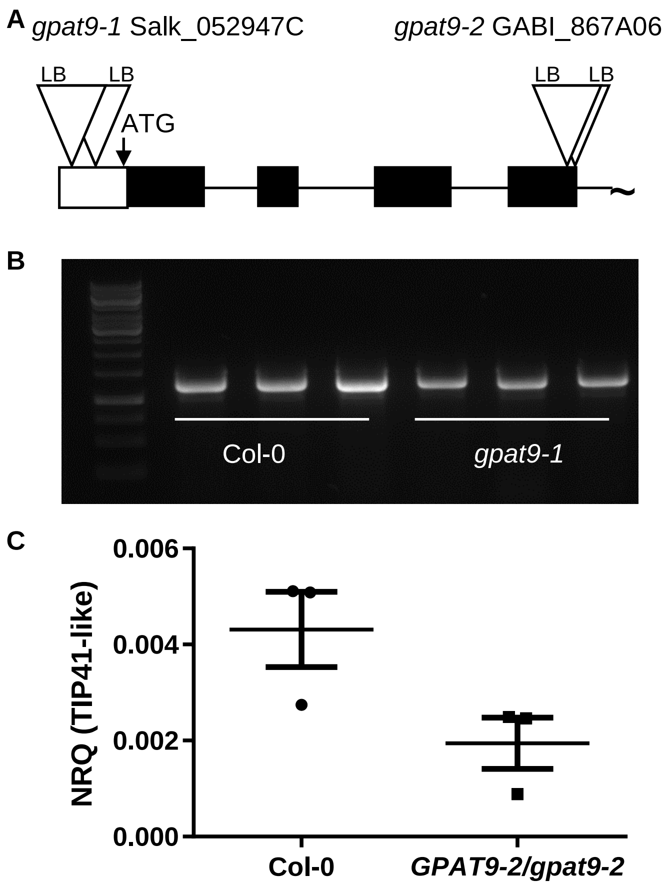


Supplemental Figure S5. Characterization of *GPAT9* T-DNA Insertions

(A) Representation of *GPAT9* T-DNA insertion locations. For both lines T-DNA left border primers will generate amplicons with gene specific primers flanking either side of the insertion suggesting there are multiple insertions with inverse orientation. The *gpat9-1* insertions are 46 bp upstream of the coding sequence. The *gpat9-2* insertion is at the end of the 4th exon. Pictured is just the first four exons out of 12 in *AtGPAT9.*

(B) RT-PCR of full length *GPAT9* coding sequence from leaves of homozygous *gpat9-1*.

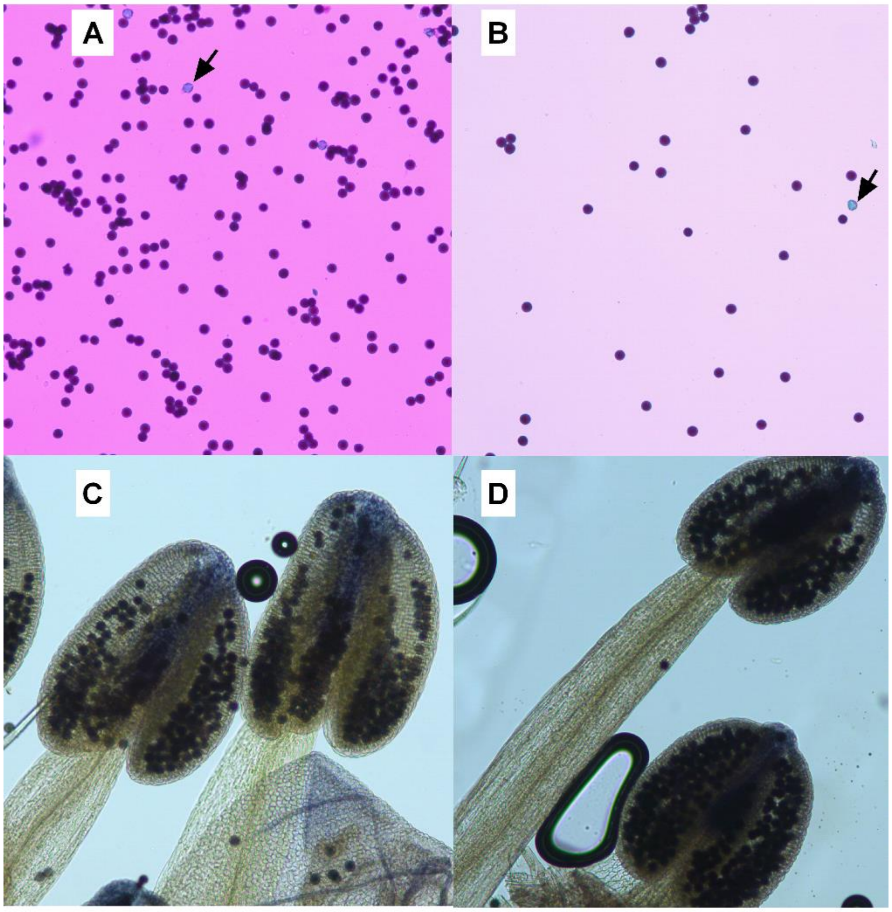
(C) qPCR results for *GPAT9* wild-type (Col-0) and *GPAT9/gpat9-2* leaves.

Methods:

(A) For insertion site sequencing the left border-gene junction was amplified by PCR with GoTaq® Flexi (Promega), gel purified by QIAquick Gel Extraction Kit (QIAGEN) and sequenced from both the left border primer and a flanking gene-specific primer by Eurofins (http://www.eurofinsgenomics.com/).

(B-C) Leaf RNA extraction with RNeasy Plant Mini Kit (QIAGEN) and treated with RNase-free DNase (Qiagen) and on-column DNase digestion. RNA was quantified using a Nanophotometer (Implen Inc). cDNA was synthesized using SuperScript III First-Strand Synthesis System for RT-PCR (Life Technologies). RT-PCR utilized standard conditions as per GoTaq® Flexi (Promega) protocol with 30 cycles of amplification. For qPCR transcript levels were analyzed by quantitative PCR (qPCR) using Platinum SYBR Green qPCR SuperMix-UDG (Life Technologies) and the Stratagene Mx3005P Quantitative PCR system (Agilent Technologies Inc). Transcript was normalized to the *TIP41-like* gene (Czechowski et al., 2005).

(A-C), the sequences for primers utilized are shown in supplemental table S1.



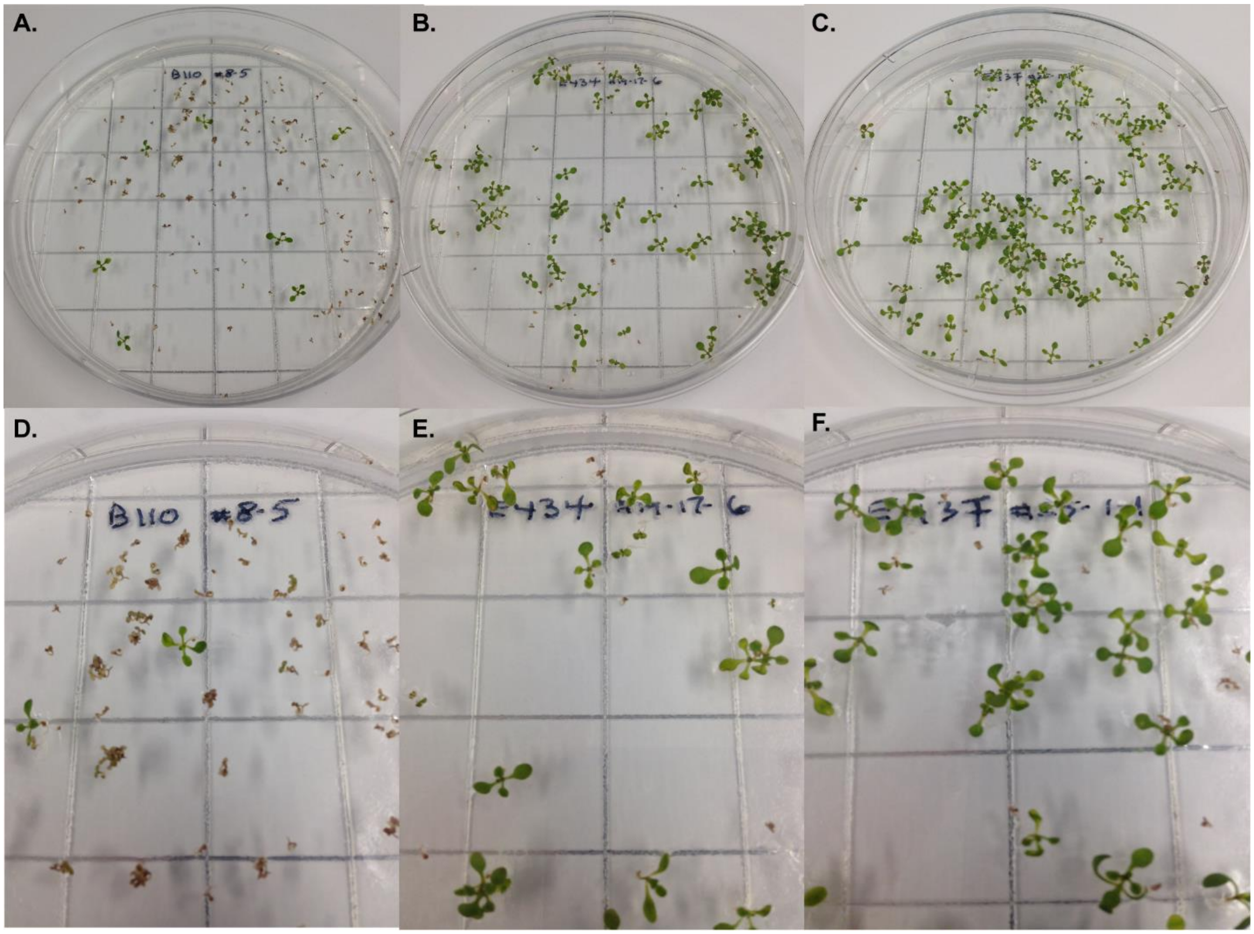
Supplemental Figure S6. Analysis Of Viability in Wild-Type and *GPAT9-2/gpat9-2* Pollen.

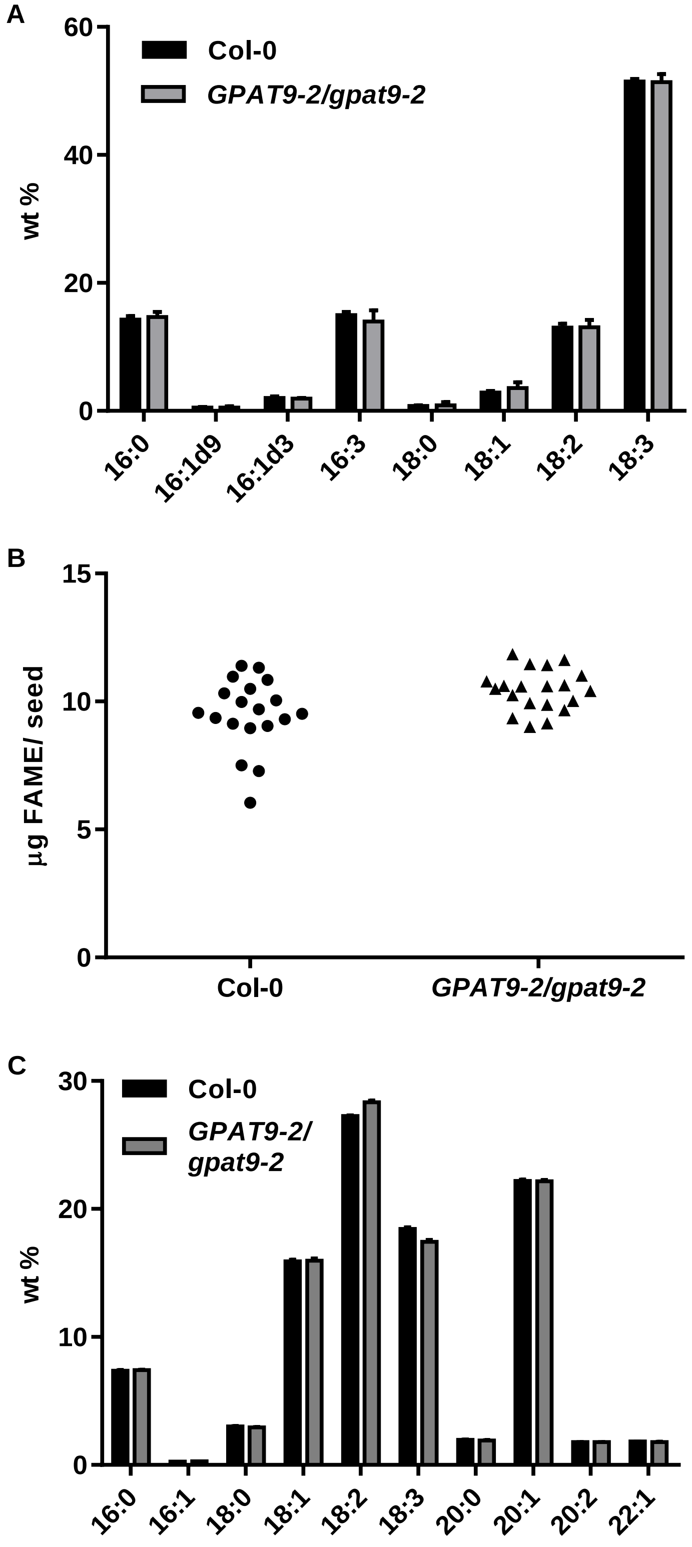
(A-B) Alexander staining (Peterson et al., 2010) for pollen abortion. Purple = non-aborted pollen, green pollen (black arrows) = aborted pollen. Pollen from wild-type (A), and *GPAT9/gpat9-2* (B) plants.

(C-D) Nitro blue tetrazolium staining for pollen viability (Regan and Moffatt, 1990). Viable pollen stain black. Anthers from wild-type (C), and *GPAT9/gpat9-2* (D) plants.

Supplemental Figure S7. Genetic Complementation of *gpat9-2* Mutants with Transgenic Plant *GPAT9*.

Hemizygous *gpat9-2* plants were transformed with different binary vectors, with or without functional full-length plant ORFs driven by the *AtGPAT9* promoter. T4 generation seeds from DsRed-fluorescent and sulfadiazine-resistant representative lines from: negative control B110 (A, D); AtGPAT9prom::AtGPAT9 (pE434, B, E); or AtGPAT9prom::VfGPAT9 (pE437, C, F) were sown on solid agar media containing sulfadiazine. Wide-angle views of the agar plates are shown in the top panels, close views of the same plates are shown in the bottom panels. Note the high proportion of stunted and aborted seedlings on the negative control plate compared to the high number of healthy, complemented seedlings established on both the E434 and E437 plates.





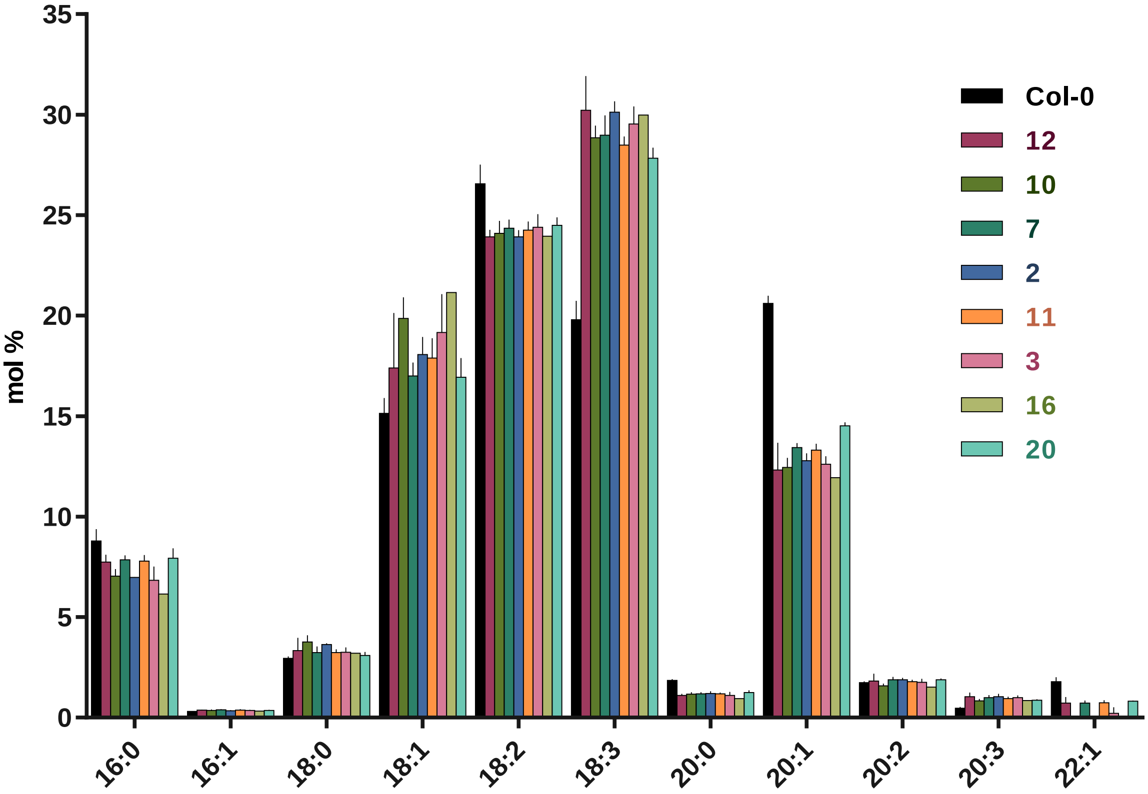
Supplemental Figure S8. Lipid Characterization of Wild-Type and *GPAT9-2/gpat9-2* Plants.

(A) The relative fatty acid composition of leaves. Average and standard deviation. *n* = 5 for wild-type (Col-0), and 13 for *GPAT9-2/gpat9-2*.

(B) Total seed fatty acid content from seeds of plants grown at the same time under 24 hr light ~150-170 µmol/m^2/sec white light. 30 seeds per FAME analysis from a single plant.
n = 19-20 individual plants per line.

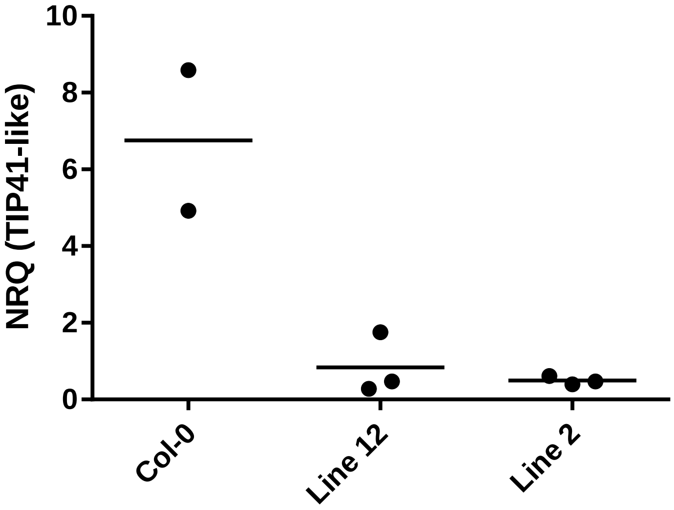
(C) The average fatty acid composition of seeds from part B. Bars are average and standard deviation.

Supplemental Figure S9. Seed Fatty Acid Composition of *GPAT9* amiRNA Knockdown Lines. Fatty acid compositions are from seed samples analyzed for total oil content in Figure 5A of the main text. Average ± S.D.

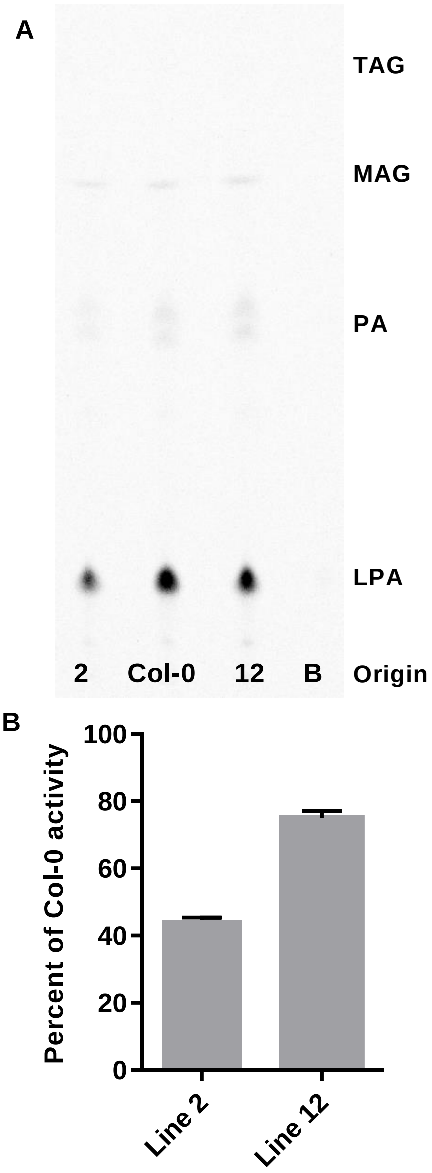


Supplemental Figure S10. Expression of *GPAT9* in Developing Seeds of Wild-Type and *GPAT9* amiRNA Knockdown Lines.

GPAT9 transcript was normalized to *TIP41-like* (Czechowski et al., 2005).Two biological replicates for Col-0, and three biological replicates for each amiRNA knockdown line. Each biological replicate is the average of three technical replicates.



Methods:
Frozen developing seeds (9-11 DAF) were separated from silique tissue by silique popping method (Bates et al., 2013). ~50 µL volume of frozen seeds per biological replicates were mechanically pulverized to a fine powder with steel beads (TissueLyser LT, QIAGEN), RNA was extracted and used for cDNA synthesis using SuperScript III First-Strand Synthesis System for RT-PCR (Life Technologies). RT-PCR utilized standard conditions as per Maxima SYBR Green/ROX qPCR Master Mix (Thermo) and BioRad CFX96™ Real-Time System and C1000™ Thermal Cycler with 45 cycles of amplification. The sequences for primers utilized are shown in supplemental table S1.



Supplemental Figure S11. Developing Seed Microsome GPAT Assays of Wild-Type and amiRNA Knockdown Lines.

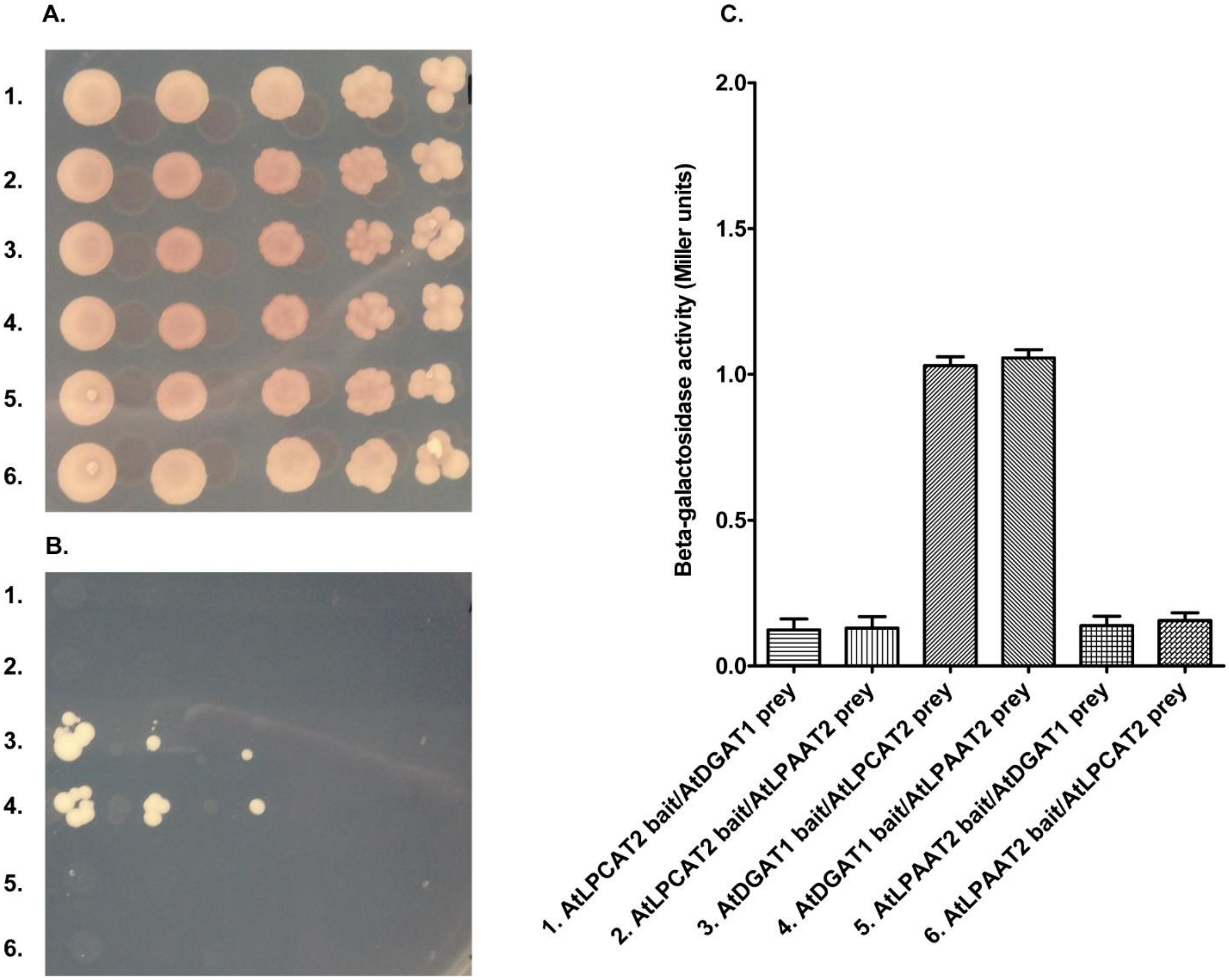
GPAT assays with developing 9-11 DAF seed microsomes utilizing 3.55 nmol [^{14}C]glycerol 3-phosphate and 25 nmol palmitoyl-CoA, for 15 min at 24°C.

(A) Phosphor image of TLC plate indicating that [^{14}C]LPA was the major product of developing seed microsome activity with palmitoyl-CoA.

(B) Percent of wild-type (Col-0) GPAT activity in *GPAT9* amiRNA knockdown lines 2 and 12. Mean and S.D. of two replicate assays.

Supplementary Figure S12. Testing of Protein:Protein Interactions Between AtLPAAT2, AtDGAT1, and AtLPCAT2.

Cub-LexA bait fusions and Nub prey fusions were produced as described in Figure 8 and in the main text. (A-B) Prototrophic growth assay of yeast strains containing various combinations of Arabidopsis acyltransferase bait plasmids co-expressed with potential NubG-fusion acyltransferase prey plasmids. Serial dilutions of cells expressing different bait-prey combinations were plated on non-selective (A) or selective (B) media. (C) Quantitative measurement of β-galactosidase activity from cell lysates of the strains used in the serial dilution assays. Cultures used for serial dilutions shown in A. and B. contained bait and prey combinations as numbered in C.



Supplementary Figure S13. Sequence Identity Comparisons Between AtGPAT1 and

AtGPAT9 to the Animalia Subset of the NCBI Protein Database.

The top hits to AtGPAT9 and AtGPAT1 are shown first, followed by the best hits from within the individual species that provided the top hits to the alternate AtGPAT sequence. See text for additional details.

```
>AtGPAT9

MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW
NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKY
HGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDH
VQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEV
WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILARLEEK
```

vs Metazoa/Animalia:

PREDICTED: glycerol-3-phosphate acyltransferase 3 [Orcinus orca]
Sequence ID: ref|XP_004282203.1|Length: 438Number of Matches: 1
Gene-associated gene details
Map Viewer-aligned genomic context
Range 1: 75 to 429GenPeptGraphics Next Match Previous Match First Match

Alignment statistics for match #1

Score	**Expect**	**Method**	**Identities**	**Positives**	**Gaps**	**Frame**
259 bits(661)	2e-82()	Compositional matrix adjust.	139/360(39%)	211/360(58%)	17/360(4%)	

Features:

```
Query  24   DYLPSGSSINEPRGK-LSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW----N  78
            D  P    ++  RG+   L D+   S    EA   IV+D  T+ F S     WN     N
Sbjct  75   DESPMEKGLSGLRGRDFELSDVFYFSKKGLEA---IVEDEVTQRFSSEELVSWNLLTRTN  131

Query  79   I---YLFP----LYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKK  131
            +   Y+ P    ++  GV+VRYC+L PLR  TLAF  I FL +   +   L  +  LR +
Sbjct  132  VNFQYISPKLTMVWVLGVIVRYCVLLPLRV-TLAFVGISFLVIGTTLVGQLP-ESSLRNR  189

Query  132  IERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIMQ  191
            +  ++    C   V + +G + YH  +   +   + VANHTS ID ++L     +A++ Q
Sbjct  190  LSELVHLTCCRICVRALSGTIHYHNKQYRPQKGGICVANHTSPIDVLILTTDGCYAMVGQ  249

Query  192  KHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVNN  251
             H G +G++Q  +++S   +WF RSE KDR +V K+LR+H+      P+LIFPEGTC+NN
Sbjct  250  VHGGLMGIIQRAMVKSCPHVWFERSEMKDRHLVTKRLREHIADKKKLPILIFPEGTCINN  309

Query  252  NYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEVWYL  311
               +MFKKG+FE+  T+ P+AIKYN  F DAFWNS K +   +LL++MTSWA+VC+VWY+
Sbjct  310  TSVMMFKKGSFEIGGTIYPVAIKYNPQFGDAFWNSSKYNMVSYLLRMMTSWAIVCDVWYM  369

Query  312  EPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILA  371
             P T   GE  ++FA RV+  I+++ GL ++PWDG LK ++      E +Q+++++ I+
Sbjct  370  PPMTREEGEDAVQFANRVKSAIAIQGGLTELPWDGGLKRAKVKDTFKEEQQKNYSKMIVG  429
```

```
>AtGPAT1

MVLPELLVILAEWVLYRLLAKSCYRAARKLRGYGFQLKNLLSLSKTQSLHNNSQHHLHNHHQQNHPNQTLQDSLDPL
FPSLTKYQELLLDKNRACSVSSDHYRDTFFCDIDGVLLRQHSSKHFHTFFPYFMLVAFEGGSIIRAILLLLSCSFLW
TLQQETKLRVLSFITFSGLRVKDMDNVSRSVLPKFFLENLNIQVYDIWARTEYSKVVFTSLPQVLVERFLREHLNAD
DVIGTKLQEIKVMGRKFYTGLASGSGFVLKHKSAEDYFFDSKKKPALGIGSSSSPQDHIFISICKEAYFWNEEESMS
KNNALPRERYPKPLIFHDGRLAFLPTPLATLAMFIWLPIGFLLAVFRISVGVFLPYHVANFLASMSGVRITFKTHNL
NNGRPEKGNSGVLYVCNHRTLLDPVFLTTSLGKPLTAVTYSLSKFSEFIAPLKTVSLKRDRKKDGEAMQRLLSKGDL
VVCPEGTTCREPYLLRFSPLFAELTEDIVPVAVDARVSMFYGTTASGLKCLDPIFFLMNPRPVYCLEILKKLPKEMT
CAGGKSSFEVANFIQGELARVLGFECTNLTRRDKYLVLAGNEGIVR
```

vs Metazoa/Animalia:

PREDICTED: ancient ubiquitous protein 1-like isoform X1 [Xiphophorus maculatus]
Sequence ID: ref|XP_005811174.1|Length: 415Number of Matches: 1
Gene-associated gene details
Map Viewer-aligned genomic context
Range 1: 20 to 262GenPeptGraphics Next Match Previous Match First Match

Alignment statistics for match #1

Score	**Expect**	**Method**	**Identities**	**Positives**	**Gaps**	**Frame**
59.3 bits(142)	3e-10()	Compositional matrix adjust.	69/256(27%)	109/256(42%)	31/256(12%)	

Features:

```
Query  336  LATLAMFIWLPIGFLLAVFRISVGV------------FLPYHVANFLASMSGVRITFKTH  383
            +A L + I+ P+G  L + RI +GV            F+   V   ++S+ G+ +  +
Sbjct  20   VALLLLLIYSPVGVCLMLMRIFIGVHVFLVSCAIPDSFVRRFVVRVMSSVLGMHVRQR--  77

Query  384  NLNNGRPEKGNSGVLYVCNHRTLLDP--VFLTTSLGKPLTAVTYSLSKFSEFIAPLKTVS  441
               N R    N+  L VCNH T  D   + L T    P    +     ++     + + S
Sbjct  78   ---NPRSRDKNTK-LCVCNHVTEFDHNIINLLTPFNTPQLEGSTGFMCWARGFMEIHSAS  133

Query  442  LKRDRKKDGEAMQRLLSKGD----LVVCPEGTTCREPYLLRFSPLFAELTEDIVPVAVDA  497
                ++  GE++QR  S       LV   E TT     LL+FS     LTE I PVA+
Sbjct  134  ---SQEAVGESLQRYCSADGAPPLLVFPEEDTTNGRAGLLKFSSWPFTLTESIQPVALRV  190

Query  498  RVSMFYGTTASGLKCLDPIFFLMNPRPVYCLEILKKLPKEMTCAGGKSSFEVANFIQGEL  557
               +   +T       D ++   +P  VY +  L  + ++     G+S+ E AN +Q  L
Sbjct  191  SRPLLSLSTVESSWLTDLLWTFFSPCTVYHVSWLPPVSRQ----DGESTQEFANKVQELL  246

Query  558  ARVLGFECTNLTRRDK  573
            A  LG   T +T+ DK
Sbjct  247  AIELGLVSTKITKADK  262
```

```
>AtGPAT9
MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW
NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKY
HGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDH
VQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEV
WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILARLEEK
```

PREDICTED: glycerol-3-phosphate acyltransferase 4-like [Xiphophorus maculatus]
Sequence ID: ref|XP_005812873.1|Length: 455Number of Matches: 1

```
Query  22   IEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW----  77
            I+D   S   + EPR +L+     D+     +A   I+DD  T+ F +   E WN
Sbjct  93   IQDLRHSAGCL-EPRFELA-----DVFFFCRKALENIIDDDVTKRFSAQKLENWNLLTRS  146

Query  78   -------NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRK  130
                   ++ +  L+  GV++RY +L P R      G  +F+ L   V   L    +LR
Sbjct  147  NHNFCYISLKVLALWILGVLIRYGVLLPFRVTVAITGIFLFIVLSTVVG--LIPCTKLRT  204

Query  131  KIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIM  190
             +   +  M     V S TG++ YH  +   +   + VANHT+ +D I+L     ++++
Sbjct  205  YLSDKVHLMGYRLCVRSLTGIITYHNRKNKPKNDGICVANHTTPVDGIILANDHCYSLVG  264

Query  191  QKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVN  250
            Q H G +G++Q  + +S   IWF R E KDR +VAK+L+DHV   + +P+LIFPEG CVN
Sbjct  265  QLHGGLLGMIQRAMAKSSPHIWFERDEVKDRRLVAKRLKDHVADENKHPVLIFPEGFCVN  324

Query  251  NNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEVWY  310
            N   +MF+KG+FE+ CT+ P AIKY+  F DAFWNS K     +LL++M+SWA+VC VWY
Sbjct  325  NTSVMMFRKGSFEIGCTIYPAAIKYDPRFGDAFWNSSKFGLVGYLLRMMSSWAIVCSVWY  384

Query  311  LEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESIL  370
            L P   + GE  ++FA RV+  I+ + GL  + WD  LK ++      E +QQ +++ +L
Sbjct  385  LPPMNRKEGEDAMQFANRVKAAIAAQGGLVDLIWDAGLKRTKVKDTFKEDQQQLYSKILL  444

Query  371  ARLEE  375
               E
Sbjct  445  GDHEN  449
```

AtGPAT9 vs Xiphophorus maculates (top AtGPAT1 hit):

PREDICTED: glycerol-3-phosphate acyltransferase 4-like [Xiphophorus maculatus]
Sequence ID: ref|XP_005812873.1|Length: 455Number of Matches: 1
Related Information
Gene-associated gene details
Map Viewer-aligned genomic context
Range 1: 93 to 449GenPeptGraphics Next Match Previous Match First Match

Score	**Expect**	**Method**	**Identities**	**Positives**	**Gaps**	**Frame**
235 bits(600)	1e-74()	Compositional matrix adjust.	131/365(36%)	200/365(54%)	19/365(5%)	

```
Features:
Query  22   IEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW----  77
            I+D   S   + EPR +L+     D+     +A   I+DD  T+ F +   E WN
Sbjct  93   IQDLRHSAGCL-EPRFELA-----DVFFFCRKALENIIDDDVTKRFSAQKLENWNLLTRS  146

Query  78   -------NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRK  130
                   ++ +  L+  GV++RY +L P R      G  +F+ L   V   L    +LR
Sbjct  147  NHNFCYISLKVLALWILGVLIRYGVLLPFRVTVAITGIFLFIVLSTVVG--LIPCTKLRT  204

Query  131  KIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIM  190
             +   +  M     V S TG++ YH  +   +   + VANHT+ +D I+L     ++++
Sbjct  205  YLSDKVHLMGYRLCVRSLTGIITYHNRKNKPKNDGICVANHTTPVDGIILANDHCYSLVG  264

Query  191  QKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVN  250
            Q H G +G++Q  + +S   IWF R E KDR +VAK+L+DHV   + +P+LIFPEG CVN
Sbjct  265  QLHGGLLGMIQRAMAKSSPHIWFERDEVKDRRLVAKRLKDHVADENKHPVLIFPEGFCVN  324

Query  251  NNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEVWY  310
            N   +MF+KG+FE+ CT+ P AIKY+  F DAFWNS K     +LL++M+SWA+VC VWY
Sbjct  325  NTSVMMFRKGSFEIGCTIYPAAIKYDPRFGDAFWNSSKFGLVGYLLRMMSSWAIVCSVWY  384

Query  311  LEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESIL  370
            L P   + GE  ++FA RV+  I+ + GL  + WD  LK ++      E +QQ +++ +L
Sbjct  385  LPPMNRKEGEDAMQFANRVKAAIAAQGGLVDLIWDAGLKRTKVKDTFKEDQQQLYSKILL  444

Query  371  ARLEE  375
               E
Sbjct  445  GDHEN  449
```

AtGPAT1 vs Orcinus orca (top AtGPAT9 species hit):

PREDICTED: neuropilin-2 isoform X6 [Orcinus orca]
Sequence ID: ref|XP_004262866.1|Length: 901Number of Matches: 1
Related Information
Gene-associated gene details
Map Viewer-aligned genomic context
Range 1: 827 to 882GenPeptGraphics Next Match Previous Match First Match

Alignment statistics for match #1

Score	**Expect**	**Method**	**Identities**	**Positives**	**Gaps**	**Frame**
30.4 bits(67)	0.041()	Compositional matrix adjust.	14/56(25%)	27/56(48%)	0/56(0%)	

Features:

```
Query  335  PLATLAMFIWLPIGFLLAVFRISVGVFLPYHVANFLASMSGVRITFKTHNLNNGRP  390
            P+     ++    G +L +  +++ + L YH   + A  +   IT+KT +  NG P
Sbjct  827  PIPAYWYYVMAAGGAVLVLVSVALALVLHYHRFRYAAKKTDHSITYKTSHYTNGAP  882
```

Supplemental Table S1. Primers utilized for PCR, RT-PCR, & qPCR.

Purpose	**Primer Name**	**Sequence (5' to 3')**
Genotyping gpat9-1 (Salk_052947C)		
Gene specific	GPAT9 salk F1	ACTTTCTTTGGAGAGTCGCTGT
Gene specific	GPAT9 salk R1	CATCAACAATGGCACCAGCA
T-DNA left border	LBb1.3	ATTTTGCCGATTTCGGAAC
Genotyping gpat9-2 (GABI_867A06)		
Gene specific	GPAT9 GK F1	GCAGGCGTGATTTGCTAGAC
Gene specific	GPAT9 GK R1	AATGCGGTCATCTGCTCCAA
T-DNA left border	o8409	ATATTGACCATCATACTCATTGC
Genotyping qrt1-4 (CS25041)		
Gene specific	Qrt F2	TTTGCCTCTCAGGGTGTTTC
Gene specific	Qrt R1	AATGAGAGCTATGCGGGAGA
T-DNA left border	LBb1.3	ATTTTGCCGATTTCGGAAC
***GPAT9* RT-PCR (Fig. S1)**		
	GPAT9 ORF start	ATGAGCAGTACGGCAGGGAGGC
	GPAT9 ORF end	TGCAAAAGTGAGTTATGTTTATTGAGA
qPCR of *GPAT9* (Fig. S1)		
	GPAT9LP1046	AGAGAGGGTCAGAGACATGA
	G9 qPCR R 1172	CGACTCTGCGAAACTCTGTTG
	qTIP41-like829F	ACATTTCAGTCTCTATCTGCGAAAGG
	qTIP41-like946R	GGATCTTCAGTTTCTGTGTCGTATGC

Supplemental Table S2. Gene identifiers for GPAT9, LPEAT1, and LPEAT2 sequences used in Figures1 and S1 in the main text. AGI locus identifiers for the three Arabidopsis genes are described at The Arabidopsis Information Resource (TAIR) homepage (https://www.arabidopsis.org/). The Genbank accession numbers are shown for tung tree GPAT9 (*Vernicia fordii*, Gidda et al., 2009) and *Ricinus communis* GPAT9 [originally annotated as a putative LPAAT, Burgal et al., (2008)]. All other identifiers are as listed for each species in the Phytozome 10.3 database (http://phytozome.jgi.doe.gov/pz/portal.html#).

*: not analyzed in this study.

Species	GPAT9	LPEAT1	LPEAT2
Arabidopsis thaliana	At5g60620	At1g80950	At2g45670
Vernicia fordii	FJ479751	*	*
Physcomitrella patens	Phpat.011G104300	*	*
Selaginella moellendorffii	152980	*	*
Aquilegia coerulea	Aquca_047_00038.1	*	*
Brachypodium distachyon	Bradi1g25790	*	*
Solanum tuberosum	PGSC0003DMT400032021	*	*
Salix purpurea	SapurV1A.0039s0700	*	*
Gossypium raimondii	Gorai.012G158300 and Gorai.005G258500	*	*
Cucumis sativus	Cucsa.099550	*	*
Zea mays	GRMZM2G165681	GRMZM2G096010	GRMZM2G116243
Setaria italica	Si030220m	Si022261m	Si006175m
Oryza sativa	LOC_Os07g34730	LOC_Os05g28960	LOC_Os06g49790
Citrus clementina	Ciclev10028668m	Ciclev10001396m	Ciclev10019536m
Glycine max	Glyma.09G119200	Glyma.04G033600	Glyma.03G019200
Prunus persica	ppa007262m	ppa006689m	ppa003784m
Populus trichocharpa	Potri.004G183300	Potri.014G042200	Potri.014G074300
Ricinus communis	ACB30546	30174.m008937	30170.m014002
Theobroma cacao	Thecc1EG006479t1	Thecc1EG033997t1	Thecc1EG005455t1
Vitis vinifera	GSVIVT01023935001	GSVIVT01009661001	GSVIVT01027580001

SUPPLEMENTAL REFERENCES

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Czechowski, T., Stitt, M., Altmann, T., Udvardi, M.K., and Scheible, W.-R. (2005). Genome-wide identification and testing of superior reference genes for transcript normalization in Arabidopsis. Plant Physiol. **139,** 5-17.

Peterson, R., Slovin, J.P., and Chen, C. (2010). A simplified method for differential staining of aborted and non-aborted pollen grains.

Regan, S.M., and Moffatt, B.A. (1990). Cytochemical Analysis of Pollen Development in Wild-Type Arabidopsis and a Male-Sterile Mutant. The Plant Cell Online **2,** 877-889.