

## Supplementary Material to “Genome-wide analysis of the Glycerol-3-Phosphate Acyltransferase (GPAT) gene family reveals the evolution and diversification of plant GPATs“

**Table S2** - Information about clade (I, II or III) of the respective protein, the more similar Arabidopsis gene, the percentage of similarity with the Arabidopsis gene, and cellular localization.

| Species                           | Protein Accession Number              | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|-----------------------------------|---------------------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Physcomitrella patens</i>      | Pp3c6_29200                           | III   | GPAT6                             | 69.4           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c2_18040                           | III   | GPAT6                             | 64.8           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c7_7840                            | III   | GPAT6                             | 72.1           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c5_1510                            | III   | GPAT6                             | 68.8           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c20_9340                           | III   | GPAT6                             | 72.0           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c6_29290                           | III   | GPAT6                             | 73.5           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c8_21680                           | III   | GPAT6                             | 71.0           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c11_26030                          | I     | GPAT9                             | 80.2           | ER                    |
| <i>Physcomitrella patens</i>      | Pp3c7_2970                            | II    | Soluble GPAT                      | 55.9           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0076s0073                      | III   | GPAT6                             | 62.6           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0011s0239                      | III   | GPAT6                             | 60.0           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0028s0065                      | III   | GPAT4                             | 56.0           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0077s0057                      | III   | GPAT6                             | 69.0           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0149s0036                      | III   | GPAT4                             | 67.3           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0147s0003                      | III   | GPAT4                             | 55.8           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0054s0107                      | III   | GPAT6                             | 65.3           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0026s0045                      | III   | GPAT6                             | 65.7           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0033s0058                      | III   | GPAT6                             | 64.5           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0016s0227                      | I     | GPAT9                             | 77.6           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0001s0271                      | I     | GPAT9                             | 76.3           | ER                    |
| <i>Sphagnum fallax</i>            | Sphfalx0164s0011                      | II    | Soluble GPAT                      | 56.6           | Chloroplast           |
| <i>Selaginella moellendorffii</i> | 80075                                 | III   | GPAT6                             | 61.3           | ER                    |
| <i>Selaginella moellendorffii</i> | 118155                                | III   | GPAT6                             | 66.6           | ER                    |
| <i>Selaginella moellendorffii</i> | 90219                                 | III   | GPAT6                             | 56.5           | ER                    |
| <i>Selaginella moellendorffii</i> | 405228                                | III   | GPAT6                             | 61.8           | ER                    |
| <i>Selaginella moellendorffii</i> | 80614                                 | III   | GPAT6                             | 72.4           | ER                    |
| <i>Selaginella moellendorffii</i> | 170163                                | III   | GPAT6                             | 69.6           | ER                    |
| <i>Selaginella moellendorffii</i> | 164779                                | III   | GPAT6, GPAT8                      | 54.8           | ER                    |
| <i>Selaginella moellendorffii</i> | 63752                                 | III   | GPAT8                             | 62.9           | ER                    |
| <i>Selaginella moellendorffii</i> | 233008                                | III   | GPAT4                             | 60.0           | ER                    |
| <i>Selaginella moellendorffii</i> | 405007                                | III   | GPAT2                             | 56.6           | Mitochondria          |
| <i>Selaginella moellendorffii</i> | 152980                                | I     | GPAT9                             | 78.9           | ER                    |
| <i>Selaginella moellendorffii</i> | 132845                                | II    | Soluble GPAT                      | 76.3           | Chloroplast           |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00003.239 | III   | GPAT2                             | 65.6           | Mitochondria          |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00179.5   | III   | GPAT1                             | 65.1           | Mitochondria          |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00133.34  | III   | GPAT8                             | 66.7           | ER                    |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00009.182 | III   | GPAT6                             | 78.5           | ER                    |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00012.248 | III   | GPAT5                             | 72.5           | ER                    |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00029.356 | III   | GPAT6                             | 74.1           | ER                    |
| <i>Amborella trichopoda</i>       | evm_27.TU.AmTr_v1.0_scaffold00048.62  | II    | Soluble GPAT                      | 68.0           | Chloroplast           |
| <i>Brachypodium distachyon</i>    | Bradi2g44377                          | III   | GPAT1                             | 59.4           | Mitochondria          |
| <i>Brachypodium distachyon</i>    | Bradi1g09480                          | III   | GPAT4                             | 67.6           | ER                    |
| <i>Brachypodium distachyon</i>    | Bradi3g26655                          | III   | GPAT6                             | 60.8           | ER                    |
| <i>Brachypodium distachyon</i>    | Bradi2g55290                          | III   | GPAT6                             | 82.8           | ER                    |

| Species                        | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|--------------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Brachypodium distachyon</i> | Bradi2g11450             | III   | GPAT2                             | 58.9           | Mitochondria          |
| <i>Brachypodium distachyon</i> | Bradi1g73935             | III   | GPAT8                             | 60.7           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi2g33165             | III   | GPAT2                             | 54.9           | Mitochondria          |
| <i>Brachypodium distachyon</i> | Bradi2g23420             | III   | GPAT5                             | 56.1           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi3g37245             | III   | GPAT2                             | 52.2           | Mitochondria          |
| <i>Brachypodium distachyon</i> | Bradi3g01350             | III   | GPAT4                             | 63.2           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi2g61040             | III   | GPAT1                             | 52.3           | Mitochondria          |
| <i>Brachypodium distachyon</i> | Bradi2g41702             | III   | GPAT2                             | 53.0           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi2g23400             | III   | GPAT5                             | 55.0           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi4g04550             | III   | GPAT2                             | 50.4           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi2g60975             | III   | GPAT2                             | 52.6           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi1g02805             | III   | GPAT2                             | 46.3           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi1g25790             | I     | GPAT9                             | 87.6           | ER                    |
| <i>Brachypodium distachyon</i> | Bradi3g34260             | II    | Soluble GPAT                      | 72.1           | Chloroplast           |
| <i>Oryza sativa</i>            | LOC_Os01g44069           | III   | GPAT1                             | 60.1           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os10g27330           | III   | GPAT6                             | 56.6           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os03g52570           | III   | GPAT6                             | 60.6           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os01g63580           | III   | GPAT6                             | 84.1           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os05g38350           | III   | GPAT6                             | 84.1           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os11g45400           | III   | GPAT2                             | 57.6           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os02g02340           | III   | GPAT4                             | 66.4           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os05g20100           | III   | GPAT2                             | 53.8           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os08g03700           | III   | GPAT8                             | 54.5           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os01g19390           | III   | GPAT2                             | 57.6           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os12g37600           | III   | GPAT2                             | 46.2           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os03g61720           | III   | GPAT2                             | 51.0           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os01g14900           | III   | GPAT2                             | 45.8           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os05g37600           | III   | GPAT6                             | 73.5           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os10g41070           | III   | GPAT1                             | 47.6           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os01g22560           | III   | GPAT1                             | 58.8           | Mitochondria          |
| <i>Oryza sativa</i>            | LOC_Os07g34730           | I     | GPAT9                             | 87.0           | ER                    |
| <i>Oryza sativa</i>            | LOC_Os10g42720           | II    | Soluble GPAT                      | 71.7           | Chloroplast           |
| <i>Panicum hallii</i>          | Pahal.E02373             | III   | GPAT1                             | 57.6           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.I01831             | III   | GPAT8                             | 62.0           | ER                    |
| <i>Panicum hallii</i>          | Pahal.B03381             | III   | GPAT6                             | 67.4           | ER                    |
| <i>Panicum hallii</i>          | Pahal.E00896.            | III   | GPAT6                             | 83.2           | ER                    |
| <i>Panicum hallii</i>          | Pahal.I00545             | III   | GPAT6                             | 62.3           | ER                    |
| <i>Panicum hallii</i>          | Pahal.E03181             | III   | GPAT2                             | 59.2           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.C02741             | III   | GPAT5                             | 62.2           | ER                    |
| <i>Panicum hallii</i>          | Pahal.I04570             | III   | GPAT1                             | 50.1           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.H00181             | III   | GPAT2                             | 53.4           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.E03539             | III   | GPAT1                             | 50.3           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.C03674             | III   | GPAT1                             | 52.3           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.I01321             | III   | GPAT1                             | 46.3           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.A00044             | III   | GPAT4                             | 62.1           | ER                    |
| <i>Panicum hallii</i>          | Pahal.F02713             | III   | GPAT1                             | 55.5           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.I04042             | III   | GPAT1                             | 54.8           | Mitochondria          |
| <i>Panicum hallii</i>          | Pahal.C02792             | III   | GPAT6                             | 65.6           | ER                    |
| <i>Panicum hallii</i>          | Pahal.B04165             | I     | GPAT9                             | 76.1           | ER                    |
| <i>Panicum hallii</i>          | Pahal.I03757             | II    | Soluble GPAT                      | 64.0           | Chloroplast           |
| <i>Setaria italica</i>         | Seita.9G101700           | III   | GPAT8                             | 67.0           | ER                    |
| <i>Setaria italica</i>         | Seita.9G261200           | III   | GPAT6, GPAT4                      | 67.0           | ER                    |
| <i>Setaria italica</i>         | Seita.5G386400           | III   | GPAT6                             | 84.1           | ER                    |
| <i>Setaria italica</i>         | Seita.9G527800           | III   | GPAT6, GPAT4                      | 59.8           | ER                    |
| <i>Setaria italica</i>         | Seita.4G285600           | III   | GPAT6, GPAT4                      | 60.6           | ER                    |
| <i>Setaria italica</i>         | Seita.3G291600           | III   | GPAT2                             | 54.7           | Mitochondria          |

| Species                | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Setaria italica</i> | Seita.3G218600           | III   | GPAT5                             | 62.3           | ER                    |
| <i>Setaria italica</i> | Seita.5G028700           | III   | GPAT2                             | 65.1           | ER                    |
| <i>Setaria italica</i> | Seita.3G223100           | III   | GPAT6                             | 72.5           | ER                    |
| <i>Setaria italica</i> | Seita.5G060100           | III   | GPAT1                             | 51.0           | ER                    |
| <i>Setaria italica</i> | Seita.8G234000           | III   | GPAT2                             | 51.6           | Mitochondria          |
| <i>Setaria italica</i> | Seita.9G023200           | III   | GPAT1                             | 48.8           | Mitochondria          |
| <i>Setaria italica</i> | Seita.3G334400           | III   | GPAT2                             | 48.6           | Mitochondria          |
| <i>Setaria italica</i> | Seita.1G116700           | III   | GPAT4                             | 62.3           | ER                    |
| <i>Setaria italica</i> | Seita.6G074300           | III   | GPAT4                             | 56.0           | ER                    |
| <i>Setaria italica</i> | Seita.3G219000           | III   | GPAT1                             | 54.6           | Mitochondria          |
| <i>Setaria italica</i> | Seita.9G527900           | III   | GPAT8                             | 62.1           | ER                    |
| <i>Setaria italica</i> | Seita.9G323800           | III   | GPAT2                             | 55.0           | Mitochondria          |
| <i>Setaria italica</i> | Seita.2G339000           | I     | GPAT9                             | 86.5           | ER                    |
| <i>Setaria italica</i> | Seita.9G307400           | II    | Soluble GPAT                      | 65.7           | Chloroplast           |
| <i>Setaria viridis</i> | Sevir.5G243800           | III   | GPAT1                             | 59.9           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.9G099900           | III   | GPAT8                             | 66.8           | ER                    |
| <i>Setaria viridis</i> | Sevir.9G264100           | III   | GPAT8                             | 66.2           | ER                    |
| <i>Setaria viridis</i> | Sevir.5G391500           | III   | GPAT6                             | 84.1           | ER                    |
| <i>Setaria viridis</i> | Sevir.9G532600           | III   | GPAT4, GPAT6                      | 59.4           | ER                    |
| <i>Setaria viridis</i> | Sevir.3G300000           | III   | GPAT2                             | 54.7           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.4G298000           | III   | GPAT6                             | 60.6           | ER                    |
| <i>Setaria viridis</i> | Sevir.5G027400           | III   | GPAT2                             | 64.3           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.9G022800           | III   | GPAT1                             | 49.0           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.3G228100           | III   | GPAT6                             | 72.5           | ER                    |
| <i>Setaria viridis</i> | Sevir.5G059700           | III   | GPAT1                             | 51.0           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.8G244100           | III   | GPAT2                             | 51.4           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.3G348800           | III   | GPAT2                             | 48.4           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.1G115700           | III   | GPAT4                             | 63.6           | ER                    |
| <i>Setaria viridis</i> | Sevir.6G073400           | III   | GPAT4                             | 57.8           | ER                    |
| <i>Setaria viridis</i> | Sevir.3G224100           | III   | GPAT1                             | 54.6           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.9G329700           | III   | GPAT2                             | 55.0           | Mitochondria          |
| <i>Setaria viridis</i> | Sevir.2G349100           | I     | GPAT9                             | 86.5           | ER                    |
| <i>Setaria viridis</i> | Sevir.9G312800           | II    | Soluble GPAT                      | 65.7           | Chloroplast           |
| <i>Sorghum bicolor</i> | Sobic.003G229700         | III   | GPAT1                             | 60.8           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.001G099300         | III   | GPAT6                             | 71.5           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.001G250200         | III   | GPAT6                             | 67.0           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.001G493300         | III   | GPAT6                             | 65.3           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.003G360700         | III   | GPAT6                             | 85.7           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.009G162000         | III   | GPAT5                             | 72.0           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.004G010300         | III   | GPAT4                             | 71.2           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.003G114200         | III   | GPAT2                             | 60.2           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.003G142500         | III   | GPAT3                             | 65.0           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.008G130800         | III   | GPAT3                             | 52.6           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.001G026100         | III   | GPAT2                             | 56.9           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.005G214400         | III   | GPAT3                             | 57.8           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.009G202600         | III   | GPAT2                             | 56.5           | Mitochondria          |
| <i>Sorghum bicolor</i> | Sobic.002G325300         | I     | GPAT9                             | 87.3           | ER                    |
| <i>Sorghum bicolor</i> | Sobic.001G283700         | II    | Soluble GPAT                      | 66.7           | Chloroplast           |
| <i>Zea mays</i>        | GRMZM2G165681            | I     | GPAT9                             | 86.8           | ER                    |
| <i>Zea mays</i>        | GRMZM2G123987            | I     | GPAT9                             | 86.8           | ER                    |
| <i>Zea mays</i>        | GRMZM2G065203            | III   | GPAT1                             | 65.9           | Mitochondria          |
| <i>Zea mays</i>        | GRMZM2G177150            | III   | GPAT1                             | 60.3           | Mitochondria          |
| <i>Zea mays</i>        | GRMZM2G147917            | III   | GPAT4, GPAT8                      | 66.3           | ER                    |
| <i>Zea mays</i>        | GRMZM2G064590            | III   | GPAT6                             | 64.7           | ER                    |
| <i>Zea mays</i>        | GRMZM2G124042            | III   | GPAT6                             | 65.8           | ER                    |
| <i>Zea mays</i>        | GRMZM2G166176            | III   | GPAT5                             | 59.0           | ER                    |

| Species                     | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|-----------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Zea mays</i>             | GRMZM2G083195            | III   | GPAT6                             | 81.9           | ER                    |
| <i>Zea mays</i>             | GRMZM2G059637            | III   | GPAT7                             | 61.7           | ER                    |
| <i>Zea mays</i>             | GRMZM2G072298            | III   | GPAT1                             | 56.1           | Mitochondria          |
| <i>Zea mays</i>             | GRMZM2G156729            | III   | GPAT2                             | 47.3           | Mitochondria          |
| <i>Zea mays</i>             | GRMZM2G070304            | III   | GPAT2                             | 55.8           | Mitochondria          |
| <i>Zea mays</i>             | GRMZM2G033767            | III   | GPAT2                             | 46.2           | Mitochondria          |
| <i>Zea mays</i>             | GRMZM2G020320            | III   | GPAT4                             | 60.0           | ER                    |
| <i>Zea mays</i>             | GRMZM2G131378            | III   | GPAT1                             | 55.4           | Mitochondria          |
| <i>Zea mays</i>             | GRMZM2G159890            | II    | Soluble GPAT                      | 66.4           | Chloroplast           |
| <i>Aquilegia coerulea</i>   | Aquca_057_00060          | III   | GPAT1                             | 71.3           | Mitochondria          |
| <i>Aquilegia coerulea</i>   | Aquca_003_00476          | III   | GPAT2                             | 74.1           | Mitochondria          |
| <i>Aquilegia coerulea</i>   | Aquca_045_00017          | III   | GPAT6                             | 86.7           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_029_00122          | III   | GPAT2                             | 66.9           | Mitochondria          |
| <i>Aquilegia coerulea</i>   | Aquca_004_00312          | III   | GPAT6                             | 86.7           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_025_00147          | III   | GPAT6                             | 68.8           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_045_00015          | III   | GPAT6                             | 81.3           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_004_00505          | III   | GPAT4                             | 61.7           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_010_00671          | III   | GPAT5                             | 71.3           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_013_00284          | III   | GPAT4                             | 85.2           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_009_00928          | III   | GPAT5                             | 76.4           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_009_00929          | III   | GPAT7                             | 74.5           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_001_00233          | I     | GPAT9                             | 92.5           | ER                    |
| <i>Aquilegia coerulea</i>   | Aquca_047_00038          | I     | GPAT9                             | 86.7           | ER                    |
| <i>Aquilegia coerulea</i>   | Aqcoe3G171100            | II    | Soluble GPAT                      | 70.2           | Chloroplast           |
| <i>Mimulus guttatus</i>     | Migut.M00497             | III   | GPAT1                             | 70.9           | Mitochondria          |
| <i>Mimulus guttatus</i>     | Migut.M00495             | III   | GPAT1                             | 69.1           | Mitochondria          |
| <i>Mimulus guttatus</i>     | Migut.J00189             | III   | GPAT6                             | 89.6           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.L01365             | III   | GPAT8                             | 70.2           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.H00880             | III   | GPAT4                             | 68.7           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.N01447             | III   | GPAT8                             | 82.1           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.F00761             | III   | GPAT5                             | 70.6           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.B01763             | III   | GPAT4                             | 83.0           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.G00542             | III   | GPAT6                             | 64.1           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.G00541             | III   | GPAT4, GPAT8                      | 63.8           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.O00899             | III   | GPAT6                             | 66.2           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.N01350             | I     | GPAT9                             | 92.4           | ER                    |
| <i>Mimulus guttatus</i>     | Migut.E00743             | II    | Soluble GPAT                      | 67.2           | Chloroplast           |
| <i>Solanum lycopersicum</i> | Solyc07g056320.2         | III   | GPAT1                             | 77.3           | Mitochondria          |
| <i>Solanum lycopersicum</i> | Solyc02g087500.1         | III   | GPAT6                             | 72.8           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc04g005840.1         | III   | GPAT6                             | 74.3           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc09g014350.2         | III   | GPAT6                             | 87.9           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc01g094700.2         | III   | GPAT4                             | 88.6           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc04g011600.2         | III   | GPAT5                             | 84.9           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc05g053030.1         | III   | GPAT5                             | 77.1           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc10g084900.1         | III   | GPAT6                             | 69.3           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc08g082340.2         | I     | GPAT9                             | 93.0           | ER                    |
| <i>Solanum lycopersicum</i> | Solyc08g076470.2         | II    | Soluble GPAT                      | 71.7           | Chloroplast           |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400044571     | III   | GPAT1                             | 77.9           | Mitochondria          |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400007387     | III   | GPAT6                             | 73.9           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400091384     | III   | GPAT6                             | 72.0           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400003553     | III   | GPAT6                             | 72.7           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400000152     | III   | GPAT4                             | 88.6           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400052335     | III   | GPAT6                             | 87.4           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400028782     | III   | GPAT6                             | 71.8           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400028781     | III   | GPAT6                             | 71.7           | ER                    |
| <i>Solanum tuberosum</i>    | PGSC0003DMT400016230     | III   | GPAT5                             | 86.1           | ER                    |

| Species                    | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|----------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Solanum tuberosum</i>   | PGSC0003DMT400028775     | III   | GPAT6                             | 67.7           | ER                    |
| <i>Solanum tuberosum</i>   | PGSC0003DMT400073428     | III   | GPAT5                             | 74.2           | ER                    |
| <i>Solanum tuberosum</i>   | PGSC0003DMT400069796     | III   | Soluble GPAT                      | 45.8           | Chloroplast           |
| <i>Solanum tuberosum</i>   | PGSC0003DMT400032021     | I     | GPAT9                             | 92.7           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.A01977             | III   | GPAT1                             | 76.7           | Mitochondria          |
| <i>Eucalyptus grandis</i>  | Eucgr.F04388             | III   | GPAT2                             | 67.3           | Mitochondria          |
| <i>Eucalyptus grandis</i>  | Eucgr.B03397             | III   | GPAT8                             | 68.6           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.K03558             | III   | GPAT2                             | 68.1           | Mitochondria          |
| <i>Eucalyptus grandis</i>  | Eucgr.F04389             | III   | GPAT2                             | 71.3           | Mitochondria          |
| <i>Eucalyptus grandis</i>  | Eucgr.A00515             | III   | GPAT6                             | 83.5           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.E00121             | III   | GPAT8                             | 88.3           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.J01235             | III   | GPAT7                             | 75.1           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.G02949             | III   | GPAT7                             | 69.9           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.I01507             | I     | GPAT9                             | 88.0           | ER                    |
| <i>Eucalyptus grandis</i>  | Eucgr.E00228             | II    | Soluble GPAT                      | 80.0           | Chloroplast           |
| <i>Eucalyptus grandis</i>  | Eucgr.E01634             | II    | Soluble GPAT                      | 72.6           | Chloroplast           |
| <i>Manihot esculenta</i>   | Manes.02G084800          | III   | GPAT1                             | 81.0           | Mitochondria          |
| <i>Manihot esculenta</i>   | Manes.01G127800          | III   | GPAT1                             | 76.4           | Mitochondria          |
| <i>Manihot esculenta</i>   | Manes.02G157300          | III   | GPAT2                             | 73.9           | Mitochondria          |
| <i>Manihot esculenta</i>   | Manes.01G230400          | III   | GPAT2                             | 71.4           | Mitochondria          |
| <i>Manihot esculenta</i>   | Manes.05G012900          | III   | GPAT2                             | 70.3           | Mitochondria          |
| <i>Manihot esculenta</i>   | Manes.01G193000          | III   | GPAT8                             | 70.5           | ER                    |
| <i>Manihot esculenta</i>   | Manes.09G103500          | III   | GPAT6                             | 87.3           | ER                    |
| <i>Manihot esculenta</i>   | Manes.08G089900          | III   | GPAT6                             | 87.1           | ER                    |
| <i>Manihot esculenta</i>   | Manes.07G118400          | III   | GPAT5                             | 78.6           | ER                    |
| <i>Manihot esculenta</i>   | Manes.01G255900          | III   | GPAT4                             | 90.0           | ER                    |
| <i>Manihot esculenta</i>   | Manes.11G106900          | I     | GPAT9                             | 93.1           | ER                    |
| <i>Populus trichocarpa</i> | Potri.005G202200         | III   | GPAT1                             | 75.5           | Mitochondria          |
| <i>Populus trichocarpa</i> | Potri.002G192600         | III   | GPAT2                             | 67.4           | Mitochondria          |
| <i>Populus trichocarpa</i> | Potri.016G063900         | III   | GPAT4                             | 70.9           | ER                    |
| <i>Populus trichocarpa</i> | Potri.006G198100         | III   | GPAT4                             | 70.9           | ER                    |
| <i>Populus trichocarpa</i> | Potri.016G113100         | III   | GPAT6                             | 86.4           | ER                    |
| <i>Populus trichocarpa</i> | Potri.006G097800         | III   | GPAT6                             | 89.5           | ER                    |
| <i>Populus trichocarpa</i> | Potri.010G201200         | III   | GPAT5                             | 82.0           | ER                    |
| <i>Populus trichocarpa</i> | Potri.008G058200         | III   | GPAT5                             | 80.0           | ER                    |
| <i>Populus trichocarpa</i> | Potri.014G085500         | III   | GPAT8                             | 84.0           | ER                    |
| <i>Populus trichocarpa</i> | Potri.001G136600         | II    | Soluble GPAT                      | 74.2           | Chloroplast           |
| <i>Ricinus communis</i>    | 30122.m000357            | I     | GPAT9                             | 94.2           | ER                    |
| <i>Ricinus communis</i>    | 28350.m000105            | III   | GPAT1                             | 78.0           | Mitochondria          |
| <i>Ricinus communis</i>    | 29736.m002070            | III   | GPAT4                             | 70.4           | ER                    |
| <i>Ricinus communis</i>    | 29822.m003441            | III   | GPAT8                             | 65.4           | ER                    |
| <i>Ricinus communis</i>    | 29908.m005967            | III   | GPAT2                             | 65.2           | Mitochondria          |
| <i>Ricinus communis</i>    | 30076.m004618            | III   | GPAT2                             | 64.4           | Mitochondria          |
| <i>Ricinus communis</i>    | 30174.m008615            | III   | GPAT8                             | 90.0           | ER                    |
| <i>Ricinus communis</i>    | 27568.m000266            | III   | GPAT5                             | 81.2           | ER                    |
| <i>Ricinus communis</i>    | 29969.m000267            | III   | GPAT6                             | 90.8           | ER                    |
| <i>Ricinus communis</i>    | 30068.m002660            | II    | Soluble GPAT                      | 68.8           | Chloroplast           |
| <i>Citrus sinensis</i>     | orange1.1g009120m.g      | III   | GPAT1                             | 77.3           | Mitochondria          |
| <i>Citrus sinensis</i>     | orange1.1g009762m.g      | III   | GPAT2                             | 71.7           | Mitochondria          |
| <i>Citrus sinensis</i>     | orange1.1g042288m.g      | III   | GPAT8                             | 68.5           | ER                    |
| <i>Citrus sinensis</i>     | orange1.1g042170m.g      | III   | GPAT2                             | 70.5           | Mitochondria          |
| <i>Citrus sinensis</i>     | orange1.1g043920m.g      | III   | GPAT8                             | 68.1           | ER                    |
| <i>Citrus sinensis</i>     | orange1.1g010860m.g      | III   | GPAT8                             | 83.8           | ER                    |
| <i>Citrus sinensis</i>     | orange1.1g018906m.g      | III   | GPAT6                             | 86.5           | ER                    |
| <i>Citrus sinensis</i>     | orange1.1g038704m.g      | III   | GPAT5                             | 91.6           | ER                    |
| <i>Citrus sinensis</i>     | orange1.1g017205m        | I     | GPAT9                             | 93.6           | ER                    |

| Species                    | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|----------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Citrus clementina</i>   | Ciclev10028672m.g        | I     | GPAT9                             | 93.6           | ER                    |
| <i>Citrus clementina</i>   | Ciclev10031163m.g        | III   | GPAT1                             | 77.2           | Mitochondria          |
| <i>Citrus clementina</i>   | Ciclev10001145m.g        | III   | GPAT2                             | 74.3           | Mitochondria          |
| <i>Citrus clementina</i>   | Ciclev10013880m.g        | III   | GPAT8                             | 68.5           | ER                    |
| <i>Citrus clementina</i>   | Ciclev10023483m.g        | III   | GPAT2                             | 70.5           | Mitochondria          |
| <i>Citrus clementina</i>   | Ciclev10033948m.g        | III   | GPAT8                             | 52.5           | ER                    |
| <i>Citrus clementina</i>   | Ciclev10011536m.g        | III   | GPAT6                             | 85.7           | ER                    |
| <i>Citrus clementina</i>   | Ciclev10031344m.g        | III   | GPAT7                             | 74.1           | ER                    |
| <i>Citrus clementina</i>   | Ciclev10019825m.g        | III   | GPAT8                             | 84.0           | ER                    |
| <i>Citrus clementia</i>    | Ciclev10001047m.g        | II    | Soluble GPAT                      | 74.0           | Chloroplast           |
| <i>Gossypium raimondii</i> | Gorai.012G158300         | I     | GPAT9                             | 88.1           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.005G258500         | I     | GPAT9                             | 90.5           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.008G098000         | III   | GPAT1                             | 78.4           | Mitochondria          |
| <i>Gossypium raimondii</i> | Gorai.006G181200         | III   | GPAT6                             | 87.7           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.010G045500         | III   | GPAT2                             | 69.4           | Mitochondria          |
| <i>Gossypium raimondii</i> | Gorai.007G078200         | III   | GPAT6                             | 67.3           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.004G145100         | III   | GPAT2                             | 65.7           | Mitochondria          |
| <i>Gossypium raimondii</i> | Gorai.012G112800         | III   | GPAT6                             | 81.0           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.011G151300         | III   | GPAT4                             | 68.7           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.004G235900         | III   | GPAT2                             | 69.3           | Mitochondria          |
| <i>Gossypium raimondii</i> | Gorai.011G267100         | III   | GPAT5                             | 78.5           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.012G071300         | III   | GPAT5                             | 80.1           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.007G100100         | III   | GPAT4                             | 87.6           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.011G267200         | III   | GPAT5                             | 74.1           | ER                    |
| <i>Gossypium raimondii</i> | Gorai.007G033500         | II    | Soluble GPAT                      | 75.7           | Chloroplast           |
| <i>Gossypium raimondii</i> | Gorai.004G182200         | II    | Soluble GPAT                      | 74.7           | Chloroplast           |
| <i>Gossypium raimondii</i> | Gorai.003G185500         | II    | Soluble GPAT                      | 74.2           | Chloroplast           |
| <i>Theobroma cacao</i>     | Thecc1EG006479           | I     | GPAT9                             | 82.7           | ER                    |
| <i>Theobroma cacao</i>     | Thecc1EG001873           | III   | GPAT1                             | 78.9           | Mitochondria          |
| <i>Theobroma cacao</i>     | Thecc1EG034986           | III   | GPAT2                             | 61.1           | Mitochondria          |
| <i>Theobroma cacao</i>     | Thecc1EG034985           | III   | GPAT2                             | 64.0           | Mitochondria          |
| <i>Theobroma cacao</i>     | Thecc1EG004855           | III   | GPAT2                             | 73.2           | Mitochondria          |
| <i>Theobroma cacao</i>     | Thecc1EG021737           | III   | GPAT6                             | 86.5           | ER                    |
| <i>Theobroma cacao</i>     | Thecc1EG018071           | III   | GPAT6                             | 68.8           | ER                    |
| <i>Theobroma cacao</i>     | Thecc1EG026783           | III   | GPAT2                             | 70.8           | Mitochondria          |
| <i>Theobroma cacao</i>     | Thecc1EG010070           | III   | GPAT4                             | 59.9           | ER                    |
| <i>Theobroma cacao</i>     | Thecc1EG042716           | III   | GPAT5                             | 76.4           | ER                    |
| <i>Theobroma cacao</i>     | Thecc1EG005317           | III   | GPAT4                             | 88.6           | ER                    |
| <i>Theobroma cacao</i>     | Thecc1EG016600           | II    | Soluble GPAT                      | 72.2           | Chloroplast           |
| <i>Arabidopsis lyrata</i>  | 919369                   | III   | GPAT1                             | 98.1           | Mitochondria          |
| <i>Arabidopsis lyrata</i>  | 470198                   | III   | GPAT2                             | 96.8           | Mitochondria          |
| <i>Arabidopsis lyrata</i>  | 943550                   | III   | GPAT3                             | 98.8           | Mitochondria          |
| <i>Arabidopsis lyrata</i>  | 478480                   | III   | GPAT5                             | 98.8           | ER                    |
| <i>Arabidopsis lyrata</i>  | 482818                   | III   | GPAT6                             | 99.4           | ER                    |
| <i>Arabidopsis lyrata</i>  | 918798                   | III   | GPAT4                             | 99.6           | ER                    |
| <i>Arabidopsis lyrata</i>  | 490527                   | III   | GPAT8                             | 98.4           | ER                    |
| <i>Arabidopsis lyrata</i>  | 349873                   | III   | GPAT4                             | 63.5           | ER                    |
| <i>Arabidopsis lyrata</i>  | 950810                   | I     | GPAT9                             | 99.5           | ER                    |
| <i>Arabidopsis lyrata</i>  | AL1G46330                | II    | Soluble GPAT                      | 99.6           | Chloroplast           |
| <i>Brassica rapa</i>       | Brara.A00307             | I     | GPAT9                             | 97.6           | ER                    |
| <i>Brassica rapa</i>       | Brara.J01416             | I     | GPAT9                             | 97.0           | ER                    |
| <i>Brassica rapa</i>       | Brara.J00449             | III   | GPAT1                             | 89.1           | Mitochondria          |
| <i>Brassica rapa</i>       | Brara.K01852             | III   | GPAT8                             | 90.4           | ER                    |
| <i>Brassica rapa</i>       | Brara.A03408             | III   | GPAT5                             | 85.7           | ER                    |
| <i>Brassica rapa</i>       | Brara.I00118             | III   | GPAT3                             | 83.2           | Mitochondria          |
| <i>Brassica rapa</i>       | Brara.C02835             | III   | GPAT3                             | 88.7           | Mitochondria          |

| Species                     | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|-----------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Brassica rapa</i>        | Brara.I05638             | III   | GPAT4                             | 93.8           | ER                    |
| <i>Brassica rapa</i>        | Brara.E02936             | III   | GPAT5                             | 87.2           | ER                    |
| <i>Brassica rapa</i>        | Brara.D02328             | III   | GPAT6                             | 94.2           | ER                    |
| <i>Brassica rapa</i>        | Brara.J00035             | III   | GPAT4                             | 96.2           | ER                    |
| <i>Brassica rapa</i>        | Brara.E00709             | III   | GPAT6                             | 94.0           | ER                    |
| <i>Brassica rapa</i>        | Brara.J02607             | III   | GPAT7                             | 90.0           | ER                    |
| <i>Brassica rapa</i>        | Brara.E02888             | III   | GPAT5                             | 78.4           | ER                    |
| <i>Brassica rapa</i>        | Brara.H00582             | II    | Soluble GPAT                      | 92.7           | Chloroplast           |
| <i>Brassica rapa</i>        | Brara.E01731             | II    | Soluble GPAT                      | 88.0           | Chloroplast           |
| <i>Brassica rapa</i>        | Brara.I02607             | II    | Soluble GPAT                      | 86.2           | Chloroplast           |
| <i>Capsella grandiflora</i> | Cagra.1671s0280          | III   | GPAT1                             | 96.2           | Mitochondria          |
| <i>Capsella grandiflora</i> | Cagra.1968s0023          | III   | GPAT2                             | 92.8           | Mitochondria          |
| <i>Capsella grandiflora</i> | Cagra.0334s0034          | III   | GPAT3                             | 93.1           | Mitochondria          |
| <i>Capsella grandiflora</i> | Cagra.1655s0027          | III   | GPAT5                             | 92.6           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.1968s0101          | III   | GPAT4                             | 95.8           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.2117s0053          | III   | GPAT7                             | 96.8           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.1261s0029          | III   | GPAT8                             | 93.8           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.1655s0038          | III   | GPAT5                             | 83.6           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.1555s0001          | III   | GPAT6                             | 93.1           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.2519s0033          | I     | GPAT9                             | 98.4           | ER                    |
| <i>Capsella grandiflora</i> | Cagra.3957s0001          | II    | Soluble GPAT                      | 97.4           | Chloroplast           |
| <i>Capsella rubella</i>     | Carubv10026601m.g        | I     | GPAT9                             | 98.1           | ER                    |
| <i>Capsella rubella</i>     | Carubv10012249m          | III   | GPAT1                             | 96.0           | Mitochondria          |
| <i>Capsella rubella</i>     | Carubv10008716m          | III   | GPAT2                             | 86.6           | Mitochondria          |
| <i>Capsella rubella</i>     | Carubv10000657m          | III   | GPAT3                             | 89.8           | Mitochondria          |
| <i>Capsella rubella</i>     | Carubv10013500m          | III   | GPAT5                             | 94.6           | ER                    |
| <i>Capsella rubella</i>     | Carubv10023060m          | III   | GPAT6                             | 94.6           | ER                    |
| <i>Capsella rubella</i>     | Carubv10008926m          | III   | GPAT4                             | 96.0           | ER                    |
| <i>Capsella rubella</i>     | Carubv10000788m          | III   | GPAT7                             | 96.4           | ER                    |
| <i>Capsella rubella</i>     | Carubv10000780m          | III   | GPAT8                             | 93.8           | ER                    |
| <i>Capsella rubella</i>     | Carubv10015640m          | III   | GPAT5                             | 84.2           | ER                    |
| <i>Capsella rubella</i>     | Carubv10012611m.g        | II    | Soluble GPAT                      | 98.0           | Chloroplast           |
| <i>Eutrema salsugineum</i>  | Thhalv10007168m          | III   | GPAT1                             | 94.0           | Mitochondria          |
| <i>Eutrema salsugineum</i>  | Thhalv10020574m          | III   | GPAT5                             | 91.6           | ER                    |
| <i>Eutrema salsugineum</i>  | Thhalv10007347m          | III   | GPAT2                             | 91.1           | Mitochondria          |
| <i>Eutrema salsugineum</i>  | Thhalv10028577m          | III   | GPAT3                             | 87.5           | Mitochondria          |
| <i>Eutrema salsugineum</i>  | Thhalv10007431m          | III   | GPAT4                             | 93.8           | ER                    |
| <i>Eutrema salsugineum</i>  | Thhalv10016551m          | III   | GPAT6                             | 94.8           | ER                    |
| <i>Eutrema salsugineum</i>  | Thhalv10028601m          | III   | GPAT4                             | 90.8           | ER                    |
| <i>Eutrema salsugineum</i>  | Thhalv10015521m          | III   | GPAT7                             | 93.2           | ER                    |
| <i>Eutrema salsugineum</i>  | Thhalv10013846m.g        | I     | GPAT9                             | 97.9           | ER                    |
| <i>Eutrema salsugineum</i>  | Thhalv10007540m.g        | II    | Soluble GPAT                      | 91.3           | Chloroplast           |
| <i>Cucumis sativus</i>      | Cucsa.099550             | I     | GPAT9                             | 90.7           | ER                    |
| <i>Cucumis sativus</i>      | Cucsa.185470             | III   | GPAT1                             | 72.6           | Mitochondria          |
| <i>Cucumis sativus</i>      | Cucsa.339200             | III   | GPAT6                             | 67.7           | ER                    |
| <i>Cucumis sativus</i>      | Cucsa.176200             | III   | GPAT6                             | 85.1           | ER                    |
| <i>Cucumis sativus</i>      | Cucsa.165180             | III   | GPAT5                             | 77.2           | ER                    |
| <i>Cucumis sativus</i>      | Cucsa.135570             | III   | GPAT4                             | 84.8           | ER                    |
| <i>Cucumis sativus</i>      | Cucsa.204890             | III   | GPAT2                             | 64.9           | Mitochondria          |
| <i>Cucumis sativus</i>      | Cucsa.312830             | II    | Soluble GPAT                      | 72.6           | Chloroplast           |
| <i>Glycine max</i>          | Glyma.14G028300          | III   | GPAT1                             | 78.0           | Mitochondria          |
| <i>Glycine max</i>          | Glyma.02G286500          | III   | GPAT1                             | 75.5           | Mitochondria          |
| <i>Glycine max</i>          | Glyma.18G107100          | III   | GPAT1                             | 73.8           | Mitochondria          |
| <i>Glycine max</i>          | Glyma.08G309200          | III   | GPAT1                             | 72.2           | Mitochondria          |
| <i>Glycine max</i>          | Glyma.14G167300          | III   | GPAT2                             | 66.3           | Mitochondria          |
| <i>Glycine max</i>          | Glyma.13G085700          | III   | GPAT2                             | 66.8           | Mitochondria          |

| Species                          | Protein Accession Number | Clade | The more similar Arabidopsis gene | Similarity (%) | Cellular localization |
|----------------------------------|--------------------------|-------|-----------------------------------|----------------|-----------------------|
| <i>Glycine max</i>               | Glyma.03G221100          | III   | GPAT2                             | 70.3           | Mitochondria          |
| <i>Glycine max</i>               | Glyma.19G218100          | III   | GPAT2                             | 69.8           | Mitochondria          |
| <i>Glycine max</i>               | Glyma.02G010600          | III   | GPAT2                             | 67.2           | Mitochondria          |
| <i>Glycine max</i>               | Glyma.07G146800          | III   | GPAT6                             | 88.1           | ER                    |
| <i>Glycine max</i>               | Glyma.14G167400          | III   | GPAT2                             | 68.6           | Mitochondria          |
| <i>Glycine max</i>               | Glyma.03G221300          | III   | GPAT2                             | 74.7           | Mitochondria          |
| <i>Glycine max</i>               | Glyma.10G011000.         | III   | GPAT2                             | 67.6           | Mitochondria          |
| <i>Glycine max</i>               | Glyma.18G197800          | III   | GPAT6                             | 81.1           | ER                    |
| <i>Glycine max</i>               | Glyma.01G113200          | III   | GPAT6                             | 88.2           | ER                    |
| <i>Glycine max</i>               | Glyma.03G078600          | III   | GPAT6                             | 84.7           | ER                    |
| <i>Glycine max</i>               | Glyma.20G070400          | III   | GPAT6                             | 71.1           | ER                    |
| <i>Glycine max</i>               | Glyma.10G119900          | III   | GPAT6                             | 71.7           | ER                    |
| <i>Glycine max</i>               | Glyma.02G249300          | III   | GPAT5                             | 81.1           | ER                    |
| <i>Glycine max</i>               | Glyma.03G008300          | III   | GPAT8                             | 86.2           | ER                    |
| <i>Glycine max</i>               | Glyma.07G069700          | III   | GPAT8                             | 87.4           | ER                    |
| <i>Glycine max</i>               | Glyma.14G067200          | III   | GPAT5                             | 78.4           | ER                    |
| <i>Glycine max</i>               | Glyma.06G255600          | III   | GPAT6                             | 79.5           | ER                    |
| <i>Glycine max</i>               | Glyma.09G119200          | I     | GPAT9                             | 92.3           | ER                    |
| <i>Glycine max</i>               | Glyma.08G085800          | I     | GPAT9                             | 92.0           | ER                    |
| <i>Glycine max</i>               | Glyma.05G131100          | I     | GPAT9                             | 91.7           | ER                    |
| <i>Glycine max</i>               | Glyma.01G014200          | II    | Soluble GPAT                      | 69.0           | Chloroplast           |
| <i>Glycine max</i>               | Glyma.09G207900          | II    | Soluble GPAT                      | 65.7           | Chloroplast           |
| <i>Medicago truncatula</i>       | Medtr4g127910            | I     | GPAT9                             | 91.0           | ER                    |
| <i>Medicago truncatula</i>       | Medtr2g438210            | I     | GPAT9                             | 88.7           | ER                    |
| <i>Medicago truncatula</i>       | Medtr5g091660            | III   | GPAT1                             | 66.6           | Mitochondria          |
| <i>Medicago truncatula</i>       | Medtr3g448430            | III   | GPAT1                             | 66.3           | Mitochondria          |
| <i>Medicago truncatula</i>       | Medtr5g061520            | III   | GPAT2                             | 67.5           | Mitochondria          |
| <i>Medicago truncatula</i>       | Medtr4g415290            | III   | GPAT6                             | 89.5           | ER                    |
| <i>Medicago truncatula</i>       | Medtr7g067380            | III   | GPAT6                             | 87.6           | ER                    |
| <i>Medicago truncatula</i>       | Medtr1g040500            | III   | GPAT6                             | 62.3           | ER                    |
| <i>Medicago truncatula</i>       | Medtr8g030620            | III   | GPAT8                             | 87.3           | ER                    |
| <i>Medicago truncatula</i>       | Medtr1g086650            | III   | GPAT2                             | 70.1           | Mitochondria          |
| <i>Medicago truncatula</i>       | Medtr5g080360            | III   | GPAT5                             | 77.1           | ER                    |
| <i>Medicago truncatula</i>       | Medtr5g029230            | II    | Soluble GPAT                      | 68.7           | Chloroplast           |
| <i>Phaseolus vulgaris</i>        | Phvul.006G033100         | III   | GPAT1                             | 77.6           | Mitochondria          |
| <i>Phaseolus vulgaris</i>        | Phvul.008G191600         | III   | GPAT1                             | 79.4           | Mitochondria          |
| <i>Phaseolus vulgaris</i>        | Phvul.008G169500         | III   | GPAT2                             | 71.7           | Mitochondria          |
| <i>Phaseolus vulgaris</i>        | Phvul.008G106700         | III   | GPAT6                             | 88.9           | ER                    |
| <i>Phaseolus vulgaris</i>        | Phvul.008G169400         | III   | GPAT2                             | 68.3           | Mitochondria          |
| <i>Phaseolus vulgaris</i>        | Phvul.007G233600         | III   | GPAT6                             | 71.9           | ER                    |
| <i>Phaseolus vulgaris</i>        | Phvul.007G212600         | III   | GPAT2                             | 75.7           | Mitochondria          |
| <i>Phaseolus vulgaris</i>        | Phvul.010G099700         | III   | GPAT4                             | 89.4           | ER                    |
| <i>Phaseolus vulgaris</i>        | Phvul.L005200            | III   | GPAT6                             | 87.2           | ER                    |
| <i>Phaseolus vulgaris</i>        | Phvul.003G022900         | I     | GPAT9                             | 92.6           | ER                    |
| <i>Phaseolus vulgaris</i>        | Phvul.002G191600         | I     | GPAT9                             | 92.3           | ER                    |
| <i>Phaseolus vulgaris</i>        | Phvul.002G136600         | II    | Soluble GPAT                      | 67.0           | Chloroplast           |
| <i>Chlamydomonas reinhardtii</i> | Cre06.g273250            | I     | GPAT9                             | 57.0           | ER                    |
| <i>Chlamydomonas reinhardtii</i> | Cre02.g143000            | II    | Soluble GPAT                      | 53.2           | Chloroplast           |
| <i>Volvox carteri</i>            | Vocar.0002s0353          | I     | GPAT9                             | 57.9           | ER                    |
| <i>Volvox carteri</i>            | Vocar.0054s0035          | II    | Soluble GPAT                      | 54.9           | Chloroplast           |
| <i>Coccomyxa subellipsoidea</i>  | 4945                     | I     | GPAT9                             | 71.2           | ER                    |
| <i>Coccomyxa subellipsoidea</i>  | 31435                    | II    | Soluble GPAT                      | 51.7           | Chloroplast           |
| <i>Micromonas pusilla</i>        | 36845                    | I     | GPAT9                             | 72.0           | ER                    |
| <i>Micromonas pusilla</i>        | 158788                   | II    | Soluble GPAT                      | 39.6           | Chloroplast           |
| <i>Micromonas sp.</i>            | 94289                    | I     | GPAT9                             | 64.3           | ER                    |
| <i>Micromonas sp.</i>            | 106290                   | II    | Soluble GPAT                      | 46.7           | Chloroplast           |



| <b>Species</b>                  | <b>Protein Accession Number</b> | <b>Clade</b> | <b>The more similar Arabidopsis gene</b> | <b>Similarity (%)</b> | <b>Cellular localization</b> |
|---------------------------------|---------------------------------|--------------|--|-----------------------|------------------------------|
| <i>Ostreococcus lucimarinus</i> | 51690                           | I            | GPAT9                                    | 63.7                  | ER                           |
| <i>Ostreococcus lucimarinus</i> | 30035                           | II           | Soluble GPAT                             | 48.5                  | Chloroplast                  |
| <i>Ostreococcus lucimarinus</i> | 119500                          | II           | Soluble GPAT                             | 48.5                  | Chloroplast                  |

ER: Endoplasmic reticulum