|  |
| --- |
| **Table S1.** Primer sequences of target genes used in qRT-PCR analysis for verification of microarray data of genes highly-expressed in giant leucaena foliage versus root. |
| **Accession no.** | **Gene** | **Forward primer (5' → 3')** | **Reverse Primer (5' → 3')** |
| GDSA01054472 | ABC transporter G family  | AGTGGCAAGCATTGTCCCTAACTTCCTCA | GCAATCTGAAGAAGCCTCCTGCAAGGATCA |
| GDSA01148410 | Aldehyde dehydrogenase | TTCACAGGAAGTGCCCGGGTGGGACGTATT  | AGCAGGGCATTTCCCACCCAACTCCAAAGT |
| GDSA01236003 | Auxin transporter WAT1 | AGGCTTCTTACAGTGGCCTATGCGGGAAT | AAGAGGGCCTTTCATGTTCACGCACCATGT |
| GDSA01169979 | GDSL esterase/lipase | AGCTGAGGCATATGGGTTGCCGTATTTGT | TGTAGCTCCAGCCACTGCGAAATTCACC |
| GDSA01167380 | Leaf lectin II sGSII | TCCGTTGATGACCCTGATTCGCTGGCAAAG | TGCCGTCTAAGGCCACAGCTCCAAGA  |
| GDSA01161960 | Lipoxygenase | AGGACGAGCCTTGGTGGCCGGTTCTT | TTAACCGCCGCGTGGTGACCCGACGTTATC |
| GDSA01236287 | Long chain acyl-CoA synthetase 1 | GGGCAGCCTTGAGCAGTGAAGTCGAAGAA | TCAGCGTAGTGCACCCACATGTTTCAGTCA |
| GDSA01168382 | Mimosinase | GAAAGGCAGGAATCACAGTGAAGAG | GGAGACTCTAGCCACACCAACTTA |
| GDSA01173290 | Oxidoreductase protein HOTHEAD | GGCGAGAACTTCGCCGGTGGTTCTCCCAAA  | TTCCGACGTCCTCTGCTTCGGCGGAAGTTT |
| GDSA01213396 | Transmembrane protein UPF0481 | TGGGAGAGAATTATGCACGTAGTGGCTTCC | AGATGCTATTCTCCAGGGAGTGCTCCAGTA |
| GDSA01234114 | UDP-glycosyltransferase | TGAGGACGATGCCCTTTGAGCTTGAGAA | ATGCCATGTTCACATCTGCCACCACAC |
| GDSA01170676 | Vinorine synthase | TCGTCGAAACCGTCCTAGGTGTCCAATTCA | TAAGACAGCGCGTCGCCAACCTTGT |
| GDSA01233524 | Xyloglucan endotransglucosylase/hydrolase 6 | TTCCGACTGTACCTCGGACCCAACAAACT | ACGAACCCACCTGTACCTTCTCGCTTCT |
| GDSA01182796 | β-amyrin synthase | AGTGGCTAGAAGTGCTAAATCC | CTAGAGCCTGTATTGCTGATCC  |

**Table S-2.** Gene sequences that are highly expressed in giant leucaena foliage compared to the root.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Accession no. | Fold change  | P-value | Gene  |  Blast hit acc no. |
| GDRZ01156473 | 131.3 | 0.031726536 | 40S ribosomal protein S3-1 | KYP74033.1 |
| GDSA01236003 | 121.8 | 0.014077216 | Auxin transporter WAT1-related protein | XP\_006585457.1 |
| GDSA01213396 | 107.3 | 0.024704878 | Transmembrane protein UPF0481 | XP\_016646954.1 |
| GDSA01158382 | 97.1 | 0.014946603 | NAD-dependent aldehyde dehydrogenase family protein | XP\_013456185.1 |
| GDSA01169979 | 93.1 | 0.020034870 | GDSL esterase/lipase | XP\_019440215.1 |
| GDRZ01156568 | 92.5 | 0.032974041 | Cytochrome P450 | XP\_010092134.1 |
| GDSA01183641 | 82.2 | 0.028019403 | Caffeoylshikimate esterase-like | XP\_017439323.1 |
| GDSA01189889 | 74.8 | 0.021575057 | S-norcoclaurine synthase 2 | XP\_016193223.1 |
| GDSA01105057 | 73.9 | 0.023653943 | Chlorophyll a-b binding protein 1D | XP\_009609717.2 |
| GDSA01144134 | 65.4 | 0.040203571 | Axial regulator YABBY 5 | KYP55712.1 |
| GDSA01148410 | 56.4 | 0.029012959 | Aldehyde dehydrogenase family 3 member F1-like | XP\_004486968.1 |
| GDSA01182796 | 54.7 | 0.018767897 | β-amyrin synthase | ADE88148.1 |
| GDSA01234114 | 54.4 | 0.060978367 | UDP-glycosyltransferase | XP\_020219978.1 |
| GDSA01235589 | 51.7 | 0.014705280 | GDSL esterase/lipase | KHN18937.1 |
| GDSA01175641 | 51.4 | 0.017628555 | Pentatricopeptide repeat-containing protein | XP\_017413921.1 |
| GDSA01234291 | 46.8 | 0.003438241 | UDP-glycosyltransferase | XP\_019429574.1 |
| GDSA01216251 | 46.0 | 0.016729440 | Protein sieve element occlusion B-like | XP\_016173306.1 |
| GDSA01148623 | 43.4 | 0.016697118 | GDSL esterase/lipase | KHN14076.1 |
| GDSA01235664 | 35.5 | 0.020730218 | Hyp1 | XP\_007161534.1 |
| GDSA01167380 | 34.1 | 0.017064767 | Leaf lectin II sGSII | AAB82745.1 |
| GDSA01161196 | 31.7 | 0.020309245 | Polyol transporter 5 | KYP64906.1 |
| GDSA01161960 | 30.7 | 0.024075870 | Lipoxygenase | BAB84352.1 |
| GDSA01202363 | 28.5 | 6.82850E-05 | Hyp2 | OMO84346.1 |
| GDSA01173290 | 27.1 | 0.027380893 | Oxidoreductase protein HOTHEAD | KHN14126.1 |
| GDSA01208592 | 25.0 | 0.027803025 | PHD finger protein ALFIN-like 7-like isoform X1 | XP\_006470803.1 |
| GDSA01180243 | 24.4 | 0.001419713 | Zinc–finger homeobox domain protein 6 | XP\_021274153.1 |
| GDSA01202054 | 23.8 | 0.016274935 | GDSL esterase/lipase | XP\_018832078.1 |
| GDSA01210192 | 20.5 | 0.028704741 | Photosynthetic NDH subunit of luminal location 2, chloroplastic-like | XP\_019459581.1 |
| GDSA01233524 | 20.3 | 0.027795655 | Xyloglucan endotransglucosylase/hydrolase protein 6 | KHN36328.1 |
| GDSA01236287 | 19.6 | 0.016441591 | Long chain acyl-CoA synthetase 1 | XP\_019441273.1 |
| GDSA01159196 | 19.4 | 0.015945098 | Hyp3 | XP\_007136249.1 |
| GDSA01203183 | 19.0 | 0.003260194 | Hyp-N 1 | - |
| GDSA01235002 | 18.9 | 0.022499018 | Long-chain-alcohol oxidase FAO4A | XP\_015963133.1 |
| GDSA01222594 | 18.1 | 0.021590344 | Golgin subfamily A member 6-like protein 1  | XP\_016183454.1 |
| GDSA01200937 | 16.7 | 0.000284476 | Chloroplast import apparatus 2 isoform X2 | XP\_010656744.1 |
| GDSA01147873 | 16.2 | 0.023748172 | Abscisic acid 8'-hydroxylase 2 isoform X1 | XP\_019420664.1 |
| GDSA01170676 | 16.2 | 0.026874665 | Vinorine synthase-like | XP\_003538872.1 |
| GDSA01217062 | 16.1 | 0.013715461 | Oxidoreductase protein HOTHEAD-like | KHN15686.1 |
| GDSA01140408 | 16.0 | 0.006529756 | Hyp-N2 | - |
| GDRZ01156632 | 15.8 | 0.249630426 | Katanin p60 ATPase-containing subunit A1-like isoform X2 | XP\_015869493.1 |
| GDSA01167031 | 15.3 | 0.019008396 | ER glycerol-3-phosphate acyltransferase | EEF31034.1 |
| GDSA01217884 | 15.0 | 0.021559614 | BTB/POZ domain-containing protein | XP\_019421015.1 |
| GDSA01145835 | 14.9 | 0.018598287 | Hyp-N3 | - |
| GDSA01185590 | 14.7 | 0.021167167 | Fructose-1,6-bisphosphatase, chloroplastic | NP\_001238269.2 |
| GDSA01210839 | 14.5 | 0.006785621 | Chitinase  | XP\_013463477.1 |
| GDRZ01156652 | 14.1 | 0.003343524 | Dehydration-induced protein 19 homolog 5-like isoform X2 | XP\_020212459.1 |
| GDSA01200779 | 13.7 | 0.020173372 | Rhomboid-like protein 9, chloroplastic isoform X1  | XP\_019088808.1 |
| GDRZ01103799 | 13.7 | 0.027288370 | Glucose-1-phosphate adenylyltransferase large subunit 3, chloroplastic/amyloplatic isoform X1 | XP\_015941335.1 |
| GDSA01235414 | 13.0 | 0.011658194 | Mannan endo-1,4-beta-mannosidase 1 | KHN43366.1 |
| GDSA01121806 | 12.5 | 0.000442470 | WRKY transcription factor 14 | KYP47933.1 |
| GDSA01054472 | 12.3 | 0.025111590 | ABC transporter G family member 2-like | XP\_017415706.1 |
| GDSA01217973 | 12.2 | 0.008946004 | Zinc-finger homeodomain protein 2-like | XP\_011010389.1 |
| GDRZ01157225 | 12.2 | 0.021957598 | Neutral invertase isoform 2 | EOY06816.1 |
| GDSA01195932 | 12.2 | 0.001457470 | Adenylate isopentenyltransferase 3, chloroplastic-like | XP\_019426932.1 |
| GDSA01232321 | 11.9 | 0.016029674 | Hyp-N4 | - |
| GDSA01224856 | 11.6 | 0.037032673 | NADPH-dependent 6'-deoxychalcone synthase-like | XP\_020219411.1 |
| GDSA01117917 | 11.5 | 0.040771493 | Receptor-like protein kinase | XP\_004498297.1 |
| GDSA01234520 | 11.4 | 0.040142277 | Trihelix transcription factor GT-2 | KHN00764.1 |
| GDRZ01213094 | 11.1 | 0.019733693 | Oxygen-evolving enhancer protein 1, chloroplatic | XP\_019424234.1 |
| GDSA01141022 | 10.7 | 0.003287311 | G-type lectin S-receptor-like serine/threonine-protein kinase | XP\_020201912.1 |
| GDRZ01108853 | 10.6 | 0.011602874 | Vicianin hydrolase | XP\_002512142.1 |
| GDSA01192237 | 10.5 | 0.000146230 | Fructose-bisphosphate aldolase, chloroplastic | XP\_020972792.1 |
| GDSA01226325 | 10.2 | 0.003804561 | 3S,6E-nerolidol synthase 1-like | XP\_020238817.1 |
| GDRZ01212177 | 10.0 | 0.000629203 | Ankyrin repeat-containing protein NPR4-like | XP\_020221095.1 |
| GDSA01199781 | 10.0 | 0.021227316 | Hyp4 | GAU15042.1 |
| GDSA01188869 | 9.8 | 0.004663689 | Beta-1,3-glucanase  | BAE53384.1 |
| GDSA01000399 | 9.5 | 0.009315316 | Hyp-N5 | - |
| GDSA01184548 | 9.3 | 0.018422002 | UDP-glycosyltransferase | XP\_003549170.1 |
| GDSA01227549 | 9.2 | 0.032441396 | LRR receptor-like protein kinase | XP\_020230734.1 |
| GDSA01229274 | 9.2 | 0.026420192 | Hyp-N6 | - |
| GDSA01148484 | 9.2 | 0.007298933 | Protodermal factor 1  | XP\_012084370.1 |
| GDSA01216510 | 9.2 | 0.016299765 | Photosystem II 10 kDa polypeptide, chloroplastic | XP\_015888354.1 |
| GDSA01177009 | 9.0 | 0.013452357 | Peroxidase 15 | KHN14344.1 |
| GDSA01184953 | 8.7 | 0.013238045 | Serine/threonine protein kinase | XM\_019373967.1 |
| GDSA01227726 | 8.4 | 0.031225782 | Peptidyl-prolyl cis-trans isomerase FKBP17-2, chloroplastic | XP\_021909102.1 |
| GDSA01193912 | 8.4 | 0.024674540 | Sulfate transporter 1.3 isoform X2 | XP\_019430824.1 |
| GDRZ01106942 | 8.4 | 0.016920734 | Alpha-1, 4 glucan phosphorylase L-2 isozyme chloroplastic/amyloplastic-like Isofomr X2  | XP\_004505374.1 |
| GDSA01185736 | 8.3 | 0.032978538 | Carboxylesterase 17 | XP\_003551853.1 |
| GDSA01182238 | 8.1 | 0.027238394 | Photosynthetic NDH subunit of subcomplex B 1, chloroplastic | XP\_015947205.1 |
| GDSA01146543 | 8.0 | 0.006686981 | Cysteine protease | BAC77521.1 |
| GDRZ01209068 | 8.0 | 0.008961573 | Cyclopropane-fatty-acyl-phospholipid synthase | XP\_013468649.1 |
| GDSA01226522 | 8.0 | 0.005703044 | NRT1/PTR family | KHN18517.1 |
| GDSA01167101 | 8.0 | 0.045673067 | Amino acid permease 2 | KHN25477.1 |
| GDSA01184071 | 7.9 | 0.001811435 | GDSL esterase/lipase | XP\_020240415.1 |
| GDSA01199832 | 7.9 | 0.024899825 | Crocetin glucosyltransferase, chloroplastic-like | XP\_003552552.1 |
| GDSA01154492 | 7.9 | 0.016397333 | NRT1/PTR 5.1 family | XP\_014520517.1 |
| GDSA01205386 | 7.9 | 0.025030708 | NADPH-quinone oxidoreductase U, chloroplastic | XP\_010049275.1 |
| GDSA01234388 | 7.7 | 0.026904179 | Cellulose synthase-like protein B1 | APR64071.1 |
| GDSA01147825 | 7.7 | 0.008045204 | Cellulose synthase-like protein H1 isoform  | XP\_017433640.1 |
| GDSA01221660 | 7.6 | 0.001153216 | Zinc-binding alcohol dehydrogenase family protein | XP\_013453840.1 |
| GDSA01149975 | 7.6 | 0.015921446 | Salicylate O-methyltransferase | KHN22769.1 |
| GDSA01175596 | 7.5 | 0.022246902 | Universal stress protein A-like protein | XP\_015968899.1 |
| GDSA01157452 | 7.4 | 0.020025238 | Ferredoxin-plastoquinone reductase PGR5-like protein, chloroplastic | XP\_012835498.1 |
| GDSA01200126 | 7.2 | 0.020262057 | G-type lectin S-receptor-like serine/threonine kinase | XP\_003608282.1 |
| GDSA01151357 | 7.1 | 0.004740461 | Nerol synthase | AGV54642.1 |
| GDSA01189762 | 7.1 | 0.028853525 | Transcription factor bHLH84  | KHN36961.1 |
| GDSA01219259 | 7.1 | 0.040494898 | Auxin transporter-like protein 3 | KYP36581.1 |
| GDSA01224375 | 6.9 | 0.019994725 | IRK-interacting protein  | XP\_021810347.1 |
| GDRZ01101502 | 6.9 | 0.005054311 | BTB/POZ domain-containing protein | XP\_019421018.1 |
| GDSA01171798 | 6.7 | 0.021076022 | Photosystem II subunit psbP-like protein chloroplastic | XP\_003552675.1 |
| GDRZ01148350 | 6.7 | 0.023162646 | Salicylate O-carboxymethyltransferase  | KHN22769.1 |
| GDSA01230640 | 6.7 | 0.011747346 | Auxin-binding protein ABP19a-like | XP\_019417162.1 |
| GDSA01174270 | 6.7 | 0.019641897 | S-adenosyl-L-methionine-dependent methyltransferase superfamily | NP\_001235165.2 |
| GDSA01145511 | 6.6 | 0.015161486 | Lipoxygenase 3, chloroplastic | XP\_015943087.2 |
| GDSA01208937 | 6.5 | 0.036525524 | Protein TSS tetratricoeptide repeat | XP\_003522940.1 |
| GDRZ01102371 | 6.5 | 0.031955294 | Myb-related transcription factor  | AGN52053.1 |
| GDSA01206650 | 6.5 | 0.024266808 | CLP protease regulatory subunit CLPX1 | XP\_020412043.1 |
| GDSA01186397 | 6.4 | 0.011481921 | Vicianin hydrolase | XP\_016170175.1 |
| GDSA01209353 | 6.4 | 0.004034736 | Transcription factor TCP-l3-like | XP\_003552583.1 |
| GDSA01231055 | 6.4 | 0.017814622 | (3S,6E)-nerolidol synthase 1-like | XP\_003528418.1 |
| GDSA01218014 | 6.3 | 0.016220498 | Protein curvature thylakoid1A, chloroplastic | XP\_004953819.1 |
| GDSA01221996 | 6.3 | 0.073524800 | Hyp5 | XP\_020978931.1 |
| GDSA01220639 | 6.1 | 0.001538930 | Oxidoreductase protein HOTHEAD | KHN15686.1 |
| GDSA01209168 | 6.1 | 0.034091541 | Linoleate 9S-lipoxygenase 5 | XP\_020211492.1 |
| GDSA01205461 | 6.1 | 0.046488898 | Hyp6 | XP\_007156800.1 |
| GDSA01177790 | 6.1 | 0.011563580 | Tetraspanin-8-like | XP\_021890645.1 |
| GDSA01178938 | 6.0 | 0.002354074 | Zinc finger protein CONSTANS-like 16-like isoform X1 | XP\_019426713.1 |
| GDSA01168382 | 6.0 | 0.016776566 | Mimosinase | BAF80449.1 |
| GDRZ01156901 | 6.0 | 0.022579950 | Hyp-N7 | - |
| GDSA01231064 | 5.9 | 0.004785883 | Trihelix transcription factor GTL2-like | XP\_015875344.1 |
| GDSA01235498 | 5.9 | 0.018826357 | Squamosa promoter-binding-like protein 13A | XP\_019464709.1 |
| GDRZ01207925 | 5.9 | 0.020407992 | Alpha-1,4-glucan phosphorylase L-2 isozyme chloroplastic/amyloplastic | KHN20530.1 |
| GDRZ01016369 | 5.9 | 0.021610147 | Calcium-permeabel cation channel CSC1-like protein | XP\_017603599.1 |
| GDSA01206259 | 5.9 | 0.000633965 | MLP protein 28, defense-related | XP\_022155376.1 |
| GDSA01130708 | 5.8 | 0.034667392 | Myb/SANT-like DNA-binding domain protein | XP\_003628341.2 |
| GDSA01208585 | 5.7 | 0.018063346 | Long-chain-alcohol oxidase FAO4A-like | XP\_003534338.2 |
| GDSA01198323 | 5.7 | 0.036718005 | Phospholipase A1-IIdelta | XP\_004505480.2 |
| GDSA01230030 | 5.6 | 0.025341910 | UDP galactose/UDP glucose transporter 2-like | XP\_003552365.1 |
| GDRZ01157095 | 5.6 | 0.013133558 | Hyp7 | EEF48199.1 |
| GDSA01143728 | 5.5 | 0.029779790 | 7-deoxyloganentin glucosyltransferase-like | XP\_006603934.1 |
| GDSA01207952 | 5.3 | 0.002329332 | Omega-hydroxypalmitate O-feruloyl transferase | XP\_004493124.1 |
| GDSA01144775 | 5.3 | 0.039790488 | Rust resistance kinase Lr10 | XP\_015934465.1 |
| GDSA01187783 | 5.3 | 0.018019679 | Serine carboxypeptidase-like 18 isoform X2 | XP\_020986941.1 |
| GDSA01218807 | 5.2 | 0.003192109 | UDP-glycosyltransferase | XP\_019427015.1 |
| GDRZ01108186 | 5.2 | 0.027832848 | Photosystem I subunit O | XP\_015936067.1 |
| GDSA01172374 | 5.2 | 0.040848313 | Acyltransferase | KHN18660.1 |
| GDSA01147380 | 5.1 | 0.016289958 | Hyp-N8 | - |
| GDRZ01105958 | 5.0 | 0.010033246 | Ankyrin-2 | KYP40681.1 |

**Table S-3**. Gene sequences analyzed by qRT-PCR that showed >2-fold upregulation in the leaves, green stem, and embryonic leaf compared to the root in giant leucaena.

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| --- | --- | --- | --- |
|  |  | **qRT-PCR fold change** | **Microarray** **fold change** |
| **NCBI sequence accession no.** | **Gene function** | **Leaflet** | **Stem** | **Embryonic leaf** | **Shoot** |
| GDSA01054472 | ABC transporter G | 37.5 | 4.6 | 5.0 | 12.4 |
| GDSA01148410 | Aldehyde dehydrogenase | 20.8 | 10.5 | 9.9 | 55.8 |
| GDSA01236003 | Auxin transporter WAT1 | 8.3 | 3.5 | 1.8 | 121.1 |
| GDSA01182796 | β-amyrin synthase  | 152.3 | 56.1 | 13.5 | 54.3 |
| GDSA01169979 | GDSL esterase/lipase | 37.7 | 6.7 | 2.5 | 92.3 |
| GDSA01167380 | Leaf lectin II sGSII | 2.5 | 4.3 | 1.4 | 34.2 |
| GDSA01161960 | Lipoxygenase  | 37.2 | 23.0 | 4.1 | 30.8 |
| GDSA01236287 | Long chain acyl-CoA synthetase | 316.0 | 83.3 | 14.7 | 19.7 |
| GDSA01213396 | Transmembrane protein UPF0481 | 27.9 | 14.4 | 7.4 | 107.48 |
| AB298597 | Mimosinase | 158.4 | 20.0 | 194.0 | 6.1 |
| GDSA01173290 | Oxidoreductase protein HOTHEAD | 18.2 | 5.9 | 6.7 | 27.2 |
| GDSA01170676 | Vinorine synthase | 1.4 | 0.5 | 0.2 | 16.3 |
| GDSA01234114 | UDP-glycosyltransferase  | 51.9 | 5.6 | 5.9 | 53.7 |
| GDSA01233524 | Xyloglucan endotransglucosylase/hydrolase  | 22.6 | 7.5 | 2.5 | 20.4 |
|  |  |  |  |  |  |