Table2 Photosynthesis related genes in KEGG pathway analyses

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| Gene\_ID | KO\_ENTRY | Description | log2(fc) | regulation |
| Ghir\_A01G001730 | K08902 | PREDICTED: photosystem II repair protein PSB27-H1, chloroplastic-like [Gossypium arboreum] | -6.78 | down |
| Ghir\_A01G003530 | K02113 | PREDICTED: ATP synthase subunit delta, chloroplastic-like [Gossypium hirsutum] | -3.40 | down |
| Ghir\_A01G013120 | K02110 | hypothetical protein Lo\_he\_he1Pt0180 (plastid) [Lobelia heterophylla subsp. heterophylla] | -4.68 | down |
| Ghir\_A01G015030 | K02723 | PREDICTED: photosystem II core complex proteins psbY, chloroplastic-like [Gossypium hirsutum] | -5.64 | down |
| Ghir\_A01G018230 | K03542 | PREDICTED: photosystem II 22 kDa protein, chloroplastic-like [Gossypium hirsutum] | -8.55 | down |
| Ghir\_A02G003190 | K02692 | PREDICTED: photosystem I reaction center subunit II, chloroplastic-like [Gossypium arboreum] | -6.41 | down |
| Ghir\_A02G015490 | K02111 | PREDICTED: uncharacterized protein LOC107887112 [Gossypium hirsutum] | -1.87 | down |
| Ghir\_A03G017800 | K02636 | PREDICTED: cytochrome b6-f complex iron-sulfur subunit, chloroplastic-like [Gossypium raimondii];PREDICTED: cytochrome b6-f complex iron-sulfur subunit, chloroplastic-like isoform X2 [Gossypium hirsutum];PREDICTED: cytochrome b6-f complex iron-sulfur subunit, chloroplastic-like [Gossypium arboreum] | -3.61 | down |
| Ghir\_A03G017810 | K02636 | PREDICTED: cytochrome b6-f complex iron-sulfur subunit, chloroplastic-like isoform X2 [Gossypium hirsutum] | -3.23 | down |
| Ghir\_A03G021120 | K02639 | PREDICTED: ferredoxin-like [Gossypium raimondii] | -8.02 | down |
| Ghir\_A03G021130 | K02639 | PREDICTED: ferredoxin-1-like [Gossypium hirsutum] | -6.10 | down |
| Ghir\_A03G023470 | K02698 | PREDICTED: photosystem I reaction center subunit psaK, chloroplastic-like [Gossypium hirsutum] | -6.72 | down |
| Ghir\_A04G000200 | K08905 | PREDICTED: photosystem I reaction center subunit V, chloroplastic-like [Gossypium hirsutum] | -9.20 | down |
| Ghir\_A04G004030 | K02703 | photosystem II protein D1 [Nicotiana tabacum] | -1.06 | down |
| Ghir\_A04G005210 | K03541 | PREDICTED: photosystem II 10 kDa polypeptide, chloroplastic-like [Gossypium hirsutum] | -6.00 | down |
| Ghir\_A04G014510 | K02108 | ATP synthase CF0 subunit IV (chloroplast) [Gossypium turneri] | -2.29 | down |
| Ghir\_A05G008230 | K14332 | hypothetical protein GOBAR\_AA23210 [Gossypium barbadense] | -5.20 | down |
| Ghir\_A05G013330 | K02695 | PREDICTED: photosystem I reaction center subunit VI, chloroplastic-like [Gossypium hirsutum] | -6.18 | down |
| Ghir\_A05G014780 | K02694 | Photosystem I reaction center subunit III, chloroplastic -like protein [Gossypium arboreum] | -5.64 | down |
| Ghir\_A05G018640 | K02638 | PREDICTED: hippocampus abundant transcript-like protein 1 isoform X2 [Gossypium hirsutum] | -6.81 | down |
| Ghir\_A05G018990 | K02641 | PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Gossypium raimondii];hypothetical protein B456\_009G194200 [Gossypium raimondii] | -7.51 | down |
| Ghir\_A05G024010 | K03542 | PREDICTED: photosystem II 22 kDa protein, chloroplastic-like [Gossypium hirsutum] | -8.33 | down |
| Ghir\_A05G030750 | K02717 | PREDICTED: psbP-like protein 1, chloroplastic [Gossypium hirsutum] | -4.22 | down |
| Ghir\_A05G032480 | K02109 | ATP synthase CF0 subunit I (plastid) [Gossypium laxum] | -3.11 | down |
| Ghir\_A05G036510 | K02717 | PREDICTED: photosynthetic NDH subunit of lumenal location 1, chloroplastic-like [Gossypium hirsutum] | -6.34 | down |
| Ghir\_A05G039300 | K02717 | PREDICTED: oxygen-evolving enhancer protein 2, chloroplastic-like [Gossypium hirsutum] | -7.33 | down |
| Ghir\_A05G039690 | K02701 | PREDICTED: probable polygalacturonase isoform X1 [Gossypium hirsutum] | -4.95 | down |
| Ghir\_A06G012890 | K02689 | 'photosystem I P700 apoprotein A1 (chloroplast) [Vicia sativa] | -3.23 | down |
| Ghir\_A06G012950 | K08901 | PREDICTED: oxygen-evolving enhancer protein 3, chloroplastic-like [Gossypium hirsutum] | -5.81 | down |
| Ghir\_A06G015110 | K02694 | Photosystem I reaction center subunit III, chloroplastic -like protein [Gossypium arboreum] | -2.66 | down |
| Ghir\_A06G015290 | K08906 | PREDICTED: cytochrome c6, chloroplastic-like [Gossypium hirsutum] | 1.48 | up |
| Ghir\_A06G016010 | K02115 | PREDICTED: ATP synthase gamma chain, chloroplastic-like [Gossypium hirsutum] | -3.59 | down |
| Ghir\_A07G003360 | K02109 | PREDICTED: uncharacterized protein LOC105803296 [Gossypium raimondii] | -4.58 | down |
| Ghir\_A07G009770 | K02699 | PREDICTED: photosystem I reaction center subunit XI, chloroplastic-like [Gossypium hirsutum] | -6.65 | down |
| Ghir\_A07G011880 | K14332 | hypothetical protein GOBAR\_AA39582 [Gossypium barbadense] | -17.71 | down |
| Ghir\_A07G016270 | K08903 | PREDICTED: subtilisin-like protease SBT1.2 [Gossypium hirsutum] | -5.00 | down |
| Ghir\_A07G017220 | K02699 | PREDICTED: photosystem I reaction center subunit XI, chloroplastic-like [Gossypium hirsutum] | -6.12 | down |
| Ghir\_A07G021870 | K02693 | hypothetical protein GOBAR\_AA30483 [Gossypium barbadense] | -3.36 | down |
| Ghir\_A07G022570 | K02721 | hypothetical protein GOBAR\_AA06646 [Gossypium barbadense] | -8.17 | down |
| Ghir\_A08G005150 | K02693 | PREDICTED: photosystem I reaction center subunit IV A, chloroplastic-like [Gossypium hirsutum] | -4.74 | down |
| Ghir\_A08G007170 | K02692 | hypothetical protein B456\_004G079200 [Gossypium raimondii] | -3.38 | down |
| Ghir\_A08G019730 | K02721 | PREDICTED: photosystem II reaction center W protein, chloroplastic-like [Gossypium hirsutum] | -5.89 | down |
| Ghir\_A10G001230 | K08901 | PREDICTED: oxygen-evolving enhancer protein 3, chloroplastic-like [Gossypium hirsutum] | -9.08 | down |
| Ghir\_A10G015420 | K02717 | PREDICTED: oxygen-evolving enhancer protein 2, chloroplastic-like isoform X1 [Gossypium arboreum] | -5.59 | down |
| Ghir\_A11G010940 | K02111 | putative ATPase, F0 complex, subunit C [Helianthus annuus] | -3.47 | down |
| Ghir\_A11G013510 | K02721 | PREDICTED: photosystem II reaction center W protein, chloroplastic-like [Gossypium hirsutum] | -7.53 | down |
| Ghir\_A11G014360 | K02693 | PREDICTED: photosystem I reaction center subunit IV B, chloroplastic-like [Gossypium raimondii] | -5.45 | down |
| Ghir\_A11G015060 | K02689 | PREDICTED: uncharacterized HIT-like protein MT1300 [Gossypium hirsutum];hypothetical protein B456\_007G158200 [Gossypium raimondii] | -2.09 | down |
| Ghir\_A11G018450 | K02641 | PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic-like [Gossypium hirsutum] | -5.45 | down |
| Ghir\_A11G019900 | K02716 | PREDICTED: oxygen-evolving enhancer protein 1, chloroplastic-like [Gossypium hirsutum] | -4.66 | down |
| Ghir\_A11G023950 | K02701;K01213 | PREDICTED: probable polygalacturonase [Gossypium arboreum];PREDICTED: probable polygalacturonase [Gossypium hirsutum] | -5.42 | down |
| Ghir\_A11G023960 | K02701 | PREDICTED: photosystem I reaction center subunit N, chloroplastic-like [Gossypium hirsutum] | -9.39 | down |
| Ghir\_A11G026980 | K02721 | PREDICTED: photosystem II reaction center W protein, chloroplastic-like [Gossypium arboreum] | -6.64 | down |
| Ghir\_A12G000450 | K02692 | PREDICTED: photosystem I reaction center subunit II, chloroplastic-like [Gossypium hirsutum] | -6.49 | down |
| Ghir\_A12G002710 | K02639 | PREDICTED: ferredoxin-2-like [Gossypium hirsutum] | -3.82 | down |
| Ghir\_A12G006120 | K02641 | hypothetical protein GOBAR\_AA09832 [Gossypium barbadense] | -7.89 | down |
| Ghir\_A12G012270 | K02113 | PREDICTED: ATP synthase delta chain, chloroplastic-like [Gossypium hirsutum] | -2.53 | down |
| Ghir\_A12G014840 | K08902 | PREDICTED: photosystem II repair protein PSB27-H1, chloroplastic-like [Gossypium hirsutum] | -4.74 | down |
| Ghir\_A12G022200 | K02639 | PREDICTED: ferredoxin-1 [Gossypium arboreum] | -2.52 | down |
| Ghir\_A12G024190 | K02704 | PREDICTED: photosystem II CP47 reaction center protein [Gossypium arboreum] | -2.79 | down |
| Ghir\_A12G024200 | K02704 | PSII 47kD protein [Gossypium barbadense] | -4.04 | down |
| Ghir\_A13G003390 | K02639 | PREDICTED: ferredoxin-A-like, partial [Gossypium hirsutum] | -5.89 | down |
| Ghir\_A13G007670 | K08901 | Oxygen-evolving enhancer 3-2, chloroplastic -like protein [Gossypium arboreum] | -7.13 | down |
| Ghir\_A13G012720 | K02717 | PREDICTED: uncharacterized protein LOC107895106 isoform X1 [Gossypium hirsutum];PREDICTED: uncharacterized protein ycf37-like isoform X2 [Gossypium hirsutum] | -2.33 | down |
| Ghir\_A13G013380 | K08905 | PREDICTED: photosystem I reaction center subunit V, chloroplastic-like [Gossypium hirsutum] | -5.21 | down |
| Ghir\_A13G014830 | K08901 | PREDICTED: photosynthetic NDH subunit of lumenal location 3, chloroplastic-like isoform X1 [Gossypium hirsutum] | -8.03 | down |
| Ghir\_A13G023520 | K02639 | Ferredoxin-3, chloroplastic -like protein [Gossypium arboreum] | -3.16 | down |
| Ghir\_D01G001710 | K08902 | PREDICTED: photosystem II repair protein PSB27-H1, chloroplastic-like [Gossypium hirsutum] | -7.51 | down |
| Ghir\_D01G003550 | K02113 | PREDICTED: ATP synthase subunit delta, chloroplastic-like [Gossypium hirsutum] | -4.06 | down |
| Ghir\_D01G016880 | K02723 | PREDICTED: photosystem II core complex proteins psbY, chloroplastic [Gossypium raimondii] | -5.76 | down |
| Ghir\_D01G017480 | K02110 | hypothetical protein Lo\_he\_he1Pt0180 (plastid) [Lobelia heterophylla subsp. heterophylla] | -4.58 | down |
| Ghir\_D01G019870 | K03542 | PREDICTED: photosystem II 22 kDa protein, chloroplastic-like [Gossypium raimondii] | -9.74 | down |
| Ghir\_D02G003560 | K02692 | hypothetical protein B456\_005G042000 [Gossypium raimondii] | -2.95 | down |
| Ghir\_D02G019100 | K02636 | hypothetical protein GOBAR\_DD34630 [Gossypium barbadense] | -3.37 | down |
| Ghir\_D02G019110 | K02636 | PREDICTED: cytochrome b6-f complex iron-sulfur subunit, chloroplastic-like [Gossypium raimondii] | -2.47 | down |
| Ghir\_D02G022570 | K02639 | hypothetical protein GOBAR\_DD28024 [Gossypium barbadense] | -7.49 | down |
| Ghir\_D02G022580 | K02639 | PREDICTED: ferredoxin-1-like [Gossypium hirsutum] | -6.62 | down |
| Ghir\_D02G024880 | K02698 | PREDICTED: photosystem I reaction center subunit psaK, chloroplastic [Gossypium raimondii] | -6.34 | down |
| Ghir\_D03G008190 | K02111 | ATP synthase alpha subunit [Gossypium barbadense] | -2.86 | down |
| Ghir\_D03G008260 | K02111 | ATP synthase alpha subunit [Gossypium barbadense] | -4.70 | down |
| Ghir\_D03G008270 | K02111 | hypothetical protein GOBAR\_AA29147 [Gossypium barbadense] | -1.69 | down |
| Ghir\_D04G003410 | K02701 | photosystem I reaction center subunit N, chloroplastic-like isoform X2 [Durio zibethinus] | -6.38 | down |
| Ghir\_D04G003790 | K02717 | PREDICTED: oxygen-evolving enhancer protein 2, chloroplastic-like isoform X1 [Gossypium hirsutum] | -6.91 | down |
| Ghir\_D04G006550 | K02717 | hypothetical protein GOBAR\_DD02715 [Gossypium barbadense] | -4.21 | down |
| Ghir\_D05G008250 | K14332 | PREDICTED: photosystem I subunit O-like [Gossypium hirsutum] | -5.51 | down |
| Ghir\_D05G013100 | K02695 | PREDICTED: photosystem I reaction center subunit VI, chloroplastic-like [Gossypium raimondii] | -6.03 | down |
| Ghir\_D05G014600 | K02694 | Photosystem I reaction center subunit III, chloroplastic -like protein [Gossypium arboreum] | -6.43 | down |
| Ghir\_D05G017140 | K08901 | PREDICTED: oxygen-evolving enhancer protein 3, chloroplastic-like [Gossypium hirsutum] | -2.58 | down |
| Ghir\_D05G018660 | K02638 | PREDICTED: hippocampus abundant transcript-like protein 1 isoform X2 [Gossypium raimondii] | -7.01 | down |
| Ghir\_D05G019010 | K02641 | PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Gossypium raimondii] | -7.45 | down |
| Ghir\_D05G023860 | K03542 | PREDICTED: photosystem II 22 kDa protein, chloroplastic-like [Gossypium hirsutum] | -8.43 | down |
| Ghir\_D05G030680 | K02717 | PREDICTED: psbP-like protein 1, chloroplastic [Gossypium raimondii] | -4.60 | down |
| Ghir\_D05G033990 | K03541 | PREDICTED: photosystem II 10 kDa polypeptide, chloroplastic [Gossypium raimondii] | -4.20 | down |
| Ghir\_D05G039370 | K08905 | PREDICTED: photosystem I reaction center subunit V, chloroplastic [Gossypium raimondii] | -5.39 | down |
| Ghir\_D06G013530 | K08901 | PREDICTED: oxygen-evolving enhancer protein 3, chloroplastic-like [Gossypium hirsutum] | -5.86 | down |
| Ghir\_D06G015970 | K02694 | PREDICTED: photosystem I reaction center subunit III, chloroplastic-like [Gossypium hirsutum] | -3.15 | down |
| Ghir\_D06G016790 | K02115 | PREDICTED: ATP synthase gamma chain, chloroplastic [Gossypium hirsutum] | -2.66 | down |
| Ghir\_D07G003370 | K02109 | PREDICTED: uncharacterized protein LOC105803296 [Gossypium raimondii] | -4.85 | down |
| Ghir\_D07G009830 | K02699 | PREDICTED: photosystem I reaction center subunit XI, chloroplastic-like [Gossypium hirsutum] | -6.20 | down |
| Ghir\_D07G011920 | K14332 | hypothetical protein GOBAR\_AA39582 [Gossypium barbadense] | -12.66 | down |
| Ghir\_D07G016580 | K08903 | PREDICTED: subtilisin-like protease SBT1.2 [Gossypium raimondii] | -4.09 | down |
| Ghir\_D07G017690 | K02699 | PREDICTED: photosystem I reaction center subunit XI, chloroplastic-like [Gossypium hirsutum] | -5.23 | down |
| Ghir\_D07G021960 | K02693 | PREDICTED: photosystem I reaction center subunit IV A, chloroplastic-like [Gossypium arboreum] | -3.71 | down |
| Ghir\_D07G022660 | K02721 | PREDICTED: photosystem II reaction center W protein, chloroplastic-like [Gossypium raimondii] | -6.87 | down |
| Ghir\_D08G005270 | K02693 | PREDICTED: photosystem I reaction center subunit IV, chloroplastic-like [Gossypium hirsutum] | -4.22 | down |
| Ghir\_D08G007210 | K02692 | PREDICTED: uncharacterized protein LOC107914686 [Gossypium hirsutum] | -4.02 | down |
| Ghir\_D08G020620 | K02721 | PREDICTED: photosystem II reaction center W protein, chloroplastic-like [Gossypium raimondii] | -5.24 | down |
| Ghir\_D09G022280 | K02639 | PREDICTED: ferredoxin, root R-B2 [Gossypium raimondii] | -5.03 | down |
| Ghir\_D10G002030 | K08901 | PREDICTED: oxygen-evolving enhancer protein 3, chloroplastic [Gossypium raimondii] | -8.87 | down |
| Ghir\_D10G012120 | K02717 | hypothetical protein B456\_011G126200 [Gossypium raimondii] | -7.35 | down |
| Ghir\_D11G013540 | K02721 | PREDICTED: photosystem II reaction center W protein, chloroplastic-like [Gossypium raimondii] | -6.13 | down |
| Ghir\_D11G014410 | K02693 | PREDICTED: photosystem I reaction center subunit IV B, chloroplastic-like [Gossypium raimondii] | -5.04 | down |
| Ghir\_D11G015130 | K02689 | PREDICTED: uncharacterized HIT-like protein MT1300 isoform X1 [Gossypium hirsutum];PREDICTED: uncharacterized HIT-like protein MT1300 isoform X2 [Gossypium hirsutum] | -1.97 | down |
| Ghir\_D11G018580 | K02641 | hypothetical protein GOBAR\_DD27847 [Gossypium barbadense] | -6.32 | down |
| Ghir\_D11G019970 | K02716 | PREDICTED: oxygen-evolving enhancer protein 1, chloroplastic [Gossypium hirsutum] | -5.08 | down |
| Ghir\_D11G024330 | K02701 | PREDICTED: photosystem I reaction center subunit N, chloroplastic-like [Gossypium raimondii] | -9.82 | down |
| Ghir\_D12G000420 | K02692 | PREDICTED: NF-kappa-B-activating protein-like [Gossypium hirsutum] | -2.80 | down |
| Ghir\_D12G006130 | K02641 | PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic-like [Gossypium hirsutum] | -8.57 | down |
| Ghir\_D12G012510 | K02113 | PREDICTED: ATP synthase delta chain, chloroplastic [Gossypium arboreum] | -1.27 | down |
| Ghir\_D12G015000 | K08902 | PREDICTED: photosystem II repair protein PSB27-H1, chloroplastic-like [Gossypium hirsutum] | -4.91 | down |
| Ghir\_D12G022220 | K02639 | PREDICTED: ferredoxin [Gossypium raimondii] | -2.97 | down |
| Ghir\_D13G003650 | K02639 | hypothetical protein GOBAR\_DD13197 [Gossypium barbadense] | -7.66 | down |
| Ghir\_D13G007910 | K08901 | Oxygen-evolving enhancer 3-2, chloroplastic -like protein [Gossypium arboreum] | -8.55 | down |
| Ghir\_D13G013390 | K02717 | PREDICTED: uncharacterized protein LOC107919990 isoform X1 [Gossypium hirsutum] | -2.73 | down |
| Ghir\_D13G014100 | K08905 | PREDICTED: photosystem I reaction center subunit V, chloroplastic-like [Gossypium hirsutum] | -4.18 | down |
| Ghir\_D13G015540 | K08901 | PREDICTED: photosynthetic NDH subunit of lumenal location 3, chloroplastic-like [Gossypium hirsutum] | -8.82 | down |
| Ghir\_D13G024250 | K02639 | PREDICTED: ferredoxin, root R-B2-like isoform X1 [Gossypium hirsutum] | -2.14 | down |