# Supporting Information

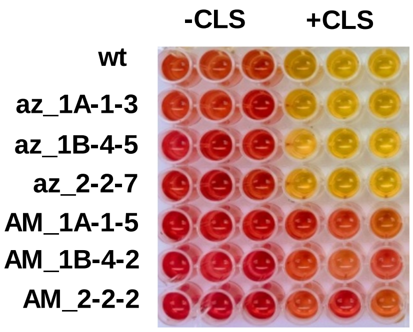

**Figure S1.** Colorimetric assay for the determination of ALS activity in leaf extracts of three independent T2 AM lines and their corresponding azygous lines in the absence and presence of 50 µg/L chlorsulfuron. Red indicates ALS activity.

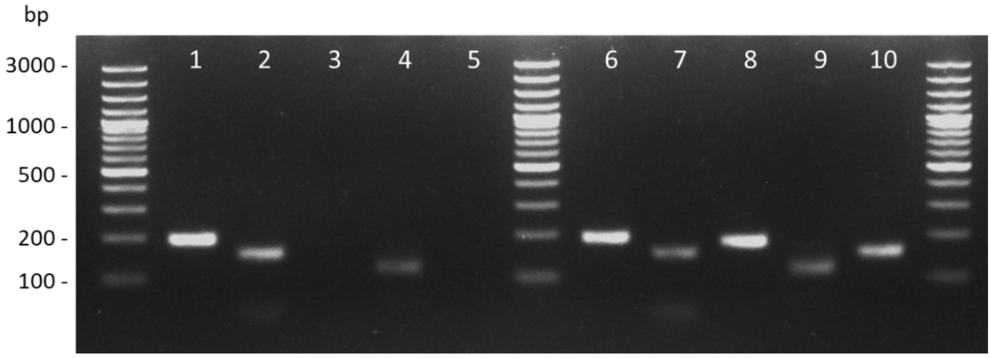

**Figure S2.** PCR reactions for specific amplification of the endogenous and transgenic copies of the ALS and MYB12 genes. PCR reactions were performed with MyTaq$^{TM}$ polymerase (Biolines) following manufacturer instruction and using as template cDNA obtained from the peel of WT (lanes 1-5) and AM (lanes 6-10) tomato fruits using the RT-qPCR primers listed on Table S6. Lanes 1 and 6: PCR of the actin gene was used as control (expected size of 285 bp); Lanes 2 and 7: eALS PCR with an expected size of 152 bp; Lanes 3 and 8: cALS PCR with an expected size of 183 bp; Lanes 4 and 9: eMYB PCR with an expected size of 116 bp; Lanes 5 and 10: cMYB PCR with an expected size of 155 bp.

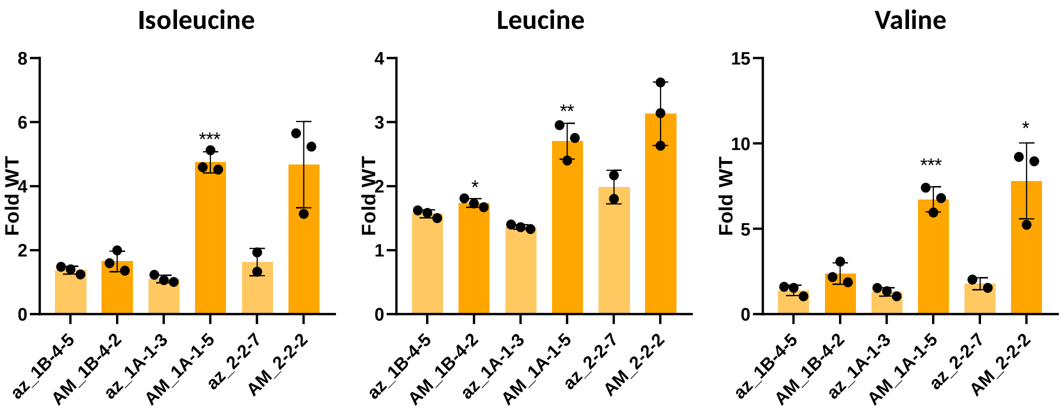

**Figure S3.** Overexpression of the acetolactate synthase gene results in increased branched chain amino acids in tomato leaves.

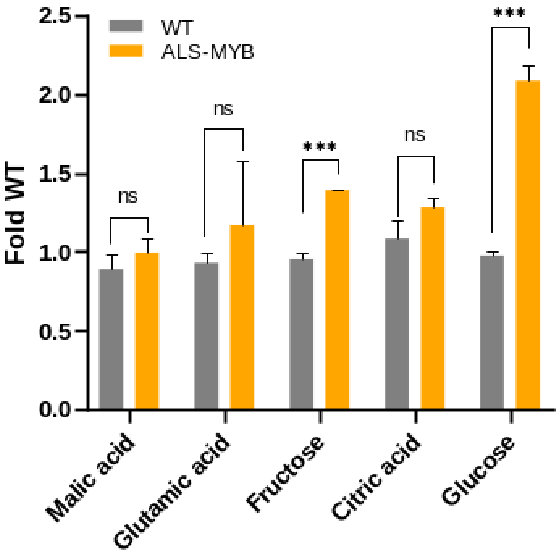

**Figure S4.** Fold change on primary metabolites content of red ripe tomato fruits of three independent T2 AM lines compared to their corresponding azygous lines determined using HPLC.

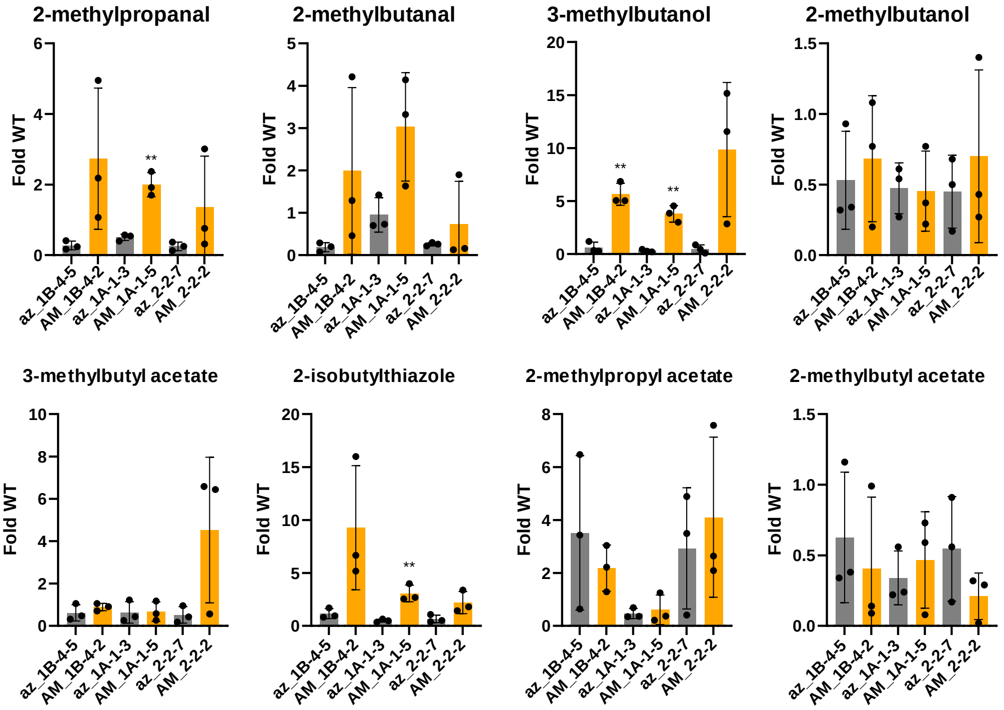

**Figure S5.** Overexpression of the acetolactate synthase gene results in unintended increase of most branched chain volatiles in tomato fruits.

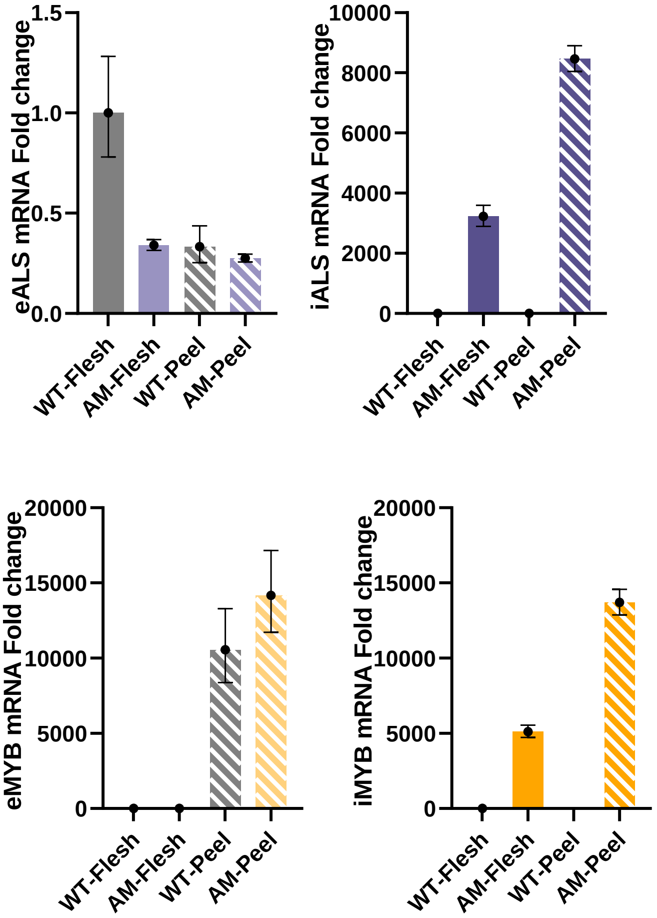

**Figure S6.** Expression levels of endogenous and intragenic ALS and MYB12 genes in tomato fruit in different tissues.

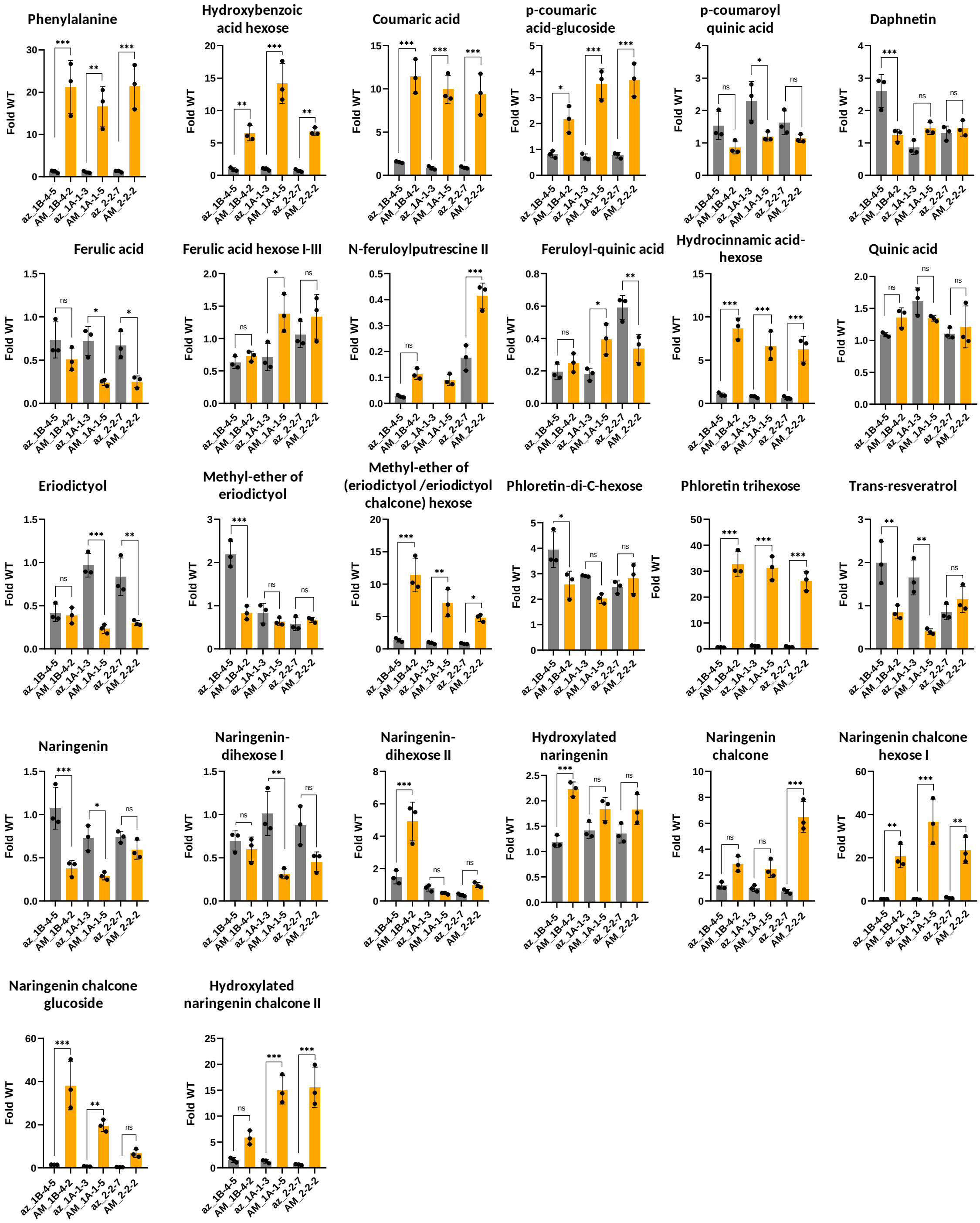

**Figure S7.** Fruit specific overexpression of the SlMyb12 gene results in increase of most phenylpropanoids in tomato fruits.

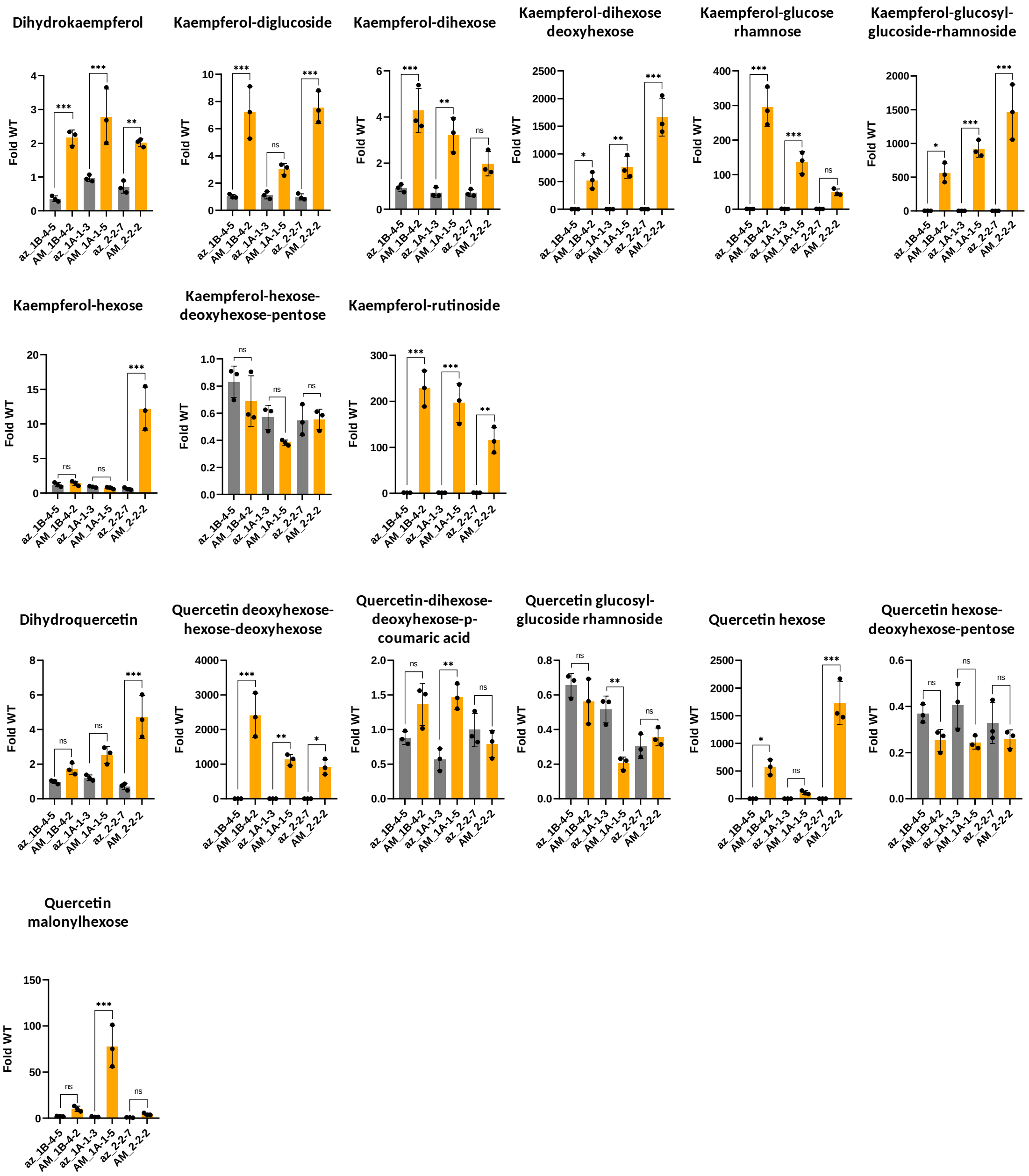

**Figure S7 (continuation).**

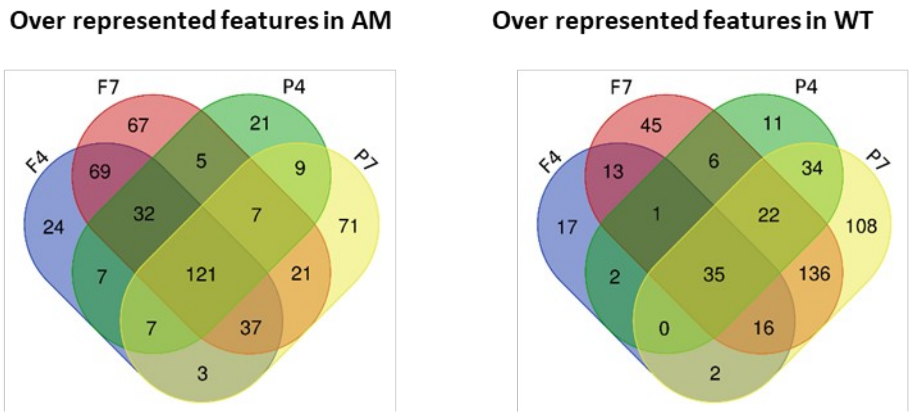

**Figure S8.** Venn diagram showing the number of independent and common features among the different samples identified with a metabolite profiling using LC-MS.

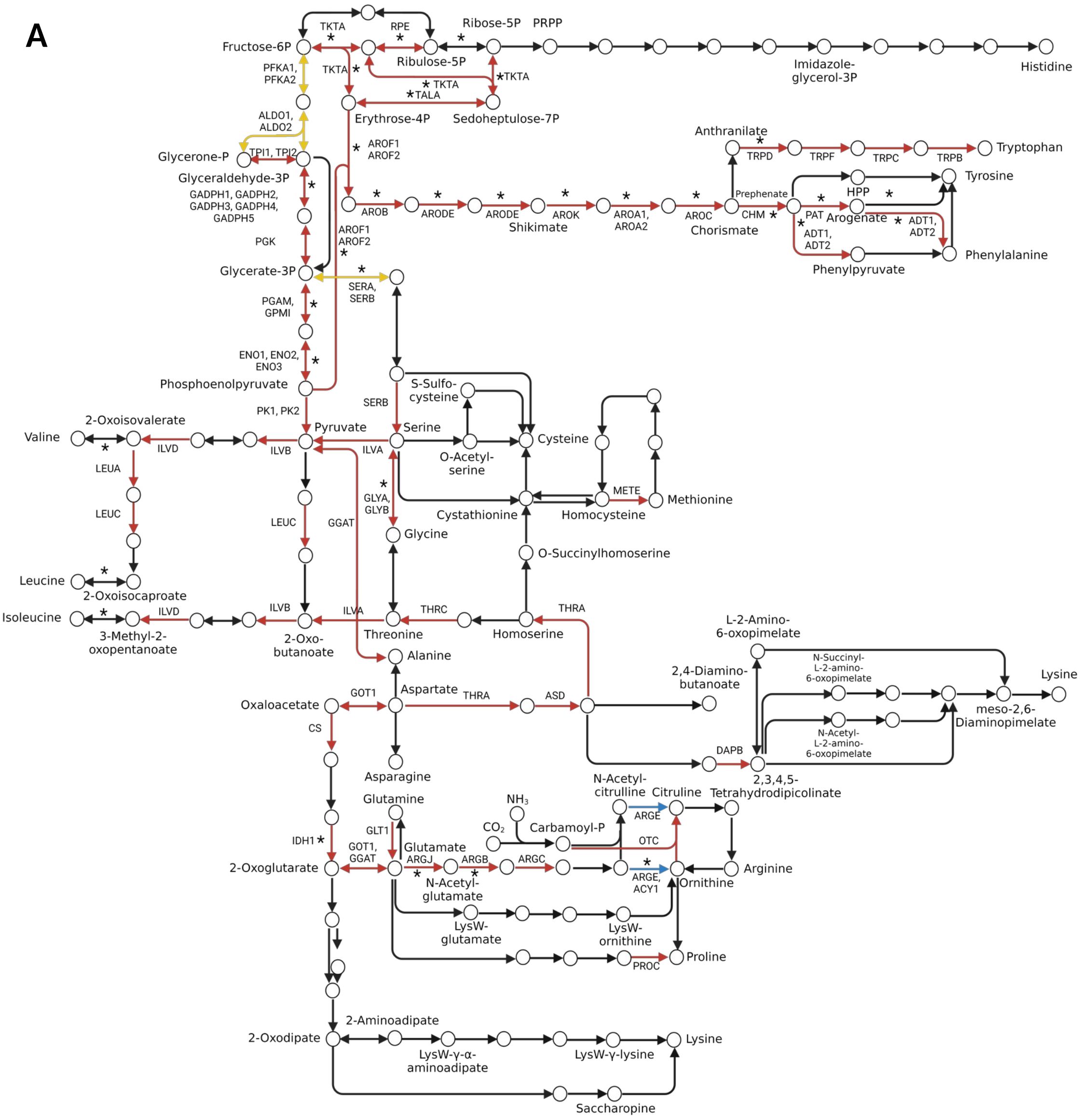

**Figure S9.** Transcriptomic analysis of ALS-MYB flesh samples shows overexpression of multiple genes involved in the amino acids biosynthetic pathway. A) A KEGG analysis shows that several genes of the amino acids biosynthetic pathway (red arrows) are overexpressed in the AM fruits compared to WT. Asterisks indicate genes also overexpressed in AtMYB12 fruits from Zhang et al. (2015). B) Log FPKMs of the genes differentially expressed among lines in the amino acids biosynthesis pathway depicted in A).

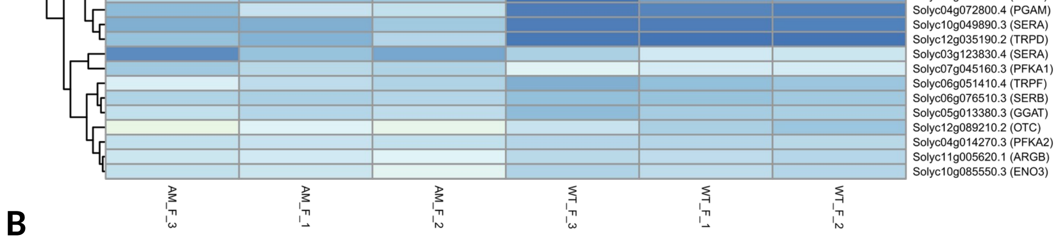

**Figure S9 (continuation).**

**Table S1.** Targeted metabolomics analysis of phenylpropanoid compounds in WT and ALS-MYB tomato fruits at red ripe (RR) stage; for each compound, information about metabolic sub-class, chemical formula, monoisotopic m/z, retention time (RT), ESI ionization (+/-), detected adduct (M-, M+H or M-H) and m/z, and validation level (STD: authentic standard; MS/MS: mass fragmentation) are reported.

| **Metabolic Class** | **Metabolite ID** | **Chemical Formula** | **Monoisotopic m/z (Da)** | **RT (min)** | **Ionization** | **Adducts** | **Detected Mass** | **Validation level** |
|---|---|---|---|---|---|---|---|---|
| AMINO ACIDS | phenylalanine | $C_9H_{11}NO_2$ | 165,07897 | 2,56 | ESI + | M+H | 166,08620 | STD |
| BENZOATES | hydroxybenzoic acid-hexose | $C_{13}H_{16}O_8$ | 300,08452 | 4,09 | ESI - | M-H | 299,07760 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | caffeic acid | $C_9H_8O_4$ | 180,04225 | 7,05 | ESI - | M-H | 179,03497 | STD |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | caffeic acid hexose IV | $C_{15}H_{18}O_9$ | 342,09508 | 6,28 | ESI - | M-H | 341,08780 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | 4-caffeoyl-quinic acid | $C_{16}H_{18}O_9$ | 354,09508 | 6,41 | ESI - | M-H | 355,10205 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | 5-caffeoyl-quinic acid | $C_{16}H_{18}O_9$ | 354,09508 | 7,77 | ESI + | M+H | 355,10208 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | coumaric acid | $C_9H_8O_3$ | 164,04734 | 5,22 | ESI + | M+H | 165,05464 | STD |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | p-coumaric acid-glucoside | $C_{15}H_{18}O_8$ | 326,10015 | 7,11 | ESI - | M-H | 325,09345 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | 4-p-coumaroylquinic acid | $C_{16}H_{18}O_8$ | 338,10015 | 7,59 | ESI - | M-H | 337,09233 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | daphnetin | $C_9H_6O_4$ | 178,02660 | 6,41 | ESI + | M+H | 179,03506 | STD |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | dicaffeoylquinic acid | $C_{25}H_{24}O_{12}$ | 516,12677 | 11,30 | ESI - | M-H | 515,11940 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | ferulic acid | $C_{10}H_9O_4$ | 194,05791 | 6,08 | ESI + | M+H | 195,06572 | STD |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | ferulic acid-hexose I-III | $C_{16}H_{20}O_9$ | 356,11073 | 7,28 | ESI - | M-H | 355,10404 | MS/MS |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | N-feruloylputrescine II | C14H20N2O3 | 264,14740 | 4,98 | ESI + | M+H | 265,15470 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | feruloyl-quinic acid | C17H20O9 | 368,11073 | 8,26 | ESI - | M-H | 367,10290 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | hydrocinnamic acid-hexose | C15H20O8 | 328,11582 | 5,97 | ESI - | M-H | 327,10850 | MS/MS |
| CINNAMATES, COUMARATES, FERULATES & SINAPATES | quinic acid | C7H12O6 | 192,06338 | 1,22 | ESI - | M-H | 191,05556 | STD |
| FLAVONOIDS | dihydrokaempferol | C15H12O6 | 288,06338 | 12,33 | ESI - | M-H | 287,05668 | STD |
| FLAVONOIDS | dihydronaringenin-chalcone | C15H14O5 | 274,08413 | 14,58 | ESI + | M+H | 275,09198 | MS/MS |
| FLAVONOIDS | dihydroquercetin | C15H12O7 | 304,05828 | 3,95 | ESI + | M+H | 305,06556 | STD |
| FLAVONOIDS | eriodyctiol | C15H12O6 | 288,06338 | 7,46 | ESI + | M+H | 289,07066 | STD |
| FLAVONOIDS | eriodictyol-hexose | C21H22O11 | 450,11621 | 9,17 | ESI - | M-H | 449,10800 | MS/MS |
| FLAVONOIDS | hydroxylated-naringenin | C15H13O6 | 289,07174 | 17,05 | ESI - | M-H | 288,06392 | MS/MS |
| FLAVONOIDS | hydroxylated-naringenin chalcone I | C15H13O6 | 289,07121 | 7,45 | ESI - | M-H | 287,05673 | MS/MS |
| FLAVONOIDS | hydroxylated-naringenin chalcone II | C15H13O6 | 289,07121 | 8,15 | ESI - | M-H | 287,05673 | MS/MS |
| FLAVONOIDS | kaempferol | C15H10O6 | 286,04773 | 14,44 | ESI + | M+H | 287,05501 | STD |
| FLAVONOIDS | luteolin | C15H10O6 | 286,04772 | 16,54 | ESI - | M-H | 285,04040 | STD |
| FLAVONOIDS | methyl-ether of eriodictyol | C16H14O6 | 302,07904 | 15,31 | ESI - | M-H | 301,07170 | MS/MS |
| FLAVONOIDS | methyl ether of (Eriodictyol/ Eriodictyol chalcone) hexose | C22H24O11 | 464,13186 | 10,83 | ESI - | M-H | 463,12401 | MS/MS |
| FLAVONOIDS | morin | C15H10O7 | 302,04266 | 12,66 | ESI + | M+H | 303,04990 | STD |
| FLAVONOIDS | myricetin | C15H10O8 | 318,03756 | 5,87 | ESI + | M+H | 319,04484 | STD |
| FLAVONOIDS | naringenin | C15H12O5 | 272,06848 | 13,69 | ESI - | M-H | 271,06120 | STD |

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|---|---|---|---|---|---|---|---|---|
| FLAVONOIDS | naringenin-dihexose I | C27H32O15 | 596,17412 | 6,82 | ESI - | M-H | 595,16680 | MS/MS |
| FLAVONOIDS | naringenin-dihexose II | C27H32O15 | 596,17412 | 11,02 | ESI - | M-H | 595,16680 | MS/MS |
| FLAVONOIDS | naringenin-hexose | C21H22O10 | 434,12130 | 12,27 | ESI - | M-H | 433,11341 | MS/MS |
| FLAVONOIDS | naringenin-chalcone | C15H12O5 | 272,06848 | 13,99 | ESI - | M-H | 271,06120 | STD |
| FLAVONOIDS | naringenin chalcone-dihexose | C27H32O15 | 596,17412 | 9,39 | ESI + | M+H | 597,18140 | MS/MS |
| FLAVONOIDS | naringenin chalcone-glucoside | C21H22O10 | 434,12129 | 10,97 | ESI - | M-H | 433,11420 | MS/MS |
| FLAVONOIDS | naringenin chalcone-hexose I | C21H22O10 | 434,1213 | 10,07 | ESI - | M-H | 433,11440 | MS/MS |
| FLAVONOIDS | naringenin chalcone-hexose II | C21H22O10 | 434,1213 | 11,19 | ESI - | M-H | 433,11400 | MS/MS |
| FLAVONOIDS | phloretin-di-C-hexose | C27H34O15 | 598,18977 | 9,02 | ESI - | M-H | 597,18250 | MS/MS |
| FLAVONOIDS | phloretin-trihexose | C33H44O20 | 760,24260 | 7,67 | ESI - | M-H | 759,23530 | MS/MS |
| FLAVONOIDS | quercetin | C15H10O7 | 302,04266 | 16,19 | ESI - | M-H | 301,03484 | STD |
| FLAVONOIDS | trans-resveratrol | C14H12O3 | 228,078640 | 12,95 | ESI - | M-H | 227,07136 | STD |
| FLAVONOID GLUCOSIDES | kaempferol-diglucoside | C27H30O16 | 610,153380 | 8,68 | ESI + | M+H | 611,16122 | STD |
| FLAVONOID GLUCOSIDES | kaempferol-dihexose | C27H28O16 | 608,13775 | 8,59 | ESI - | M-H | 607,12993 | MS/MS |
| FLAVONOID GLUCOSIDES | kaempferol-dihexose-deoxyhexose | C33H40O20 | 756,21129 | 7,21 | ESI + | M+H | 757,21860 | MS/MS |
| FLAVONOID GLUCOSIDES | kaempferol-glucose-rhamnose | C27H30O15 | 593,15120 | 11,66 | ESI - | M-H | 592,14392 | MS/MS |
| FLAVONOID GLUCOSIDES | kaempferol-glucosyl-glucoside-rhamnsoside | C33H40O20 | 756,21129 | 7,17 | ESI - | M-H | 755,20400 | MS/MS |
| FLAVONOID GLUCOSIDES | kaempferol-hexose | C21H20O11 | 448,10055 | 10,76 | ESI - | M-H | 447,09327 | STD |
| FLAVONOID GLUCOSIDES | kaempferol-hexose-deoxyhexose-pentose | C32H35O19 | 723,17669 | 8,93 | ESI - | M-H | 722,16882 | MS/MS |
| FLAVONOID GLUCOSIDES | kaempferol-manolylglucoside | C24H22O14 | 534,10095 | 7,91 | ESI + | M+H | 535,10810 | MS/MS |

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|---|---|---|---|---|---|---|---|---|
| FLAVONOID GLUCOSIDES | kaempferol-rutinoside | C27H30O15 | 594,15847 | 9,70 | ESI + | M+H | 595,16560 | STD |
| FLAVONOID GLUCOSIDES | quercetin deoxyhexose-hexose-deoxyhexose | C33H39O20 | 755,20347 | 7,17 | ESI - | M- | 755,20200 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-diglucoside | C27H30O17 | 626,14829 | 8,04 | ESI + | M+H | 627,15550 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-dihexose-deoxyhexose | C33H40O21 | 772,20621 | 6,60 | ESI - | M-H | 771,19890 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-dihexose-deoxyhexose-p-coumaric acid | C42H46O23 | 918,24299 | 10,41 | ESI - | M-H | 917,23570 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-dihexose-pentose-deoxyhexose | C38H44O25 | 902,23338 | 6,34 | ESI - | M-H | 901,22552 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin glucosyl-glucoside rhamnoside | C33H40O21 | 772,20620 | 9,02 | ESI - | M-H | 771,19890 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-hexose | C21H20O12 | 464,09549 | 9,36 | ESI - | M-H | 463,08821 | STD |
| FLAVONOID GLUCOSIDES | quercetin-hexose-hexose | C27H30O17 | 626,14830 | 8,06 | ESI - | M-H | 625,14211 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-hexose-deoxyhexose-pentose | C32H38O20 | 742,19564 | 8,39 | ESI - | M-H | 741,11883 | MS/MS |
| FLAVONOID GLUCOSIDES | quercetin-malonylhexose | C24H22O15 | 550,09586 | 9,76 | ESI + | M+H | 551,10280 | MS/MS |
| FLAVONOID GLUCOSIDES | rutin | C27H30O16 | 610,15338 | 8,97 | ESI - | M-H | 609,14610 | STD |

**Table S2.** Untargeted metabolomics analysis in WT and ALS-MYB tomato fruits at 7 days post breaker. All the compounds listed display mass accuracy below 3ppm and mass compatible formula.

| Name | Family | Conjugation | RT [min] | Formula | MW | m/z | Ref Ion | Evidence1 | Evidence2 | Evidence3 | Evidence 4 | Conf. Level[a] |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| acyl diglycoside_6[b] | acyl glycoside | none | 8.503 | C17 H30 O12 | 426.17358 | 471.17176 | [M+FA-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| acyl diglycoside_2[b] | acyl glycoside | none | 10.067 | C14 H24 O10 | 352.13683 | 351.12952 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| acyl diglycoside_3[b] | acyl glycoside | none | 10.188 | C17 H30 O12 | 426.17366 | 471.17185 | [M+FA-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| acyl diglycoside_4[b] | acyl glycoside | none | 11.296 | C14 H24 O10 | 352.13683 | 351.12949 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| acyl glycoside_1[b] | acyl glycoside | none | 12.209 | C14 H26 O9 | 338.1578 | 337.15054 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| acyl diglycoside_1[b] | acyl glycoside | none | 12.923 | C14 H24 O10 | 352.13688 | 351.12957 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| acyl diglycoside_5 | acyl glycoside | none | 13.696 | C16 H30 O10 | 382.1838 | 427.18192 | [M+FA-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | | 3 |
| acyl glycoside_2[b] | acyl glycoside | none | 14.255 | C14 H26 O9 | 338.15764 | 337.15034 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | | 3 |
| Leucine | aminoacid | none | 2.334 | C6 H13 N O2 | 131.09458 | 132.10186 | [M+H]+1 | Mass compatible <3ppm | MS/MS | | RT | 2 |
| Naringenin chalcone | chalcone | none | 25.47 | C15 H12 O5 | 272.06827 | 271.06097 | [M-H]-1 | Standard | MS/MS | mZCloud | RT | 1 |
| Taxifolin dihexoside | Dihydroflavonol | sugar | 15.701 | C15 H12 O7 | 304.05823 | 303.05096 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Naringenin dihexoside_1 | flavanone | sugar | 15.353 | C15 H12 O5 | 272.06841 | 273.07576 | [M+H]+1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Naringenin dihexoside_2 | flavanone | sugar | 15.601 | C15 H12 O5 | 272.06847 | 271.06119 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Eriodictyol 7-O-glucoside | flavanone | sugar | 16.748 | C21 H22 O11 | 450.11619 | 449.10889 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Prunin | flavanone | sugar | 17.32 | C21 H22 O10 | 434.12134 | 435.12872 | [M+H]+1 | Mass compatible | MS/MS | mZCloud | RT | 2 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | <3ppm | | | | |
| Eriodictyol hexoside_1 | flavanone | sugar | 18.736 | C21 H22 O11 | 450.11622 | 449.10893 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Naringenin glucoside_1 | flavanone | sugar | 19.081 | C21 H22 O10 | 434.12114 | 433.11384 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Eriodictyol hexoside_2 | flavanone | sugar | 19.238 | C21 H22 O11 | 450.11621 | 449.1089 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Eriodictyol hexoside_3 | flavanone | sugar | 19.795 | C21 H22 O11 | 450.11609 | 449.10881 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Eriodictyol hexoside_6 | flavanone | sugar | 20.135 | C21 H22 O11 | 450.11608 | 449.10881 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Naringenin glucoside_3 | flavanone | sugar | 21.241 | C21 H22 O10 | 434.12121 | 433.1139 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Eriodictyol hexoside_4 | flavanone | sugar | 21.28 | C21 H22 O11 | 450.11619 | 449.10887 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Naringenin glucoside_5 | flavanone | sugar | 21.406 | C30 H34 O18 | 682.1749 | 681.16771 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Naringenin glucoside_2 | flavanone | sugar | 21.483 | C21 H22 O10 | 434.12122 | 433.11386 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Naringenin glucoside_4 | flavanone | sugar | 21.807 | C21 H22 O10 | 434.12118 | 433.11383 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Eriodictyol | flavanone | none | 22.234 | C15 H12 O6 | 288.06343 | 287.05614 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Eriodictyol Chalcone | flavanone | none | 23.249 | C15 H12 O6 | 288.0633 | 287.05601 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Eriodictyol hexoside_5 | flavanone | sugar | 23.772 | C22 H18 N4 O7 | 450.11648 | 449.10918 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Naringenin coumaroyl glucoside_2 | flavanone | hydroxycinnamic acid + sugar | 25.266 | C30 H28 O13 | 596.15305 | 595.14578 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Naringenin coumaroylglucoside_1 | flavanone | hydroxycinnamic acid + sugar | 28.87 | C30 H28 O12 | 580.15814 | 579.15085 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| quercetin diglucoside | flavonol | sugar | 15.316 | C27 H30 O16 | 610.15287 | 609.14555 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Rutin | flavonol | sugar | 16.44 | C27 H30 O16 | 610.15274 | 609.14549 | [M-H]-1 | Standard | MS/MS | mZCloud | RT | 1 |
| Quercetin-3β-D-glucoside | flavonol | sugar | 16.78 | C21 H20 O12 | 464.09535 | 463.08801 | [M-H]-1 | Standard | MS/MS | mZCloud | RT | 1 |
| Kaempferol hexoside rhamnoside | flavonol | sugar | 18.157 | C27 H30 O15 | 594.15829 | 593.15098 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Kaempferol-3-glucoside | flavonol | sugar | 18.556 | C21 H20 O11 | 448.10062 | 447.09333 | [M-H]-1 | Standard | MS/MS | mZCloud | RT | 1 |
| Tomatine_3 | Glycoalkaloid | sugar | 22.613 | C27 H45 N O2 | 433.3558 | 416.35252 | [M+H-H2O] +1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Dehydrotomatine_2 | Glycoalkaloid | sugar | 25.005 | C35 H57 N O9 | 635.40305 | 636.41032 | [M+H]+1 | Mass compatible <3ppm | MS/MS | | RT | 2 |
| Tomatine_2 | Glycoalkaloid | sugar | 25.162 | C65 H77 N O16 | 1127.52777 | 1126.52049 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 2 |
| Dehydrotomatine_1 | Glycoalkaloid | sugar | 25.167 | C40 H61 N5 O8 | 739.45053 | 740.45779 | [M+H]+1 | Mass compatible <3ppm | | | RT | 2 |
| Tomatine_1 | Glycoalkaloid | sugar | 25.332 | C55 H74 O22 | 1086.47243 | 363.16413 | [M+3H]+3 | Mass compatible <3ppm | | | RT | 2 |
| Gentisic acid hexoside | hydroxybenzoic acid | sugar | 5.954 | C13 H16 O9 | 316.0795 | 315.07222 | [M-H]-1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Pyrogallol-2-O-glucuronide | hydroxybenzoic acid | sugar | 6.638 | C12 H14 O9 | 302.06384 | 301.05657 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Vanilloyl-beta-D-glucose | hydroxybenzoic acid | sugar | 6.814 | C14 H18 O9 | 330.0953 | 329.08802 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Salicylic Acid-Glucoside | hydroxybenzoic acid | sugar | 6.851 | C13 H16 O8 | 300.08453 | 299.0773 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Dihydroxybenzoic acid pentoside | hydroxybenzoic acid | sugar | 8.17 | C12 H14 O8 | 286.06878 | 285.0615 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| 2-O-caffeoylglucaric acid | hydroxycinnamic acid | sugar | 6.525 | C15 H16 O11 | 372.06924 | 371.06196 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Caffeoyl glucoside_2 | hydroxycinnamic acid | sugar | 6.649 | C15 H18 O9 | 342.09499 | 341.08771 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Caffeoylquinic acid_1 | hydroxycinnamic acid | quinic acid | 8.21 | C16 H18 O9 | 354.09504 | 355.10251 | [M+H]+1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Coumaric acid glucoside_1 | hydroxycinnamic acid | sugar | 8.364 | C15 H18 O8 | 326.10003 | 325.09285 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Caffeoyl glucoside_1 | hydroxycinnamic acid | sugar | 8.707 | C15 H18 O9 | 342.09507 | 341.08779 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Ferulic acid glucoside_1 | hydroxycinnamic acid | sugar | 9.865 | C16 H20 O9 | 356.11057 | 355.10329 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Chlorogenic acid | hydroxycinnamic acid | quinic acid | 10.16 | C16 H18 O9 | 354.09494 | 355.10252 | [M+H]+1 | Standard | MS/MS | | RT | 1 |
| Coumaric acid glucoside_3 | hydroxycinnamic acid | sugar | 10.558 | C15 H18 O8 | 326.10008 | 325.0928 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| sinapaldehyde glucoside | hydroxycinnamic acid | sugar | 10.641 | C17 H22 O9 | 370.12617 | 369.11889 | [M-H]-1 | Mass compatible <3ppm | | | RT | 3 |
| Coumaric acid glucoside_2 | hydroxycinnamic acid | sugar | 10.807 | C15 H18 O8 | 326.10004 | 325.0928 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Coumaric acid glucoside_4 | hydroxycinnamic acid | sugar | 11.415 | C15 H18 O8 | 326.10023 | 325.09296 | [M-H]-1 | Mass compatible <3ppm | MS/MS | | RT | 3 |
| Ferulic acid glycoside_2 | hydroxycinnamic acid | sugar | 11.952 | C16 H20 O9 | 378.09281 | 379.10009 | [M+H]+1 | Mass compatible <3ppm | MS/MS | mZCloud | RT | 2 |
| Abietin | hydroxycinnamic acid | sugar | 12.588 | C16 H22 O8 | 342.13136 | 341.12408 | [M-H]-1 | Mass compatible <3ppm | | | RT | 3 |
| Isochlorogenic acid | hydroxycinnamic acid | quinic acid | 19.985 | C25 H24 O12 | 516.12686 | 499.12361 | [M+H-H2O] +1 | Mass compatible <3ppm | MS/MS | | RT | 2 |

a. To assign confidence levels, the following diagnostic evidences are indicated: evidence 2 (MS2 data available), evidence 3 (match in mzCloud MS/MS database), evidence 4 (compatible RT with proposed structure). Confidence level was assigned as follows (adapted from the criteria recommended in Blaženović et al., 2018):

- Level 1 Confident 2D structure: Reference standard match
- Level 2 Probable structure: At least two additional diagnostic evidences from 2, 3 and 4
- Level 3 Possible structure or class: At least one additional diagnostic evidence from 2, 3 and 4

b. In these acylsugars, 3-methylbutanoate was identified as an acyl chain with the MS2

*Reference:* Blaženović, I., Kind, T., Ji, J., & Fiehn, O. (2018). Software tools and approaches for compound identification of LC-MS/MS data in metabolomics. *Metabolites*, *8*(2), 31.

**Table S3.** List of differentially expressed genes between AM and WT flesh samples ordered by fold-change.

| Gene | Description | KEGG | Log$_2$ fold-change | FDR | FPKM Average | |
|---|---|---|---|---|---|---|
| | | | | | AM_F | WT_F |
| Solyc09g059170.3 | Glycosyltransferase (AHRD V3.3 *** A4GRT2_9SOLA) | FG2 | -13.15020455 | 9.5613E-52 | 298.5768787 | 0.028617333 |
| Solyc09g059060.1 | Quinone-oxidoreductase QR1, chloroplastic (AHRD V3.3 *-* QR1_TRIVS),Pfam:PF13602 | NA | -12.76761477 | 4.29235E-73 | 60.864845 | 0 |
| Solyc09g059070.3 | Quinone-oxidoreductase chloroplastic-like (AHRD V3.3 *-* A0A2K3P901_TRIPR) | NA | -11.99135761 | 3.95332E-48 | 20.813088 | 0 |
| Solyc03g096160.3 | Protein yippee-like (AHRD V3.3 *** A0A1U8GAE4_CAPAN) | NA | -11.84436271 | 7.48474E-63 | 10.90678467 | 0 |
| Solyc10g083440.2 | Glycosyltransferase (AHRD V3.3 *** A0A2G3BGM7_CAPCH) | BZ1 | -11.83158655 | 6.3457E-255 | 151.0940197 | 0.036416333 |
| Solyc08g062520.2 | homeobox-leucine zipper protein ROC8 (AHRD V3.3 *** A0A2I4EBE3_9ROSI) | HD-ZIP | -11.5124068 | 5.62262E-55 | 2.845491 | 0 |
| Solyc05g047530.3 | trans-cinnamate 4-monooxygenase | CYP73A | -11.49002639 | 1.37513E-12 | 142.0290783 | 0.046958667 |
| Solyc05g052240.3 | Chalcone-flavonone isomerase family protein (AHRD V3.3 *** A0A2G2ZJB2_CAPAN) | chalcone isomerase | -10.71153681 | 4.93423E-18 | 902.3850503 | 0.511204 |
| Solyc02g083860.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1QGX7_ARTAN) | F3H | -10.48820639 | 1.88475E-17 | 676.3905843 | 0.446773667 |
| Solyc02g089780.3 | dihydroflavonol 4-reductase/flavanone protein (AHRD V3.3 *-* AT3G02420.2) | NA | -10.08824345 | 2.2762E-32 | 225.5794527 | 0.199770333 |
| Solyc09g091510.3 | chalcone synthase 1 | CHS | -10.08192877 | 1.38328E-10 | 720.5945127 | 0.641138667 |
| Solyc01g079620.4 | colorless fruit epidermis | MYBP | -9.984525758 | 1.6284E-161 | 49.91320167 | 0.046887 |
| Solyc09g042670.4 | Unknown protein | NA | -9.954745765 | 1.22302E-63 | 20.760418 | 0.013240333 |
| Solyc03g044330.1 | Acetolactate synthase (AHRD V3.3 *** C0L093_TOBAC) | ILVB | -9.672729686 | 1.88894E-92 | 6167.554525 | 7.684817333 |
| Solyc09g059020.4 | Quinone-oxidoreductase QR1, chloroplastic (AHRD V3.3 *** QR1_TRIVS) | CEQORH | -9.275119428 | 7.0026E-197 | 52.137952 | 0.078941667 |
| Solyc06g006000.3 | Maternal effect embryo arrest 59 (AHRD V3.3 *** B6T4K8_MAIZE) | NA | -9.070673894 | 2.78715E-13 | 28.52280067 | 0.044019667 |
| Solyc00g500353.1 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G2VZP0_CAPBA) | PAL | -8.990075082 | 3.73674E-42 | 4.199248667 | 0.005643667 |
| Solyc05g053550.3 | chalcone synthase 2 | CHS | -8.930426554 | 2.76877E-13 | 477.246277 | 0.947261333 |
| Solyc09g061791.1 | Cytochrome P450 (AHRD V3.3 *** A0A2U1L5B3_ARTAN) | NA | -8.577693003 | 7.9943E-20 | 5.260968667 | 0.011347667 |
| Solyc00g500095.1 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G2VZP0_CAPBA) | PAL | -7.989478834 | 6.6046E-30 | 4.033011667 | 0.010614667 |
| Solyc11g013110.2 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G49390.1) | FLS | -7.904396822 | 1.22302E-63 | 1713.514201 | 7.169820667 |
| Solyc06g060570.3 | dihydrofolate reductase-like (AHRD V3.3 *** A0A2I4ECQ2_9ROSI) | NA | -7.900777113 | 5.42272E-18 | 14.73618067 | 0.051807667 |
| Solyc05g055700.3 | Zinc-binding dehydrogenase (AHRD V3.3 *** A0A2U1MNF4_ARTAN) | NA | -7.806721746 | 3.07173E-63 | 13.03428167 | 0.055745333 |
| Solyc03g121010.4 | Unknown protein | NA | -7.408140856 | 2.73849E-20 | 6.727808333 | 0.032616333 |
| Solyc03g042560.3 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G2YQ27_CAPAN) | PAL | -7.393417148 | 4.89248E-24 | 2.680221333 | 0.013789333 |

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|---|---|---|---|---|---|---|
| Solyc03g115220.4 | Flavonoid 3'-monooxygenase (AHRD V3.3 *** A0A2G2WR53_CAPBA) | CYP75B1 | -7.067411164 | 7.7663E-23 | 57.72727967 | 0.438377667 |
| Solyc07g008240.3 | Non-symbiotic hemoglobin like (AHRD V3.3 *** A0A2R6R1Q2_ACTCH) | NA | -7.013198048 | 2.66593E-14 | 61.26280867 | 0.479395 |
| Solyc03g119980.3 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** O04083_ARATH) | CSE | -6.824222039 | 3.64091E-24 | 18.21060233 | 0.152694 |
| Solyc01g074000.3 | Histone H3 (AHRD V3.3 *** D8L9K7_WHEAT) | H3 | -6.576203848 | 5.02773E-29 | 10.21922267 | 0.091002 |
| Solyc09g015020.1 | Class I heat shock protein (AHRD V3.3 *** A0A2K3KSJ8_TRIPR) | HSP20 | -6.523610669 | 3.92197E-07 | 112.270743 | 1.170219667 |
| Solyc05g025890.3 | Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** Q8GUT5_ARATH) | NA | -6.201464386 | 6.67178E-11 | 14.64726167 | 0.190405333 |
| Solyc06g072660.4 | DEK (AHRD V3.3 *-* A0A200R412_9MAGN) | DEK | -6.145700678 | 1.79341E-25 | 2.376141333 | 0.030559667 |
| Solyc06g084030.3 | Methyltransferase type 11 (AHRD V3.3 *** A0A200QEQ4_9MAGN) | NA | -6.039153592 | 1.91499E-74 | 25.00169967 | 0.376577667 |
| Solyc07g047680.3 | F-box protein SNE (AHRD V3.3 *** A0A2G3BZC0_CAPCH) | NA | -6.004149708 | 2.39644E-18 | 9.837961333 | 0.138979 |
| Solyc01g079110.4 | Histone H3 (AHRD V3.3 *** A0A2G3DHD8_CAPCH) | H3 | -5.972744027 | 1.17795E-23 | 5.096710667 | 0.069782 |
| Solyc06g075010.4 | 60 kDa chaperonin (AHRD V3.3 *** B2IXD2_NOSP7) | NA | -5.959712643 | 9.47756E-47 | 39.517377 | 0.646651667 |
| Solyc01g086820.4 | Histone H3 (AHRD V3.3 *-* A0A2P6TS80_CHLSO) | H3 | -5.901983061 | 6.2533E-12 | 7.706828333 | 0.124799 |
| Solyc11g072860.2 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | H4 | -5.843443903 | 2.00936E-07 | 30.77453833 | 0.518857333 |
| Solyc03g114500.4 | Enolase (AHRD V3.3 *** A0A2G2WR88_CAPBA) | ENO | -5.815913006 | 2.96543E-25 | 106.660833 | 1.943702667 |
| Solyc02g032910.3 | glycine rich protein precursor (AHRD V3.3 *-* NP_001233996.1) | NA | -5.68394298 | 5.03263E-09 | 7.007236333 | 0.131846 |
| Solyc03g097030.3 | 4-coumarate:CoA ligase (AHRD V3.3 *** Q42880_LITER) | 4CL | -5.600601984 | 6.29457E-05 | 3.093476667 | 0.058731333 |
| Solyc04g050050.3 | SUN-like protein 13 | NA | -5.570583209 | 2.49382E-24 | 4.414370667 | 0.090670333 |
| Solyc01g096670.4 | Cytochrome P450 (AHRD V3.3 *** A0A2U1MC34_ARTAN) | CYP98A | -5.548396926 | 2.25777E-65 | 17.71237733 | 0.375834667 |
| Solyc05g005920.4 | protein NRT1/ PTR FAMILY 1.2-like (AHRD V3.3 *** A0A2I4HMB7_9ROSI) | SLC15A3_4 | -5.462892211 | 3.75668E-05 | 2.814622 | 0.061400333 |
| Solyc10g008910.1 | Histone H3 (AHRD V3.3 *** B3TM40_ELAGV) | H3 | -5.400199382 | 7.77074E-07 | 19.38308633 | 0.459807 |
| Solyc05g010320.4 | Chalcone-flavonone isomerase family protein (AHRD V3.3 *** A0A193AUW5_SOLME) | chalcone isomerase | -5.389297177 | 1.3952E-08 | 4.844835667 | 0.108142333 |
| Solyc02g021260.3 | B3 domain-containing protein (AHRD V3.3 *-* A0A1Q3DFU3_CEPFO) | NA | -5.331341226 | 2.58645E-29 | 2.470870333 | 0.059648333 |
| Solyc02g085660.1 | Glycosyltransferase (AHRD V3.3 *** A0A2I4ENI5_9ROSI) | UGT72E | -5.32272534 | 1.32473E-10 | 24.194911 | 0.608372 |
| Solyc06g072160.3 | Alcohol dehydrogenase 1 (AHRD V3.3 *** A0A1U8H3Z9_CAPAN) | ADH | -5.29218681 | 1.21474E-30 | 7.418668 | 0.189062667 |
| Solyc12g035190.2 | Anthranilate phosphoribosyltransferase (AHRD V3.3 *** A0A2U1N166_ARTAN) | TRPD | -5.190615636 | 3.46856E-11 | 5.181326667 | 0.136966 |
| Solyc02g086310.2 | lipid-transfer protein 7k-LTP precursor (AHRD V3.3 --* NP_001306883.1) | NA | -5.064869846 | 2.61792E-13 | 81.04396567 | 2.465957 |
| Solyc04g078340.3 | Cytochrome P450 (AHRD V3.3 *-* A0A200QZM5_9MAGN) | NA | -5.060306791 | 9.01554E-25 | 8.754092667 | 0.260326667 |
| Solyc10g050990.2 | Unknown protein | NA | -4.885309758 | 9.31032E-07 | 588.4448193 | 19.98058867 |
| Solyc08g066360.3 | Malic enzyme (AHRD V3.3 *** A0A2G2W5J3_CAPBA) | MAEB | -4.864062261 | 3.86236E-11 | 7.382468667 | 0.249904667 |

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|---|---|---|---|---|---|---|
| Solyc05g050980.3 | 3-phosphoshikimate 1-carboxyvinyltransferase (AHRD V3.3 *** A0A0M8KSM3_NICAT) | AROA | -4.822213987 | 2.04533E-70 | 25.115069 | 0.896876333 |
| Solyc10g018015.1 | Unknown protein | NA | -4.766882986 | 6.44532E-21 | 12.36240967 | 0.440776333 |
| Solyc09g074475.1 | Unknown protein | NA | -4.71676248 | 9.43153E-07 | 18.097113 | 0.658792667 |
| Solyc04g011390.1 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | H4 | -4.685800614 | 2.16877E-37 | 28.424249 | 1.09191 |
| Solyc06g075675.1 | Myb/SANT-like domain-containing protein (AHRD V3.3 *-* A0A2U1P375_ARTAN) | NA | -4.613422404 | 2.26507E-45 | 15.19781433 | 0.63025 |
| Solyc04g012010.3 | Disease resistance protein (AHRD V3.3 *** A0A2U1Q201_ARTAN) | NA | -4.544059784 | 1.21864E-47 | 5.755710333 | 0.249375667 |
| Solyc01g099630.4 | xyloglucan endotransglucosylase-hydrolase 1 | xyloglucan:xyloglucosyl transferase | -4.522159575 | 3.22388E-05 | 10.93693267 | 0.479012667 |
| Solyc07g025380.3 | DNA ligase-like protein (AHRD V3.3 *** AT1G75150.3) | NA | -4.474957505 | 6.37778E-25 | 1.237446667 | 0.053312333 |
| Solyc12g088390.1 | Zinc-finger protein (AHRD V3.3 *** Q40899_PETHY) | NA | -4.468722128 | 3.89382E-14 | 17.21487033 | 0.771700333 |
| Solyc07g026650.3 | 1-aminocyclopropane-1-carboxylate oxidase 5 | aminocyclopropanecarboxylate oxidase | -4.439549907 | 1.26759E-07 | 41.41221367 | 1.970156 |
| Solyc09g097960.3 | NAD(P)-linked oxidoreductase, aldo/keto reductase family protein (AHRD V3.3 *** A0A1Y1HY98_KLENI) | NA | -4.42730436 | 5.7228E-10 | 43.636401 | 2.060629 |
| Solyc07g007350.1 | Sterile alpha motif (SAM) domain protein (AHRD V3.3 *** Q1G3Q5_ARATH) | NA | -4.377076569 | 1.1699E-52 | 24.954861 | 1.196323667 |
| Solyc09g092480.1 | Glycosyltransferase (AHRD V3.3 *** A0A2I4GJH4_9ROSI) | NA | -4.354422012 | 9.08801E-19 | 15.671731 | 0.773227333 |
| Solyc04g072800.4 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (AHRD V3.3 *** A0A2G3CNK4_CAPCH) | PGAM | -4.309498719 | 3.4371E-13 | 8.950383667 | 0.453837333 |
| Solyc04g080550.4 | Isoflavone reductase-like protein (AHRD V3.3 *** A0A2G2V5Y4_CAPBA) | PCBER1 | -4.286320294 | 2.20778E-12 | 12.76449667 | 0.668348 |
| Solyc09g007910.4 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G2YQ27_CAPAN) | PAL | -4.258387437 | 1.74987E-15 | 284.1167147 | 15.177004 |
| Solyc01g099620.3 | Respiratory burst oxidase-like protein (AHRD V3.3 *** C1IHQ9_9ROSI) | RBOH | -4.240602032 | 1.77777E-08 | 2.594177667 | 0.139051 |
| Solyc05g008140.4 | Unknown protein | NA | -4.182680822 | 5.31565E-23 | 12.96976767 | 0.710020667 |
| Solyc07g005100.4 | Chitinase/lysozyme (AHRD V3.3 *** Q43591_TOBAC) | chitinase | -4.085787442 | 3.64091E-24 | 15.355256 | 0.896173667 |
| Solyc08g067310.1 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G2W7U9_CAPBA) | NA | -4.070931708 | 2.74079E-38 | 10.34751667 | 0.616939 |
| Solyc06g072013.1 | Unknown protein | NA | -3.922556784 | 1.18735E-25 | 14.056168 | 0.911365 |
| Solyc06g050340.3 | high mobility group B protein 7 isoform X1 (AHRD V3.3 *-* XP_025887246.1) | NA | -3.903752227 | 6.60647E-17 | 5.419476 | 0.360455667 |
| Solyc11g071640.3 | Glycosyl hydrolase family protein (AHRD V3.3 *** A0A1P8BG25_ARATH) | BGLX | -3.893759432 | 0.000556454 | 3.205217 | 0.219901333 |
| Solyc03g083360.3 | Pectinesterase (AHRD V3.3 *** A0A2G3CX60_CAPCH) | NA | -3.830099143 | 1.32207E-06 | 9.461324333 | 0.684465667 |
| Solyc12g011160.2 | 3-hydroxyisobutyryl-CoA hydrolase-like protein 5 (AHRD V3.3 *** A0A2G2YT91_CAPAN) | HIBCH | -3.82307757 | 4.56319E-35 | 111.149193 | 7.847044 |
| Solyc08g063000.4 | Nucleosome assembly protein family (AHRD V3.3 *** A9TVZ4_PHYPA) | NAP1L1 | -3.798285055 | 2.78715E-13 | 15.101403 | 1.112857667 |
| Solyc04g024840.3 | GDSL esterase/lipase (AHRD V3.3 *** A0A2R6QF80_ACTCH) | NA | -3.792390948 | 4.6472E-36 | 5.518810333 | 0.398924 |

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|---|---|---|---|---|---|---|
| Solyc10g086180.2 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G2VU16_CAPBA) | PAL | -3.789046155 | 1.16203E-14 | 156.3848317 | 11.47844167 |
| Solyc01g104110.4 | 11-S seed storage protein (AHRD V3.3 *** A0A2U1KM33_ARTAN) | NA | -3.735296292 | 3.0509E-24 | 10.62837333 | 0.791793 |
| Solyc09g015380.1 | Abscisic acid receptor PYL5 (AHRD V3.3 *** A0A1U8EIS0_CAPAN) | PYL | -3.730450497 | 0.000208704 | 8.636098667 | 0.650349 |
| Solyc01g100030.5.1 | deoxyuridine triphosphatase | DUT | -3.725520529 | 1.28244E-17 | 3.253352 | 0.242052 |
| Solyc01g110920.4 | Small auxin up-regulated RNA26 | NA | -3.703107653 | 1.01989E-09 | 13.63206333 | 1.058519 |
| Solyc03g093360.3 | PLAT/LH2 domain (AHRD V3.3 *** A0A200QDT2_9MAGN) | NA | -3.678691673 | 8.29082E-06 | 26.123761 | 2.099912 |
| Solyc06g072017.1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* A0A2U1N2C4_ARTAN) | NA | -3.677319773 | 3.74148E-13 | 8.260369333 | 0.639981333 |
| Solyc02g078380.3 | Stem-specific protein TSJT1 (AHRD V3.3 *** A0A1U8FVZ0_CAPAN) | NA | -3.674504634 | 3.23033E-12 | 11.40134 | 0.895951333 |
| Solyc09g090685.1 | Unknown protein | NA | -3.662689985 | 0.009837799 | 6.936681 | 0.527649667 |
| Solyc08g005120.3 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* A0A2U1LGD5_ARTAN) | NA | -3.626204121 | 4.26479E-15 | 6.082374667 | 0.483335667 |
| Solyc06g074790.2 | Histone H2B (AHRD V3.3 *** A0A2G3CAQ8_CAPCH) | H2B | -3.574676783 | 5.87142E-26 | 37.185911 | 3.154536667 |
| Solyc10g076480.2 | Ammonium transporter (AHRD V3.3 *** A0A2G2VSP2_CAPBA) | AMT | -3.548340922 | 5.85972E-06 | 3.738299667 | 0.318835667 |
| Solyc06g005680.4 | Two-component response regulator (AHRD V3.3 *-* C0HE02_MAIZE) | NA | -3.545063523 | 0.003582666 | 3.904082333 | 0.331393667 |
| Solyc07g032710.4 | hypothetical protein (AHRD V3.3 *-* AT5G42710.3) | NA | -3.513220048 | 1.33245E-21 | 3.711301 | 0.327414333 |
| Solyc04g080540.2 | DNA polymerase epsilon catalytic subunit A (AHRD V3.3 *** AT1G19530.2) | NA | -3.362067611 | 1.48761E-06 | 722.9996137 | 71.11397667 |
| Solyc10g005300.3 | Serine/threonine-protein kinase PBS1 (AHRD V3.3 *** A0A2G2VSF8_CAPBA) | NA | -3.346917091 | 1.54512E-18 | 1.957200667 | 0.187952333 |
| Solyc10g007100.3 | Protein DETOXIFICATION (AHRD V3.3 *** A0A218WWW8_PUNGR) | TC.MATE | -3.340708098 | 1.19691E-25 | 16.901845 | 1.679910333 |
| Solyc11g066330.2 | Major facilitator superfamily (AHRD V3.3 *** A0A2U1Q7R9_ARTAN) | NA | -3.337945025 | 1.02291E-07 | 2.464718 | 0.239612667 |
| Solyc02g090120.1 | hypothetical protein (AHRD V3.3 -** AT5G66985.1) | NA | -3.332397226 | 3.4711E-07 | 537.0917663 | 53.749298 |
| Solyc02g031990.1 | VQ motif-containing protein 22 (AHRD V3.3 *** A0A2G2XD74_CAPBA) | NA | -3.327819034 | 0.000943756 | 38.021232 | 3.913361333 |
| Solyc08g080040.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** F4J670_ARATH) | ANS | -3.319745012 | 6.80837E-10 | 4.700180333 | 0.470804667 |
| Solyc02g094160.1 | Ribonucleoside-diphosphate reductase small chain (AHRD V3.3 *** A0A1U8FR86_CAPAN) | RRM2 | -3.264543965 | 3.84367E-19 | 4.357572333 | 0.446378333 |
| Solyc09g007920.4 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G3BJ81_CAPCH) | PAL | -3.25839395 | 1.18691E-09 | 908.8073733 | 97.31142167 |
| Solyc01g005590.2 | Unknown protein | NA | -3.254759569 | 1.86436E-11 | 10.20341133 | 1.058748 |
| Solyc02g093300.3 | DNA polymerase (AHRD V3.3 *** H9E8V2_SOLLC) | POLA1 | -3.243710753 | 2.35575E-18 | 2.039281 | 0.21671 |
| Solyc01g087820.2 | Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC) | NA | -3.216873164 | 6.68114E-12 | 5.267331667 | 0.578458333 |
| Solyc01g097970.4 | Deoxyuridine 5'-triphosphate nucleotidohydrolase (AHRD V3.3 *** A0A2G2W7R1_CAPBA) | DUT | -3.172980934 | 2.15553E-20 | 5.196336667 | 0.577338333 |
| Solyc03g007060.3 | Cell cycle regulated microtubule associated protein (AHRD V3.3 *** A0A1P8B7D6_ARATH) | NA | -3.111566127 | 1.5426E-08 | 1.68575 | 0.197041333 |

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|---|---|---|---|---|---|---|
| Solyc07g054810.1 | Unknown protein | NA | -3.108504294 | 0.002516354 | 18.009496 | 2.006982 |
| Solyc10g049890.3 | D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** A0A2G2VSK7_CAPBA) | SERA | -3.059421295 | 1.15861E-09 | 3.491604333 | 0.42412 |
| Solyc02g093580.4 | Tomato 9612 mRNA | PEL | -3.048203397 | 5.6201E-13 | 2.416598667 | 0.291840333 |
| Solyc01g111980.3 | Lysine histidine transporter-like 8 (AHRD V3.3 *** A0A2G2XYM3_CAPAN) | NA | -3.045989026 | 2.96934E-07 | 158.3006793 | 19.6667 |
| Solyc12g057060.2 | Glycosyltransferase (AHRD V3.3 *** A0A2G3CNS7_CAPCH) | NA | -3.026746809 | 1.6837E-07 | 4.801511667 | 0.596584333 |
| Solyc12g099260.2 | Citrate synthase-like (AHRD V3.3 *** A0A200R252_9MAGN) | ACLY | -3.026455019 | 7.90141E-18 | 2.320765333 | 0.285459 |
| Solyc02g088340.4 | WRKY transcription factor 3 | NA | -3.004983742 | 4.41935E-12 | 156.0221027 | 19.82455433 |
| Solyc11g066890.1 | Arogenate dehydratase (AHRD V3.3 *** A0A2G3BBC7_CAPCH) | ADT | -3.002080312 | 4.00427E-49 | 161.674225 | 20.181363 |
| Solyc08g041770.3 | Hyp O-arabinosyltransferase-like protein (AHRD V3.3 *** AT5G13500.3) | HPAT | -3.001445126 | 0.000711806 | 7.309233 | 0.940299667 |
| Solyc03g025830.4 | Myosin heavy chain-related protein (AHRD V3.3 *** Q9C8T4_ARATH) | NA | -2.996748973 | 9.18437E-08 | 1.457748333 | 0.181037 |
| Solyc03g031830.1 | RING/U-box superfamily protein (AHRD V3.3 *** Q8GXD8_ARATH) | NA | -2.996509481 | 1.61627E-20 | 7.199883 | 0.899597 |
| Solyc01g008920.4 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1L7S8_ARTAN) | NA | -2.977191614 | 1.34814E-30 | 15.54515133 | 1.966717333 |
| Solyc12g042480.3 | Cytochrome (AHRD V3.3 *** A0A2G2Y725_CAPAN) | CYP736A | -2.972624199 | 0.021725302 | 4.550525667 | 0.593164333 |
| Solyc09g018220.3 | Tobacco mosaic virus resistance-2 | NA | -2.954536079 | 1.91549E-08 | 5.587407333 | 0.737314333 |
| Solyc10g084400.2 | Glutathione S-transferase (AHRD V3.3 *** Q76KW1_PEA) | GST | -2.940865506 | 9.91714E-43 | 148.447871 | 19.38159167 |
| Solyc06g053150.1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A2U1NSJ9_ARTAN) | NA | -2.928322671 | 8.66667E-12 | 3.341066 | 0.438618333 |
| Solyc06g008620.1 | TolB protein-related protein (AHRD V3.3 *** A0A2U1LVX5_ARTAN) | NA | -2.915834016 | 5.49219E-15 | 6.210105 | 0.831179333 |
| Solyc03g033330.3 | RING/U-box superfamily protein (AHRD V3.3 *** A0A2U1ML59_ARTAN) | NA | -2.908484014 | 4.90025E-06 | 4.732312333 | 0.636575667 |
| Solyc09g092490.3 | Glycosyltransferase (AHRD V3.3 *-* A0A2I4GJH4_9ROSI) | NA | -2.903796434 | 2.56662E-09 | 35.52907233 | 4.681395 |
| Solyc06g083440.3 | Cytochrome b5 (AHRD V3.3 *** A0A2G3CCB6_CAPCH) | CYB5 | -2.895105889 | 2.06897E-22 | 8.982302 | 1.207203333 |
| Solyc03g025840.3 | Cytochrome b561/ferric reductase transmembrane protein family (AHRD V3.3 *** A0A178UZ09_ARATH) | CYB561 | -2.893608777 | 1.14938E-23 | 420.8840637 | 56.867364 |
| Solyc11g012160.2 | Fumarylacetoacetase (AHRD V3.3 *** A0A2G3AZK7_CAPCH) | FAH | -2.888284435 | 8.06988E-56 | 304.639384 | 41.412815 |
| Solyc02g079750.4 | Quinone reductase (AHRD V3.3 *** F8WQS4_NICBE) | WRBA | -2.860241865 | 4.03238E-42 | 211.8482667 | 29.229807 |
| Solyc07g062130.3 | trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 (AHRD V3.3 *** A0A2I4GY66_9ROSI) | RHM | -2.845179078 | 0.000209974 | 17.657423 | 2.533418333 |
| Solyc10g078740.2 | Enoyl-[acyl-carrier-protein] reductase [NADH] (AHRD V3.3 *** B6TFF6_MAIZE) | FABI | -2.833150305 | 5.82091E-05 | 2.955153 | 0.418027667 |
| Solyc09g091650.3 | Replication factor C subunit 1 (AHRD V3.3 *-* A0A1Z5JWY4_FISSO) | CTF18 | -2.826141916 | 4.99904E-19 | 3.032951333 | 0.428621 |
| Solyc01g107100.3 | beta-1%2C4-xylosidase (AHRD V3.3 *** AT3G19615.1) | NA | -2.824992458 | 5.38989E-11 | 17.46941833 | 2.515959333 |
| Solyc02g068820.3 | Receptor-like protein kinase (AHRD V3.3 *** A0A2R6Q6W2_ACTCH) | NA | -2.812805803 | 9.59177E-10 | 2.511489667 | 0.355321333 |

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|---|---|---|---|---|---|---|
| Solyc01g099200.3 | Lipoxygenase (AHRD V3.3 *** K4B0V7_SOLLC) | LOX1_5 | -2.807669836 | 2.09836E-08 | 11.46730167 | 1.620455333 |
| Solyc01g100930.3 | GDSL esterase/lipase (AHRD V3.3 *** A0A1U8GQF3_CAPAN) | NA | -2.798934819 | 1.67308E-10 | 3.574676333 | 0.517354333 |
| Solyc06g036130.4 | Protein DETOXIFICATION (AHRD V3.3 *** Q6V7U8_SOLLC) | TC.MATE | -2.791503574 | 2.07631E-29 | 189.8956247 | 27.68024367 |
| Solyc11g056680.1 | Leucine-rich repeat receptor-like protein (AHRD V3.3 *** H6V788_MALDO) | NA | -2.784107441 | 6.79487E-17 | 22.08899067 | 3.179652 |
| Solyc04g077620.1 | Uncharacterized conserved protein UCP031279 (AHRD V3.3 -** AT1G10140.1) | NA | -2.737354838 | 5.29206E-06 | 51.541359 | 7.963816333 |
| Solyc09g011630.3 | Glutation-S-transferase | GST | -2.71424951 | 3.25343E-07 | 18.645843 | 2.912372333 |
| Solyc01g098400.3 | Histidine phosphotransfer protein (AHRD V3.3 *** A0A0A1WCB7_NICAT) | AHP | -2.70308117 | 3.33243E-10 | 6.806130667 | 1.028671333 |
| Solyc04g045530.4 | DNA primase large subunit (AHRD V3.3 *** A0A2G3BK14_CAPCH) | PRI2 | -2.686681562 | 0.000606031 | 1.883893333 | 0.298511333 |
| Solyc11g072630.2 | mitogen-activated protein kinase 4 | ERK | -2.68160259 | 1.41002E-17 | 26.30998733 | 4.15196 |
| Solyc02g032950.3 | WRKY transcription factor 16 | NA | -2.677978114 | 0.000718107 | 2.831254667 | 0.444725667 |
| Solyc05g014540.3 | DNA polymerase alpha subunit B (AHRD V3.3 *** A0A2G3B930_CAPCH) | POLA2 | -2.677669818 | 4.90872E-14 | 2.124192 | 0.334087 |
| Solyc06g034110.3 | Tomato acid phosphatase | NA | -2.663967114 | 1.78715E-49 | 64.246864 | 10.233056 |
| Solyc02g092860.3 | Cytochrome P450 (AHRD V3.3 *** Q9XFX1_CICAR) | CYP81E | -2.662985113 | 3.73018E-05 | 9.295514667 | 1.494595667 |
| Solyc01g102330.3 | Carbohydrate esterase, putative (DUF303) (AHRD V3.3 *** Q0WNN6_ARATH) | NA | -2.654519552 | 0.000505689 | 42.36501867 | 6.890628 |
| Solyc02g080290.3 | Beta-glucosidase 46 (AHRD V3.3 *** A0A1U8FUJ5_CAPAN) | BGLB | -2.651043567 | 7.53146E-08 | 9.623926 | 1.573451 |
| Solyc02g093970.4 | Protein kinase domain (AHRD V3.3 *** A0A200QYA9_9MAGN) | NA | -2.645787282 | 5.04449E-14 | 1.550922 | 0.248505 |
| Solyc09g007890.1 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G3BJ62_CAPCH) | PAL | -2.630966174 | 6.69582E-08 | 76.71023833 | 12.67136867 |
| Solyc05g006740.4 | Glutathione S-transferase (AHRD V3.3 *** A0A200QY01_9MAGN) | GST | -2.626155348 | 3.03578E-10 | 6.105787 | 0.989751333 |
| Solyc03g097170.3 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1LGD5_ARTAN) | NA | -2.623483651 | 0.001913466 | 3.058024667 | 0.506618 |
| Solyc01g005390.3 | Nudix hydrolase (AHRD V3.3 *** A0A2U1MBD3_ARTAN) | diphosphoinositol-polyphosphate diphosphatase | -2.58174923 | 0.001500473 | 33.59321833 | 5.73147 |
| Solyc02g070800.2 | DUF561 domain-containing protein (AHRD V3.3 *** A0A1Q3DH97_CEPFO) | NA | -2.580548482 | 2.07766E-07 | 19.90550067 | 3.360105667 |
| Solyc04g008100.3 | RING-type E3 ubiquitin transferase (AHRD V3.3 *** A0A2G2ZH40_CAPAN) | NA | -2.568009775 | 6.71002E-05 | 42.64587267 | 7.387659 |
| Solyc02g086270.4 | Protein kinase family protein (AHRD V3.3 *** A0A2U1MH78_ARTAN) | NA | -2.563990967 | 0.017562647 | 4.662009667 | 0.809210333 |
| Solyc12g010410.3 | Homeobox protein knotted-1-like 3 (AHRD V3.3 *** A0A1U8H944_CAPAN) | NA | -2.5608222 | 4.83175E-05 | 32.48239267 | 5.640577333 |
| Solyc02g065170.3 | L-ascorbate oxidase-like protein (AHRD V3.3 *** A0A2G3D2Z5_CAPCH) | NA | -2.556692294 | 0.000334567 | 3.994987 | 0.695016333 |
| Solyc07g049290.3 | Protein NRT1/ PTR FAMILY 6.4 (AHRD V3.3 *** A0A2G2Z2Y2_CAPAN) | NA | -2.531938215 | 2.28895E-07 | 2.875017333 | 0.504446667 |
| Solyc05g041540.4 | Carboxypeptidase (AHRD V3.3 *** A0A2G3BBI5_CAPCH) | SCPL-IV | -2.524800854 | 2.0586E-12 | 17.52233033 | 3.073793333 |
| Solyc05g053540.3 | Dihydroxy-acid dehydratase (AHRD V3.3 *** A0A2G3CHU1_CAPCH) | ILVD | -2.523995467 | 2.23948E-12 | 120.15301 | 21.21513567 |

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|---|---|---|---|---|---|---|
| Solyc01g106620.2 | pathogenesis-related protein 1-like (AHRD V3.3 *** A0A2I4HRD5_9ROSI) | PR1 | -2.521315448 | 0.007134707 | 4.914199333 | 0.854102333 |
| Solyc01g099410.3 | Histone H2A (AHRD V3.3 *** A0A0H5QLQ1_9EUKA) | H2A | -2.517685312 | 1.02133E-23 | 43.01931033 | 7.608207333 |
| Solyc03g112330.3 | U-box domain-containing protein 52-like (AHRD V3.3 *** A0A2K3L2U5_TRIPR) | NA | -2.516961865 | 1.76813E-08 | 3.550557 | 0.627225667 |
| Solyc08g006470.4 | Zinc finger protein (AHRD V3.3 *** A0A2U1NTB4_ARTAN) | REI1 | -2.507418953 | 0.003693136 | 2.449492667 | 0.437965667 |
| Solyc09g011550.3 | Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN) | GST | -2.50558955 | 1.72132E-08 | 3.905110667 | 0.679746667 |
| Solyc07g053640.1 | Arabinogalactan-protein (AHRD V3.3 *-* Q41256_NICAL) | NA | -2.496344648 | 7.82074E-17 | 27.90541667 | 4.929289 |
| Solyc09g089740.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1NTU8_ARTAN) | NA | -2.494639491 | 4.17592E-07 | 3.398716 | 0.601283667 |
| Solyc04g074480.3 | DAHP synthase 2 precursor | AROF | -2.480656957 | 1.09073E-15 | 54.63823533 | 9.961101333 |
| Solyc02g085390.4 | ATP-dependent DNA helicase DDM1 (AHRD V3.3 *** A0A1U8FMX5_CAPAN) | HELLS | -2.48000302 | 9.6188E-12 | 1.008600333 | 0.179122 |
| Solyc09g010000.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1NTU8_ARTAN) | NA | -2.474418504 | 4.01381E-05 | 13.47145733 | 2.490251667 |
| Solyc12g094660.2 | Disease resistance protein (AHRD V3.3 *** A0A2U1Q8K0_ARTAN) | NA | -2.471199968 | 9.42745E-06 | 5.189907333 | 0.956893 |
| Solyc04g018055.1 | Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *-* A0A2G3C9S8_CAPCH) | GAPDH | -2.466724861 | 3.42551E-07 | 5.784454333 | 1.038910333 |
| Solyc02g088460.4 | Chorismate mutase (AHRD V3.3 *** B5LAU1_CAPAN) | chorismate mutase | -2.46401914 | 9.52809E-15 | 37.25519067 | 6.886815 |
| Solyc02g094390.3 | S-acyltransferase (AHRD V3.3 *** A0A1U8FK29_CAPAN) | ZDHHC9_14_18 | -2.462237654 | 1.12904E-07 | 16.716332 | 3.093085 |
| Solyc01g108910.4 | maternal effect embryo arrest 14 (AHRD V3.3 *** AT2G15890.1) | NA | -2.459424064 | 0.000682889 | 90.07878833 | 16.52337733 |
| Solyc04g007470.3 | Drought responsive Zinc finger protein | NA | -2.458865736 | 2.02238E-05 | 13.96710133 | 2.495006 |
| Solyc09g089730.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1NTU8_ARTAN) | NA | -2.457187646 | 2.66593E-14 | 16.22497367 | 2.968067 |
| Solyc01g081410.4 | Major facilitator superfamily protein (AHRD V3.3 *** F4KD53_ARATH) | NA | -2.45368634 | 6.6346E-11 | 1.960088 | 0.353217333 |
| Solyc07g052480.3 | isocitrate lyase LEU18678 | ACEA | -2.445924107 | 3.52017E-26 | 17.77550767 | 3.262584 |
| Solyc12g036130.1 | ABC transporter C family member 2 (AHRD V3.3 *-* A0A2G3DGG8_CAPCH) | NA | -2.445142669 | 6.39935E-07 | 3.990375 | 0.7177 |
| Solyc10g086650.1 | Glyoxal oxidase (AHRD V3.3 *** A0A200R4V9_9MAGN) | NA | -2.441621872 | 2.18484E-19 | 13.36113967 | 2.495612333 |
| Solyc01g096740.4 | Protein ZINC INDUCED FACILITATOR-LIKE 1 (AHRD V3.3 *** A0A1J3IH30_NOCCA) | NA | -2.436139592 | 2.46381E-18 | 27.45080867 | 5.12302 |
| Solyc09g075910.1 | Receptor-like protein kinase (AHRD V3.3 *** A0A2U1PPA0_ARTAN) | NA | -2.421270513 | 0.045256767 | 6.934030333 | 1.322537667 |
| Solyc10g055810.2 | chitinase Z15140 | CHIB | -2.416414443 | 0.002491979 | 16.696618 | 3.191448667 |
| Solyc01g080910.2 | polyadenylate-binding protein 1-B-binding protein (AHRD V3.3 *** AT5G44860.2) | NA | -2.414970713 | 9.95912E-19 | 54.63772433 | 10.332681 |
| Solyc01g100000.3 | F-box domain, Phloem protein 2-like protein (AHRD V3.3 *** A0A2U1MNC1_ARTAN) | NA | -2.412531719 | 0.011155744 | 16.105999 | 3.087251 |
| Solyc09g064940.2 | Phenazine biosynthesis PhzF protein (AHRD V3.3 *** A0A200Q4V2_9MAGN) | NA | -2.40044779 | 1.07332E-10 | 1830.003622 | 353.5313367 |
| Solyc07g018300.3 | Replication protein A 32 kDa subunit A (AHRD V3.3 *** A0A1J3JLU8_NOCCA) | RFA2 | -2.398095183 | 4.18072E-05 | 4.866262333 | 0.917592667 |

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|---|---|---|---|---|---|---|
| Solyc09g059270.3 | ER lumen protein retaining receptor (AHRD V3.3 *** A0A200QBW0_9MAGN) | NA | -2.391130278 | 2.55544E-26 | 293.9839277 | 56.59170933 |
| Solyc06g074530.1 | Arogenate dehydratase (AHRD V3.3 *** A0A2G2VAY6_CAPBA) | ADT | -2.390788437 | 0.001342399 | 232.4379783 | 45.59390433 |
| Solyc09g042700.4 | proactivator polypeptide-like 1 (AHRD V3.3 *** A0A2I4EIU6_9ROSI) | PSAP | -2.388647762 | 1.09731E-16 | 22.30549833 | 4.258914 |
| Solyc08g077060.3 | Zinc finger, LSD1-type (AHRD V3.3 *** A0A2U1LIJ4_ARTAN) | NA | -2.378952528 | 0.003341592 | 7.233476667 | 1.419909667 |
| Solyc06g063260.4 | alpha-1,2-Mannosidase (AHRD V3.3 *** A0A2G2WKP9_CAPBA) | MAN1A_C | -2.375846488 | 7.432E-10 | 1.34847 | 0.258211667 |
| Solyc11g073010.1 | Exocyst subunit Exo70 family protein (AHRD V3.3 *** A0A2G2VNA4_CAPBA) | EXOC7 | -2.35911235 | 6.46139E-06 | 5.485121667 | 1.093011333 |
| Solyc09g057660.3 | Peptidylprolyl isomerase (AHRD V3.3 *** A0A2G2WN61_CAPBA) | FKBP4_5 | -2.358803755 | 1.13605E-35 | 61.01299067 | 12.03007533 |
| Solyc12g009180.2 | Cupin_5 domain-containing protein (AHRD V3.3 *** A0A1Q3BA35_CEPFO) | K09705 | -2.354497487 | 2.50252E-11 | 24.39079867 | 4.845642667 |
| Solyc03g117600.3 | Transferase (AHRD V3.3 *** A0A200QII6_9MAGN) | HCT | -2.348574463 | 2.44394E-14 | 7.514580333 | 1.486436667 |
| Solyc09g007730.4 | Pkinase domain-containing protein (AHRD V3.3 *** A0A1Q3B9U2_CEPFO) | NA | -2.337340854 | 0.002980238 | 4.822388333 | 0.963809667 |
| Solyc04g082270.3 | DUF241 domain-containing protein (AHRD V3.3 *** A0A1Q3B6H2_CEPFO) | NA | -2.336740509 | 8.0795E-09 | 7.048261 | 1.421504667 |
| Solyc06g069580.3 | Heparanase-like protein 1 (AHRD V3.3 *** A0A2G2ZC77_CAPAN) | HPSE | -2.336703802 | 3.07005E-14 | 5.082577 | 1.006237333 |
| Solyc05g052870.4 | Glycosyltransferase (AHRD V3.3 *** A0A2U1NU39_ARTAN) | NA | -2.335245399 | 5.63369E-09 | 2.052591333 | 0.410129667 |
| Solyc08g005800.4 | Pectin acetylesterase (AHRD V3.3 *** A0A1U8F2I8_CAPAN) | NOTUM | -2.334597833 | 0.005791151 | 6.434318667 | 1.300428 |
| Solyc10g078240.2 | Cytochrome P450 (AHRD V3.3 *** A0A2U1MC34_ARTAN) | CYP98A | -2.332362212 | 4.5672E-21 | 52.845582 | 10.63233567 |
| Solyc02g070780.4 | DNA helicase (AHRD V3.3 *** A0A2G2XDX1_CAPBA) | MCM3 | -2.329763201 | 1.43008E-09 | 7.692772333 | 1.531812 |
| Solyc07g045440.1 | Fasciclin-like arabinogalactan protein 2 (AHRD V3.3 *** A0A2G3BYC2_CAPCH) | NA | -2.328949194 | 1.89321E-06 | 2.830201333 | 0.563706667 |
| Solyc06g053810.3 | p-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** Q0WUY1_ARATH) | NA | -2.327391933 | 7.43602E-06 | 2.578648 | 0.511774 |
| Solyc01g108100.3 | cold regulated protein 27 (AHRD V3.3 *** AT5G42900.2) | NA | -2.325346607 | 0.016177764 | 18.29973533 | 3.727148667 |
| Solyc05g012510.3 | Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** A0A2G2VL62_CAPBA) | PYG | -2.318584191 | 2.47232E-07 | 8.630421 | 1.759291 |
| Solyc07g054790.1 | Wound-responsive family protein (AHRD V3.3 *** A0A2K3L288_TRIPR) | NA | -2.31750891 | 0.000130054 | 204.302363 | 41.46887533 |
| Solyc09g090900.4 | 3-isopropylmalate dehydratase large subunit (AHRD V3.3 *** A0A2G3CJZ4_CAPCH) | LEUC | -2.308923811 | 0.042523259 | 5.989426333 | 1.252768667 |
| Solyc06g065100.3 | R2R3MYB transcription factor 3 | MYBP | -2.304292206 | 1.57432E-16 | 19.25837133 | 3.931211 |
| Solyc02g071490.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** Q9SB32_ARATH) | NA | -2.294538053 | 2.88767E-10 | 2.780818333 | 0.563688333 |
| Solyc11g066400.1 | Zinc finger protein (AHRD V3.3 *** A0A200R5F9_9MAGN) | NA | -2.277022339 | 9.72751E-08 | 7.292424667 | 1.520152 |
| Solyc11g071800.2 | Strictosidine synthase (AHRD V3.3 *** A0A200Q9R0_9MAGN) | NA | -2.269570767 | 2.31144E-14 | 13.39276167 | 2.810044667 |
| Solyc03g096840.4 | hypothetical protein (AHRD V3.3 *** AT5G17165.1) | NA | -2.266871066 | 0.000220405 | 55.64295533 | 11.78598467 |
| Solyc09g059430.3 | RPM1-interacting protein 4 (AHRD V3.3 *** A0A1P8SF00_NICBE) | RIN4 | -2.247690465 | 2.26478E-08 | 17.817074 | 3.828639667 |

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|---|---|---|---|---|---|---|
| Solyc01g091190.3 | 5-enolpyruvylshikimate-3-phosphate synthase | AROA | -2.242261146 | 3.92207E-16 | 140.2620343 | 29.96184833 |
| Solyc07g043550.3 | UDP-glucose 4-epimerase (AHRD V3.3 *** A0A1Y1ITM0_KLENI) | UXE | -2.240167474 | 1.65832E-10 | 1.878892667 | 0.396488 |
| Solyc08g080650.3 | PATHOGENESIS RELATED PROTEIN P23 | NA | -2.23963135 | 0.0002612 | 8.680361667 | 1.870505333 |
| Solyc07g053480.4 | Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT) | RAB11A | -2.228699744 | 1.02281E-07 | 6.775741 | 1.470621 |
| Solyc01g010310.4 | Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 *** A0A1P8AZV6_ARATH) | NA | -2.208844585 | 1.19016E-05 | 5.624468333 | 1.231900667 |
| Solyc11g005800.2 | Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A2U1QNA9_ARTAN) | CHAF1B | -2.208630938 | 1.52912E-15 | 3.262919 | 0.709452 |
| Solyc01g079500.4 | DNA replication licensing factor MCM7 (AHRD V3.3 *** A0A1U8FE76_CAPAN) | MCM7 | -2.200517874 | 1.17196E-08 | 5.157961 | 1.123643667 |
| Solyc02g077090.4 | Protein CHUP1, chloroplastic (AHRD V3.3 *-* A0A2G3D559_CAPCH) | NA | -2.191416791 | 6.71768E-05 | 1.847561333 | 0.409185667 |
| Solyc02g080530.3 | Peroxidase (AHRD V3.3 *** K4B9S4_SOLLC) | peroxidase | -2.190597417 | 0.017762483 | 12.28732867 | 2.728769 |
| Solyc08g068680.4 | aromatic amino acid decarboxylase 1A | SDC | -2.188711456 | 0.021705868 | 77.106321 | 17.43643167 |
| Solyc08g080630.4 | Ethylene-responsive proteinase inhibitor 1 (AHRD V3.3 *** A0A1U8G7N9_CAPAN) | NA | -2.180223776 | 1.19055E-07 | 10.808632 | 2.401235667 |
| Solyc01g099340.3 | Protein indeterminate-domain 12 (AHRD V3.3 *** A0A2G2W7U4_CAPBA) | NA | -2.176321529 | 6.38749E-15 | 30.07607733 | 6.743801 |
| Solyc05g005760.4 | NHL domain-containing protein (AHRD V3.3 *** A0A2K3PAQ7_TRIPR) | NA | -2.174557235 | 1.71384E-09 | 4.870985 | 1.095668333 |
| Solyc09g097770.3 | Cell wall protein (AHRD V3.3 *** Q40142_SOLLC) | NA | -2.171048121 | 1.02011E-05 | 8.490998 | 1.904590667 |
| Solyc02g086456.1 | titin isoform X6 (AHRD V3.3 *-* XP_010316304.1) | NA | -2.169195779 | 0.00680576 | 51.90874467 | 11.70878767 |
| Solyc01g107990.3 | PI-PLC X domain-containing protein (AHRD V3.3 *** A0A2G2W995_CAPBA) | NA | -2.165017474 | 8.65589E-25 | 8.955297667 | 2.009881333 |
| Solyc02g094330.3 | Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** F4JEV5_ARATH),Pfam:PF01190 | NA | -2.159490626 | 0.000124202 | 3.007211667 | 0.687145667 |
| Solyc12g036150.1 | ABC transporter C family member 2 (AHRD V3.3 *-* A0A2G2WC67_CAPBA) | NA | -2.152257551 | 1.00804E-10 | 3.611097667 | 0.818008333 |
| Solyc09g018750.3 | CBS domain protein (AHRD V3.3 *** A0A2K3NEI1_TRIPR) | NA | -2.144673565 | 2.68645E-26 | 176.5090637 | 40.223708 |
| Solyc08g066740.3 | Early nodulin-like protein 1 (AHRD V3.3 *** A0A1J3CHP6_NOCCA) | NA | -2.139849116 | 2.57466E-06 | 3.919606333 | 0.893134667 |
| Solyc07g008520.3 | Protein NRT1/ PTR FAMILY 8.1 (AHRD V3.3 *** A0A2G2WCL3_CAPBA) | SLC15A3_4 | -2.139108434 | 2.31682E-09 | 3.517154333 | 0.805967667 |
| Solyc07g056270.3 | Receptor-like protein kinase (AHRD V3.3 *** A0A2K3P4G5_TRIPR) | NA | -2.13611485 | 0.001423207 | 1.543108 | 0.351641667 |
| Solyc01g111880.4 | MAP kinase kinase kinase 11 | NA | -2.132876233 | 0.000212886 | 5.432848333 | 1.265686333 |
| Solyc03g116740.3 | Phosphatidylcholine:diacylglycerol cholinephosphotransferase 1 (AHRD V3.3 *** A0A1U8FVJ4_CAPAN) | NA | -2.132581486 | 6.45377E-11 | 3.726150333 | 0.855766 |
| Solyc09g082810.3 | Unknown protein | NA | -2.132260541 | 0.02743384 | 7.875007667 | 1.838536333 |
| Solyc05g053100.3 | Dihydrolipoyl dehydrogenase-like protein (AHRD V3.3 *** A0A2K3PDU3_TRIPR) | DLD | -2.125976906 | 6.86414E-18 | 4.520763 | 1.038735 |
| Solyc01g107780.4 | Glycosyltransferase (AHRD V3.3 *** A0A1Q3DDW3_CEPFO) | TOGT1 | -2.121324152 | 6.35283E-06 | 2.604707333 | 0.597414 |
| Solyc03g116230.4 | Chitin-binding lectin 1 (AHRD V3.3 *-* LECT_SOLTU) | NA | -2.097068725 | 1.13106E-07 | 1118.57491 | 263.4169107 |

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|---|---|---|---|---|---|---|
| Solyc12g019410.3 | Protein kinase domain (AHRD V3.3 *** A0A200QJI2_9MAGN) | NA | -2.095299118 | 4.85554E-14 | 3.415027333 | 0.806464667 |
| Solyc07g055710.3 | Heat stress transcription factor A-5 (AHRD V3.3 *** A0A2G2Z4R4_CAPAN) | HSFF | -2.09297115 | 0.019824695 | 6.193389333 | 1.484484333 |
| Solyc06g068990.4 | Mitogen-activated protein kinase (AHRD V3.3 *** A0A2G2WLN1_CAPBA) | NA | -2.09141813 | 8.01906E-15 | 6.914608333 | 1.632729667 |
| Solyc02g086454.1 | titin isoform X6 (AHRD V3.3 *-* XP_010316304.1) | NA | -2.088022394 | 0.007467716 | 46.78440733 | 11.177527 |
| Solyc02g085100.3 | Glucose-6-phosphate 1-epimerase (AHRD V3.3 *** A0A2G3AQU6_CAPCH) | glucose-6-phosphate 1-epimerase | -2.078581757 | 1.47276E-18 | 16.04720967 | 3.798163333 |
| Solyc12g057110.2 | 14-3-3 protein (AHRD V3.3 *** P93786_SOLTU) | YWHAE | -2.077458373 | 1.46387E-08 | 11.68082633 | 2.786268333 |
| Solyc04g009850.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1NTU8_ARTAN) | NA | -2.076038966 | 3.34463E-06 | 3.741446 | 0.890769667 |
| Solyc03g112960.1 | Pectinesterase (AHRD V3.3 *-* A0A200PZQ0_9MAGN) | NA | -2.064358322 | 3.75423E-06 | 6.300622667 | 1.525569333 |
| Solyc12g009520.2 | receptor-like protein 12 (AHRD V3.3 *** A0A1S4DP57_TOBAC) | NA | -2.063923832 | 0.016943943 | 1.054722667 | 0.253302333 |
| Solyc07g006890.1 | Cytochrome P450 (AHRD V3.3 *** A0A200Q4B5_9MAGN) | CYP94A5 | -2.061466125 | 0.007050948 | 203.4463397 | 49.978819 |
| Solyc09g065180.3 | binding protein precursor AF106660 | NA | -2.061327283 | 3.64622E-17 | 8.400976 | 2.018880333 |
| Solyc11g007390.1 | Glycosyltransferase (AHRD V3.3 *-* A0A2I4G8J4_9ROSI) | NA | -2.058191324 | 3.85117E-12 | 8.713976667 | 2.109419333 |
| Solyc09g007900.4 | Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A2G3BJ81_CAPCH) | PAL | -2.0571314 | 0.000105519 | 614.139801 | 151.064321 |
| Solyc02g079200.1 | ARM repeat superfamily protein (AHRD V3.3 *** O64785_ARATH) | NA | -2.056570375 | 1.15968E-05 | 1.858363 | 0.452154 |
| Solyc02g086452.1 | titin isoform X3 (AHRD V3.3 *-* XP_004232326.1) | NA | -2.054013643 | 0.012246444 | 37.49048633 | 9.172178 |
| Solyc01g096040.4 | Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A072U5I5_MEDTR) | APF2 | -2.048862051 | 1.83168E-15 | 160.6003417 | 39.44392933 |
| Solyc09g074230.4 | SlSFP7 | ERD6 | -2.048484341 | 6.30781E-11 | 11.98044767 | 2.934912667 |
| Solyc10g008320.1 | microtubule-associated protein (AHRD V3.3 *** AT4G28310.1) | NA | -2.041356707 | 4.47738E-10 | 6.595619667 | 1.609318333 |
| Solyc02g086458.1 | titin isoform X2 (AHRD V3.3 *-* XP_010316302.1) | NA | -2.032002856 | 0.001951643 | 85.266552 | 21.178311 |
| Solyc04g077270.4 | G-type lectin S-receptor-like serine/threonine-protein kinase (AHRD V3.3 *** A0A1U8GJN2_CAPAN) | NA | -2.027033664 | 0.022758833 | 10.48729067 | 2.645782667 |
| Solyc08g021820.3 | auxin-regulated IAA29 | IAA | -2.024916526 | 0.028427975 | 6.131590333 | 1.527077 |
| Solyc10g007880.4 | Cytochrome P450 (AHRD V3.3 *** A0A2U1MAN7_ARTAN) | NA | -2.024769957 | 2.74041E-11 | 2.621718333 | 0.648972667 |
| Solyc07g007750.3 | Defensin protein (AHRD V3.3 *** B1N678_SOLLC),Pfam:PF00304 | NA | -2.020191811 | 9.95548E-10 | 6.395152333 | 1.580454667 |
| Solyc06g071290.3 | Aldehyde dehydrogenase (AHRD V3.3 *** A0A0K9R405_SPIOL) | BETB | -2.016526886 | 0.000227828 | 2.18119 | 0.547159333 |
| Solyc03g113130.3 | plant cysteine oxidase 2-like (AHRD V3.3 *** A0A2G3A1M0_CAPAN) | PCO | -2.006435921 | 0.000436891 | 7.614735667 | 1.936062 |
| Solyc02g089730.1 | Endo-1,3(4)-beta-glucanase 1 (AHRD V3.3 *** A0A1J3K097_NOCCA) | endo-1,3(4)-beta-glucanase | -2.003906748 | 0.002180929 | 2.116524333 | 0.535348333 |
| Solyc02g087770.3 | Aldose 1-epimerase (AHRD V3.3 *** A0A1U8G0C5_CAPAN) | GALM | -2.000359189 | 9.65691E-14 | 18.31072867 | 4.645264667 |

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|---|---|---|---|---|---|---|
| Solyc02g067490.3 | Actin cross-linking protein (DUF569) (AHRD V3.3 *** Q9XIF7_ARATH) | NA | -1.994205856 | 0.001855366 | 8.380178333 | 2.116101333 |
| Solyc12g044190.3 | Pvr4 (AHRD V3.3 *** A0A1D5AHY8_CAPAN) | NA | -1.989334224 | 1.08994E-08 | 2.284718667 | 0.581100333 |
| Solyc08g080640.2 | NP24 protein precursor | NA | -1.98686195 | 1.89783E-05 | 136.2806243 | 35.094068 |
| Solyc02g084600.4 | Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* A0A061DFG6_THECC) | NA | -1.985477723 | 0.036392411 | 4.110955667 | 1.033375333 |
| Solyc01g097820.4 | Adenine phosphoribosyltransferase-like protein, putative (DUF2358) (AHRD V3.3 *** Q94K63_ARATH) | NA | -1.983405227 | 9.36357E-06 | 5.279863667 | 1.343010667 |
| Solyc03g115770.3 | Two-component response regulator-like APRR5 (AHRD V3.3 *** A0A2G3CZB4_CAPCH) | TOC1 | -1.980665393 | 4.36717E-08 | 39.92076267 | 10.22200567 |
| Solyc12g042380.2 | Stress up-regulated Nod 19 (AHRD V3.3 *** A0A200R3S5_9MAGN) | NA | -1.975602818 | 5.39442E-29 | 174.8580017 | 44.88454167 |
| Solyc03g123620.4 | Pectinesterase (AHRD V3.3 *** A0A2G3D1E1_CAPCH) | NA | -1.974385995 | 0.003017909 | 26.505775 | 6.911172 |
| Solyc08g006410.4 | Glycosyltransferase (AHRD V3.3 *** B9VJL9_9SOLA) | SGT1 | -1.973231504 | 0.000530699 | 1.612561667 | 0.409684667 |
| Solyc09g065880.4 | F-box/LRR-repeat protein 17 (AHRD V3.3 *** A0A2G3CVF9_CAPCH) | NA | -1.964910844 | 2.252E-05 | 2.093447333 | 0.544271667 |
| Solyc02g093250.3 | Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** A0A1U8FPA5_CAPAN) | caffeoyl-CoA O-methyltransferase | -1.961946907 | 0.021247868 | 7.977669667 | 2.062550667 |
| Solyc01g102390.4 | Germin-like protein (AHRD V3.3 *** O65358_SOLTU) | NA | -1.946600847 | 4.39229E-08 | 15.853171 | 4.118526333 |
| Solyc04g005130.3 | bHLH transcription factor 027 | NA | -1.945345459 | 6.54705E-06 | 3.344059 | 0.873861 |
| Solyc01g110130.3 | DNA helicase (AHRD V3.3 *** A0A2G3BW33_CAPCH) | MCM4 | -1.942596754 | 1.28422E-06 | 13.65802133 | 3.588022333 |
| Solyc08g068640.4 | Serine decarboxylase (AHRD V3.3 *** A0A2G2W5V8_CAPBA) | SDC | -1.940714616 | 0.02947277 | 2.878231 | 0.766722667 |
| Solyc04g071890.3 | Peroxidase (AHRD V3.3 *** K4BTH6_SOLLC) | peroxidase | -1.936328378 | 0.048654386 | 4.328649667 | 1.163807 |
| Solyc06g074730.4 | Argonaute 5 | ELF2C | -1.928523291 | 0.003130546 | 0.935995 | 0.246683667 |
| Solyc03g026110.4 | SUN-like protein 8 | NA | -1.926027923 | 4.78278E-07 | 11.85418967 | 3.164625333 |
| Solyc09g018080.3 | protein DETOXIFICATION 53 (AHRD V3.3 *-* XP_019071047.2) | NA | -1.925699364 | 4.28397E-07 | 8.401367333 | 2.214630667 |
| Solyc05g018050.1 | RING/U-box superfamily protein (AHRD V3.3 *-* A0A2U1KYA3_ARTAN) | NA | -1.925636236 | 0.004686294 | 12.43109467 | 3.320516667 |
| Solyc11g062060.3 | Zinc finger protein (AHRD V3.3 *** A0A200QA40_9MAGN) | NA | -1.922983988 | 7.54729E-05 | 12.29551367 | 3.237887333 |
| Solyc09g008550.4 | NCS1 family nucleobase:cation symporter-1 (AHRD V3.3 *** A0A328X9Z8_9BURK) | TC.NCS1 | -1.912475843 | 3.38032E-09 | 8.966404667 | 2.370828667 |
| Solyc02g088200.4 | Putative eukaryotic LigT (AHRD V3.3 *-* AT3G16230.2) | ASCC1 | -1.90751727 | 0.001220218 | 6.527229 | 1.773784 |
| Solyc12g057040.2 | cryptochrome 1b | CRY1 | -1.903914985 | 4.75405E-12 | 10.02048133 | 2.709205 |
| Solyc06g005430.1 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | H4 | -1.902684884 | 8.15338E-19 | 44.02565167 | 11.87595967 |
| Solyc10g078920.3 | Thioredoxin-like 3-1, chloroplastic (AHRD V3.3 *** A0A2G3BHN6_CAPCH) | NA | -1.89982328 | 1.09141E-05 | 21.48951667 | 5.76901 |
| Solyc02g085180.5.1 | alpha/beta fold family protein | NA | -1.889786474 | 1.24896E-08 | 5.572579667 | 1.502317 |
| Solyc04g071650.4 | Cellulose synthase (AHRD V3.3 *** K4BTF5_SOLLC) | CESA | -1.889461629 | 0.001414653 | 4.700195667 | 1.301185333 |

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|---|---|---|---|---|---|---|
| Solyc10g083880.2 | tonoplast intrinsic protein 1.3 | TIP | -1.884234021 | 5.03493E-05 | 37.326631 | 10.14444333 |
| Solyc03g114950.2 | ABC transporter B family member 27 (AHRD V3.3 *** A0A1U8FW31_CAPAN) | NA | -1.881100055 | 3.38077E-10 | 14.10322 | 3.874546667 |
| Solyc05g051780.4 | Gamma-glutamyltranspeptidase 1 (AHRD V3.3 *** A0A2G2WRQ3_CAPBA),Pfam:PF01019 | GGT1_5 | -1.880989964 | 2.94637E-07 | 8.229835 | 2.271189 |
| Solyc09g011650.4 | Glutathione S-transferase (AHRD V3.3 *** A0A173GPJ1_9ASPA) | GST | -1.877859254 | 3.4814E-16 | 13.16930967 | 3.618719333 |
| Solyc12g036120.1 | ABC transporter C family member 2 (AHRD V3.3 *-* A0A2G3DGG8_CAPCH) | NA | -1.877265733 | 1.90592E-07 | 3.192434 | 0.861083667 |
| Solyc01g094460.3 | AT-hook motif nuclear-localized protein 9-like (AHRD V3.3 *** A0A2I4E613_9ROSI) | NA | -1.871393066 | 0.005500366 | 1.318754 | 0.356008333 |
| Solyc01g079950.3 | Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A2U1ML86_ARTAN) | NA | -1.871196072 | 0.015582839 | 3.166197333 | 0.883404333 |
| Solyc12g008660.1 | Zinc finger transcription factor 73 | NA | -1.87034151 | 0.017762483 | 11.40416333 | 3.151023333 |
| Solyc09g066070.4 | homeobox-leucine zipper protein ROC8 (AHRD V3.3 *** A0A2I4EBE3_9ROSI) | HD-ZIP | -1.866124928 | 9.59177E-10 | 17.896464 | 4.986076333 |
| Solyc07g007400.3 | Leucine-rich repeat-like protein (AHRD V3.3 *-* Q6K620_ORYSJ) | NA | -1.863256814 | 0.013798401 | 64.39912367 | 17.58144133 |
| Solyc03g083560.1 | Protein EXORDIUM-like 7 (AHRD V3.3 *** A0A2G2X692_CAPBA) | NA | -1.857017139 | 1.50265E-07 | 47.80485533 | 13.424335 |
| Solyc11g011210.2 | Gibberellin-regulated protein 12 (AHRD V3.3 *** A0A1U8GMV5_CAPAN) | NA | -1.856866949 | 1.03182E-16 | 605.7571413 | 167.7419127 |
| Solyc01g006280.3 | Formate--tetrahydrofolate ligase (AHRD V3.3 *** A0A2G3DED7_CAPCH) | FHS | -1.853369064 | 3.70109E-15 | 157.207255 | 43.69052267 |
| Solyc02g082180.3 | DNA helicase (AHRD V3.3 *** A0A2G2XFH5_CAPBA) | MCM6 | -1.846547644 | 9.36231E-09 | 9.107374 | 2.554447333 |
| Solyc06g150137.1 | Cytochrome P450 (AHRD V3.3 *** A0A2U1MXM4_ARTAN) | CYP73A | -1.845580048 | 4.24157E-16 | 106.01665 | 29.62105067 |
| Solyc05g007480.1 | protein PHYTOCHROME KINASE SUBSTRATE 1-like (AHRD V3.3 *** A0A2I4EE26_9ROSI) | NA | -1.842378232 | 2.25443E-05 | 3.534472 | 0.989597 |
| Solyc03g121610.3 | Serine/threonine-protein kinase PBS1 (AHRD V3.3 *** A0A2G2XXF9_CAPAN) | NA | -1.839874787 | 1.45674E-06 | 2.178697333 | 0.617698333 |
| Solyc07g062500.3 | Cytochrome (AHRD V3.3 *** A0A2G2WF27_CAPBA) | NA | -1.839273825 | 0.011059057 | 2.776898 | 0.793942667 |
| Solyc02g067580.3 | B12D protein (AHRD V3.3 *** Q9XHD5_IPOBA) | NA | -1.836025345 | 0.00066444 | 357.3989717 | 101.0915883 |
| Solyc06g008510.3 | Cdt1-like protein chloroplastic-like (AHRD V3.3 *** A0A2K3MWV0_TRIPR) | CDT1 | -1.829890785 | 0.009790554 | 1.336690667 | 0.371405 |
| Solyc11g065940.2 | ENTH/VHS-like protein (AHRD V3.3 *** A0A2U1LWI0_ARTAN) | EPN | -1.826110186 | 8.49728E-18 | 20.81643333 | 5.882505667 |
| Solyc09g011560.3 | Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN) | GST | -1.815009147 | 3.43961E-05 | 26.282149 | 7.468615333 |
| Solyc10g007070.4 | Early nodulin-like protein 1 (AHRD V3.3 *-* A0A2G3BCD1_CAPCH) | NA | -1.812838699 | 7.98786E-16 | 12.588908 | 3.591641667 |
| Solyc01g109040.4 | Cytochrome b6-f complex subunit 7 (AHRD V3.3 *** A0A1U8DXD4_CAPAN) | NA | -1.806473506 | 2.98888E-06 | 5.742195 | 1.628455667 |
| Solyc09g066060.3 | homeobox-leucine zipper protein ROC8 (AHRD V3.3 *-* A0A2I4EBE3_9ROSI) | HD-ZIP | -1.781930018 | 8.4987E-07 | 15.21256133 | 4.487078333 |
| Solyc10g083360.2 | Calmodulin-binding family protein, putative, expressed (AHRD V3.3 *** Q2QXN6_ORYSJ) | NA | -1.7781428 | 1.05966E-20 | 81.303444 | 23.978002 |
| Solyc02g031950.3 | pathogenesis-related family protein (AHRD V3.3 *** AT1G78780.5) | NA | -1.777825658 | 4.70817E-22 | 82.74081933 | 24.221913 |
| Solyc07g053950.1 | microtubule-associated protein (AHRD V3.3 *** AT4G28310.1) | NA | -1.776568052 | 3.85076E-05 | 15.42004467 | 4.527814 |
| Solyc08g075470.3 | WAT1-related protein (AHRD V3.3 *** K4CMR4_SOLLC) | NA | -1.773564491 | 1.39078E-05 | 2.452942 | 0.725241667 |

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|---|---|---|---|---|---|---|
| Solyc11g011190.1 | Exostosin-like protein (AHRD V3.3 *** A0A2U1NB95_ARTAN) | NA | -1.771166982 | 5.55723E-10 | 16.54752233 | 4.863995667 |
| Solyc02g082680.4 | RB1-inducible coiled-coil protein (AHRD V3.3 *** AT2G17550.1) | NA | -1.767447729 | 5.88734E-09 | 3.849076 | 1.127566333 |
| Solyc04g054980.3 | PLAT/LH2 domain (AHRD V3.3 *** A0A200QB70_9MAGN) | NA | -1.767064914 | 5.51089E-05 | 75.916687 | 22.80353433 |
| Solyc05g008540.3 | Origin of replication complex subunit 4 (AHRD V3.3 *** A0A2G2VJZ3_CAPBA) | ORC4 | -1.766886012 | 0.002840984 | 1.774343333 | 0.526830333 |
| Solyc07g007410.4 | Leucine-rich repeat (AHRD V3.3 *-* A0A200R908_9MAGN) | NA | -1.760370769 | 0.011336195 | 53.988706 | 15.85727633 |
| Solyc04g079720.4 | HXXXD-type acyl-transferase family protein (AHRD V3.3 *** A0A2U1N4J4_ARTAN) | NA | -1.759967396 | 5.22527E-16 | 26.440074 | 7.893751 |
| Solyc01g094760.3 | Origin of replication complex subunit 5 (AHRD V3.3 *** A0A2G3BSZ3_CAPCH) | ORC5 | -1.759457721 | 0.000794442 | 1.546905333 | 0.465069667 |
| Solyc01g006680.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1NBL4_ARTAN) | JMJ30 | -1.747551369 | 0.019208498 | 23.42993767 | 7.026513667 |
| Solyc02g093050.3 | WRKY transcription factor 8 | NA | -1.747096758 | 0.004043866 | 23.12885567 | 7.029981667 |
| Solyc12g056660.3 | Mitochondrial carrier protein (AHRD V3.3 *** A0A200QJI9_9MAGN) | SLC25A26 | -1.743134948 | 9.20977E-08 | 4.306564667 | 1.302163333 |
| Solyc12g089210.2 | Ornithine carbamoyltransferase (AHRD V3.3 *** A0A2G2YA09_CAPAN) | OTC | -1.742719453 | 0.000468372 | 26.42221867 | 7.805508333 |
| Solyc06g007580.1 | PDDEXK-like protein (AHRD V3.3 *** A0A2U1LF29_ARTAN) | NA | -1.740780074 | 0.011172428 | 14.76303233 | 4.474203 |
| Solyc01g100770.2 | DUF538 domain-containing protein (AHRD V3.3 *** A0A1Q3CLQ5_CEPFO) | NA | -1.732966611 | 8.17318E-05 | 6.374728 | 1.892983333 |
| Solyc10g084250.1 | Lectin receptor kinase-like protein (AHRD V3.3 *** S8CIF7_9LAMI) | NA | -1.732013274 | 2.38475E-05 | 1.689179667 | 0.515181333 |
| Solyc06g005160.4 | cytosolic ascorbate peroxidase 1 | L-ascorbate peroxidase | -1.730789182 | 5.7057E-19 | 630.171997 | 191.0861817 |
| Solyc12g056830.1 | ATP synthase subunit delta, chloroplastic-like (AHRD V3.3 *** A0A2I4F0A5_9ROSI) | ATPF1D | -1.726586916 | 3.57248E-10 | 40.772382 | 12.37677567 |
| Solyc04g082880.4 | Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (AHRD V3.3 *** A0A1U8GHK4_CAPAN) | PFP | -1.725421114 | 3.47098E-08 | 112.5275243 | 34.41011433 |
| Solyc07g007420.3 | F-box/LRR-repeat protein (AHRD V3.3 *** A0A2K3MS36_TRIPR) | NA | -1.723176301 | 0.004272919 | 21.453167 | 6.450418333 |
| Solyc07g053920.3 | Mannan endo-1,4-beta-mannosidase (AHRD V3.3 *** A0A2K3MXH2_TRIPR) | MAN | -1.722878126 | 0.007599125 | 1.360174 | 0.416715333 |
| Solyc12g036160.3 | ABC transporter C family member 2 (AHRD V3.3 *-* A0A2G3DGG8_CAPCH) | NA | -1.721931917 | 2.76754E-07 | 4.442275 | 1.346327 |
| Solyc05g005160.3 | ATP-citrate synthase (AHRD V3.3 *** B6TD54_MAIZE) | ACLY | -1.712363707 | 2.45615E-16 | 26.05502033 | 8.059816 |
| Solyc09g014900.3 | Cytochrome P450 (AHRD V3.3 *** A0A2U1NKI2_ARTAN) | CYP71P1 | -1.710233002 | 0.008002814 | 4.841981 | 1.509355 |
| Solyc09g074890.1 | Rapid ALkalinization Factor (AHRD V3.3 *** A0A200QWN9_9MAGN) | NA | -1.710132205 | 0.026256793 | 12.068699 | 3.734612333 |
| Solyc08g076730.4 | Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* Q0WUZ1_ARATH) | NA | -1.709978943 | 0.018512502 | 7.226419 | 2.241754667 |
| Solyc05g007010.3 | Glyoxal oxidase (AHRD V3.3 *** A0A200PQ20_9MAGN) | NA | -1.708320549 | 2.6162E-05 | 3.537075333 | 1.086447667 |
| Solyc09g098425.1 | CRIB domain-containing protein RIC1 (AHRD V3.3 *** A0A2G3CR99_CAPCH) | NA | -1.700243602 | 0.025350559 | 8.420198333 | 2.656218667 |
| Solyc07g062270.3 | Gamma-glutamyl hydrolase (AHRD V3.3 *** B2Z9Y3_SOLLC) | GGH | -1.696711681 | 1.17722E-21 | 16.548823 | 5.144659667 |
| Solyc07g006730.4 | Protein DETOXIFICATION (AHRD V3.3 *** A0A2I4FHR8_9ROSI) | TC.MATE | -1.695146218 | 0.000336549 | 4.367904 | 1.378756667 |

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|---|---|---|---|---|---|---|
| Solyc05g055430.4 | RAP release 2, galactose-binding-like domain protein, putative (DUF1997) (AHRD V3.3 *** A0A1P8BG49_ARATH) | NA | -1.694081727 | 0.007397893 | 4.209564 | 1.287904 |
| Solyc06g073190.3 | fructokinase 2 | SCRK | -1.687106691 | 9.2163E-22 | 132.6662647 | 41.48616533 |
| Solyc03g044790.3 | methylesterase AY455313 | NA | -1.684831122 | 6.33111E-05 | 6.783376 | 2.112764333 |
| Solyc06g005420.1 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | H4 | -1.676229002 | 1.92229E-14 | 112.022397 | 35.00501067 |
| Solyc06g051410.4 | N-(5'-phosphoribosyl)anthranilate isomerase (AHRD V3.3 *** S8D1B0_9LAMI) | TRPF | -1.674775226 | 0.000295424 | 11.70507333 | 3.712525 |
| Solyc01g110000.3 | Beta-galactosidase (AHRD V3.3 *** A0A2G3BW46_CAPCH) | NA | -1.674262418 | 0.000161054 | 3.201559 | 1.015235 |
| Solyc03g095600.1 | KIP1-like (AHRD V3.3 *-* A0A200R3P8_9MAGN) | NA | -1.67253659 | 5.36137E-07 | 1.644923 | 0.516603333 |
| Solyc12g095760.2 | Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (AHRD V3.3 *** A0A2G3B4E8_CAPCH) | PFP | -1.672430427 | 0.005608328 | 16.47116667 | 5.292433333 |
| Solyc08g006350.3 | Glycosyltransferase (AHRD V3.3 *** B9VJL9_9SOLA) | SGT1 | -1.669072162 | 3.64115E-11 | 32.48695567 | 10.257547 |
| Solyc02g005606.1 | serine/threonine-protein phosphatase 7 long form homolog (AHRD V3.3 *-* XP_019069006.1) | NA | -1.663441559 | 0.034562572 | 26.33023033 | 8.414891667 |
| Solyc07g049700.1 | Disease resistance protein (AHRD V3.3 *** A0A2U1N8H9_ARTAN) | NA | -1.660682812 | 0.000126942 | 2.190022667 | 0.698910667 |
| Solyc06g064550.3 | Aspartokinase-homoserine dehydrogenase (AHRD V3.3 *** O63067_SOYBN) | THRA | -1.659502707 | 3.22385E-06 | 3.389996 | 1.091805333 |
| Solyc09g092260.4 | Chaperone protein DnaJ (AHRD V3.3 *** A0A2G3AV72_CAPCH) | NA | -1.655753442 | 0.008172851 | 9.103744 | 2.904989333 |
| Solyc09g010020.2 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1NTU8_ARTAN) | NA | -1.654336523 | 0.011621183 | 15.261617 | 4.991213 |
| Solyc05g009050.3 | Receptor-like protein kinase (AHRD V3.3 *** D3G6F0_CAPAN) | NA | -1.646913199 | 0.01082244 | 1.871084 | 0.608752333 |
| Solyc02g065765.1 | COBRA-like protein (AHRD V3.3 *** K4B708_SOLLC) | NA | -1.64428529 | 0.001435367 | 9.429053667 | 3.089318 |
| Solyc02g031960.3 | Pectate lyase (AHRD V3.3 *-* A0A2G3DIQ3_CAPCH) | NA | -1.641920567 | 0.000112689 | 22.02269833 | 7.095599667 |
| Solyc04g081400.3 | plastidic hexokinase | HK | -1.639792934 | 8.47148E-16 | 17.24279533 | 5.596234 |
| Solyc05g005330.3 | Disease resistance protein (AHRD V3.3 *** A0A2U1Q201_ARTAN) | NA | -1.635572874 | 0.001561675 | 1.957939 | 0.643061667 |
| Solyc10g006330.3 | protein PLASTID MOVEMENT IMPAIRED 1 (AHRD V3.3 *** A0A2I4GWL2_9ROSI) | NA | -1.63508984 | 7.37801E-10 | 7.402094333 | 2.387733667 |
| Solyc06g076350.3 | LePCL1 | NA | -1.632713338 | 0.010899651 | 21.76370067 | 7.117274333 |
| Solyc04g074700.4 | LES17306 homeodomain protein | HD-ZIP | -1.627432812 | 0.019122191 | 2.488519333 | 0.813888 |
| Solyc09g075420.3 | ethylene response factor E.1 | EREBP | -1.622989651 | 3.28254E-06 | 483.3107907 | 159.367147 |
| Solyc04g054830.4 | Type I inositol polyphosphate 5-phosphatase 5 (AHRD V3.3 *-* A0A199V5W7_ANACO) | NA | -1.622177148 | 0.000215693 | 1.782698667 | 0.582937333 |
| Solyc03g120450.4 | Aminotransferase (AHRD V3.3 *** A0A200PN75_9MAGN) | ISS1 | -1.619006534 | 3.32718E-05 | 2.883155667 | 0.949982 |
| Solyc09g013150.4 | Phosphate transporter (AHRD V3.3 *** A0A2H4H6T2_MALDO) | SLC17A | -1.616899976 | 0.000533466 | 162.119733 | 53.59961867 |
| Solyc03g117590.3 | Chaperone protein DnaJ (AHRD V3.3 *** A0A2G2WQF7_CAPBA) | NA | -1.61349224 | 9.79175E-08 | 32.63376633 | 10.836021 |
| Solyc12g056800.2 | Oxidoreductase (AHRD V3.3 *** A0A200QCB4_9MAGN) | NA | -1.611816678 | 0.012735925 | 2.106583333 | 0.701764667 |

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|---|---|---|---|---|---|---|
| Solyc03g025200.3 | Protein DETOXIFICATION (AHRD V3.3 *** Q6V7U8_SOLLC) | TC.MATE | -1.606603174 | 8.55958E-08 | 3.486555667 | 1.157466667 |
| Solyc04g082460.4 | Catalase (AHRD V3.3 *** A0A2G2X1I6_CAPBA) | KATE | -1.597800428 | 4.17985E-13 | 49.16808967 | 16.23458133 |
| Solyc01g005800.3 | Calmodulin binding protein (AHRD V3.3 *** A0A2K3N563_TRIPR) | NA | -1.594427546 | 0.000315717 | 3.238063 | 1.088749 |
| Solyc09g065190.3 | Ran GTPase-activating protein 1 (AHRD V3.3 *** A7M8K3_SOLTU) | RANGAP1 | -1.593796943 | 5.42884E-15 | 14.544171 | 4.842313667 |
| Solyc01g096430.4 | NADPH:quinone oxidoreductase-like (AHRD V3.3 *** A0A2I4GZV4_9ROSI) | CHRR | -1.589128343 | 7.37801E-10 | 16.91803667 | 5.700785333 |
| Solyc10g050220.2 | hypothetical protein (AHRD V3.3 *-* AT4G33980.2) | NA | -1.587671826 | 9.94976E-05 | 12.126093 | 4.063769667 |
| Solyc09g075720.4 | Protein kinase superfamily protein (AHRD V3.3 *** Q0WSF6_ARATH) | NA | -1.582416764 | 0.009683476 | 3.373039 | 1.147843667 |
| Solyc03g083470.3 | Receptor-like protein kinase (AHRD V3.3 *** A0A2K3NJB3_TRIPR) | NA | -1.582249573 | 0.027949291 | 14.11741333 | 4.845047667 |
| Solyc04g073950.2 | VQ motif protein (AHRD V3.3 *-* A0A2K3NKL0_TRIPR) | NA | -1.581138566 | 4.19246E-07 | 17.14937367 | 5.796573333 |
| Solyc11g005690.3 | TONSOKU protein (AHRD V3.3 *** Q4W7J1_TOBAC) | NA | -1.577425058 | 0.000638209 | 0.792681667 | 0.268963667 |
| Solyc12g014490.3 | 65-kDa microtubule-associated protein 1-like (AHRD V3.3 *** Q9FEV7_TOBAC),Pfam:PF03999 | PRC1 | -1.576864598 | 0.043201401 | 2.782454 | 0.950425333 |
| Solyc06g076640.3 | Tubulin beta chain (AHRD V3.3 *** A0A1U8H9E6_CAPAN) | TUBB | -1.575412819 | 3.20886E-05 | 11.71489933 | 4.007756333 |
| Solyc11g020610.3 | Neutral/alkaline invertase (AHRD V3.3 *** I0CL58_MANES) | NA | -1.570395581 | 2.94304E-07 | 3.827278 | 1.288814333 |
| Solyc05g052450.3 | Protein trichome birefringence-like 32 (AHRD V3.3 *** A0A1U8GQI0_CAPAN) | NA | -1.567839849 | 1.05889E-05 | 2.746397667 | 0.939591333 |
| Solyc01g105370.4 | 2-nitropropane dioxygenase-like protein (AHRD V3.3 *** Q9FMG0_ARATH) | NA | -1.56629747 | 0.001016891 | 29.33302933 | 10.07053167 |
| Solyc04g077020.3 | Tubulin alpha chain (AHRD V3.3 *** A0A1U8GD16_CAPAN) | TUBA | -1.563394378 | 0.00167493 | 97.85560367 | 33.88855967 |
| Solyc02g063520.3 | Homeobox-leucine zipper protein HAT22 (AHRD V3.3 *** A0A2G2XBJ3_CAPBA) | HD-ZIP | -1.563323647 | 2.66444E-05 | 4.735624 | 1.604833 |
| Solyc11g012910.2 | Gamma-glutamylcyclotransferase (AHRD V3.3 *** A0A2G2ZMV7_CAPAN) | GGCT | -1.558262366 | 1.72881E-16 | 29.13878133 | 9.983533 |
| Solyc04g055170.3 | annexin p35 | ANNAT | -1.556855251 | 2.88179E-16 | 60.37118033 | 20.78518833 |
| Solyc03g114100.1 | hypothetical protein (AHRD V3.3 *** AT1G52720.1) | NA | -1.552238935 | 0.023503751 | 11.90885733 | 4.06965 |
| Solyc05g056540.4 | Alcohol dehydrogenase-like protein (AHRD V3.3 *** Q8LDF7_ARATH) | NA | -1.549720066 | 4.13718E-14 | 37.80286133 | 13.043242 |
| Solyc06g071410.3 | MAP kinase kinase kinase 40 | NA | -1.544802227 | 0.02743384 | 2.257135 | 0.777055667 |
| Solyc04g049350.4 | chorismate synthase 1 precursor | AROC | -1.542906024 | 1.34071E-16 | 166.5517377 | 57.488668 |
| Solyc07g026930.3 | Unknown protein | NA | -1.540460771 | 0.000500243 | 1.826886 | 0.631199333 |
| Solyc11g006470.2 | Core-2 i-branching beta-n-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A2K3MQ33_TRIPR) | NA | -1.5397381 | 1.33344E-06 | 16.99407467 | 5.877643667 |
| Solyc04g049450.3 | Protein disulfide-isomerase (AHRD V3.3 *** A0A2G3AFP1_CAPAN) | PDIA1 | -1.529744461 | 5.43128E-07 | 18.84787267 | 6.633649667 |
| Solyc11g005700.1 | RING-type E3 ubiquitin transferase (AHRD V3.3 *** A0A2G2VFF2_CAPBA) | NA | -1.528750571 | 4.28676E-06 | 16.579757 | 5.834489 |
| Solyc04g079480.2 | Serpin-ZX (AHRD V3.3 *** A0A2G2X0W8_CAPBA) | SERPINB | -1.527733869 | 0.006572332 | 2.540094 | 0.902258667 |

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|---|---|---|---|---|---|---|
| Solyc10g005510.3 | Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** A0A2G3BCA8_CAPCH) | GAPDH | -1.526416028 | 3.73488E-08 | 59.676608 | 21.10016667 |
| Solyc11g066660.3 | Magnesium transporter MRS2-A, chloroplastic (AHRD V3.3 *** A0A2G2YHE9_CAPAN) | MRS2 | -1.52057737 | 0.000794968 | 9.561450667 | 3.363878 |
| Solyc08g075120.3 | Rop guanine nucleotide exchange factor 14 (AHRD V3.3 *** A0A2G3AG82_CAPAN) | NA | -1.519513364 | 5.8356E-05 | 1.680575 | 0.588509333 |
| Solyc09g047870.4 | 23S rRNA (Cytidine1920-2'-O)/16S rRNA (Cytidine1409-2'-O)-methyltransferase (AHRD V3.3 *** A0A2I0WJW4_9ASPA) | TLYA | -1.514193564 | 1.86742E-07 | 6.329354667 | 2.228406 |
| Solyc04g012060.3 | Ribonucleoside-diphosphate reductase (AHRD V3.3 *** A0A1U8FDK5_CAPAN) | RRM1 | -1.513159721 | 5.05699E-07 | 1.864320667 | 0.652719333 |
| Solyc02g083590.3 | dehydroquinate synthase | AROB | -1.510748942 | 8.44561E-12 | 127.6499227 | 45.16929 |
| Solyc07g062780.3 | E3 SUMO-protein ligase MMS21 (AHRD V3.3 *** A0A2G2Z5F2_CAPAN) | NSMCE2 | -1.509113829 | 1.71671E-05 | 2.649927 | 0.935843333 |
| Solyc09g065030.3 | Protein trichome birefringence-like 11 (AHRD V3.3 *** A0A2G2V2U5_CAPBA) | NA | -1.508718764 | 2.12557E-08 | 8.364403667 | 2.968185333 |
| Solyc10g080940.3 | Tubulin beta chain (AHRD V3.3 *** A0A1U8EJY6_CAPAN) | TUBB | -1.506612632 | 0.000315611 | 66.14860033 | 23.73096567 |
| Solyc04g051350.3 | Ribonucleoside-diphosphate reductase (AHRD V3.3 *** A0A2G3BE96_CAPCH) | RRM1 | -1.504289038 | 3.49882E-06 | 1.417591333 | 0.503651 |
| Solyc04g077670.3 | Serine carboxypeptidase-like 18 (AHRD V3.3 *** A0A2G3CPL7_CAPCH) | SCPL-I | -1.502369893 | 0.000495212 | 3.08982 | 1.105921667 |
| Solyc12g008600.2 | DUF1005 family protein (DUF1005) (AHRD V3.3 *** Q9M0F0_ARATH) | NA | -1.490951609 | 0.005609824 | 6.240396667 | 2.243646333 |
| Solyc01g101040.3 | ATP-citrate synthase (AHRD V3.3 *** B6TD54_MAIZE) | ACLY | -1.489807629 | 2.54808E-11 | 99.37329367 | 35.90842767 |
| Solyc01g087540.4 | DUF642 domain-containing protein (AHRD V3.3 *** A0A1Q3AUQ6_CEPFO) | NA | -1.483102644 | 0.018082215 | 2.295744333 | 0.834449333 |
| Solyc01g008130.4 | Glutaredoxin-related protein (AHRD V3.3 *** A0A2U1PBW7_ARTAN) | NA | -1.481841308 | 0.027281145 | 4.711111 | 1.73023 |
| Solyc03g118190.4 | Ethylene-responsive transcription factor (AHRD V3.3 *** A0A2G3CZ32_CAPCH) | NA | -1.47189394 | 2.54704E-05 | 3.160156333 | 1.13611 |
| Solyc10g076510.2 | Pyruvate decarboxylase (AHRD V3.3 *** Q8H9C6_SOLTU) | PDC | -1.469489855 | 0.001057077 | 396.4750217 | 143.9657617 |
| Solyc03g098740.1 | Biotic cell death-associated protein (AHRD V3.3 *** Q850R9_NICGU) | NA | -1.46722629 | 4.83864E-07 | 74.31021367 | 27.179368 |
| Solyc04g076880.3 | phosphoenolpyruvate carboxykinase | PCKA | -1.466905771 | 6.39536E-05 | 405.5024923 | 147.7928823 |
| Solyc10g079090.3 | Chaperone protein dnaJ 6 (AHRD V3.3 *** A0A1U8EIY5_CAPAN) | DNAJC9 | -1.464464627 | 0.000262465 | 13.016654 | 4.703404 |
| Solyc01g104720.3 | thionin-like protein (AHRD V3.3 -** AT1G25275.1) | NA | -1.459768647 | 2.64512E-08 | 2183.572672 | 801.215108 |
| Solyc06g065210.4 | Neutral/alkaline invertase (AHRD V3.3 *** I0CL58_MANES) | NA | -1.458475718 | 5.49296E-13 | 11.174252 | 4.103709333 |
| Solyc01g102400.3 | Germin-like protein (AHRD V3.3 *** O65358_SOLTU) | NA | -1.455102763 | 0.001234214 | 5.566708 | 2.057332 |
| Solyc09g066470.4 | ABC transporter-like (AHRD V3.3 *** A0A200PW10_9MAGN) | CAF16 | -1.455096177 | 1.0583E-07 | 15.48726 | 5.693377 |
| Solyc10g079050.2 | BHLH transcription factor o95 | NA | -1.451888655 | 0.001467007 | 40.38069633 | 14.619393 |
| Solyc12g008470.2 | Cytochrome B5-like protein (AHRD V3.3 *** A0A1U8EAT2_CAPAN) | NA | -1.450486576 | 0.018704227 | 18.08997433 | 6.738336333 |
| Solyc06g036250.2 | stress response NST1-like protein (AHRD V3.3 *** AT4G25690.2) | NA | -1.448527394 | 0.000329554 | 40.68742533 | 14.830704 |
| Solyc04g016470.4 | LEQA L.esculentum TomQ'a beta(1,3)glucanase | NA | -1.445069311 | 0.000572835 | 12.607757 | 4.645252 |

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|---|---|---|---|---|---|---|
| Solyc07g065660.4 | Cellulose synthase-like protein E1 (AHRD V3.3 *** A0A2G2Z684_CAPAN) | NA | -1.442115678 | 0.024831912 | 1.031548667 | 0.383583 |
| Solyc02g089690.3 | Protein trichome birefringence-like 19 (AHRD V3.3 *** A0A2G2XIK2_CAPBA) | NA | -1.440106447 | 0.037386768 | 1.644241667 | 0.610591667 |
| Solyc06g005150.3 | ascorbate peroxidase | L-ascorbate peroxidase | -1.435744818 | 1.36502E-14 | 241.4290363 | 89.83595 |
| Solyc06g005260.3 | Glutaredoxin (AHRD V3.3 *** A0A2G2XHT5_CAPBA) | GRXC | -1.435102364 | 4.86976E-12 | 300.9543153 | 112.8630397 |
| Solyc02g093980.3 | Nucleolar-like protein (AHRD V3.3 *-* F4J3H8_ARATH) | NA | -1.433992964 | 1.00139E-05 | 1.168166667 | 0.437419333 |
| Solyc01g100370.3 | Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** A0A2U1PDN0_ARTAN) | NA | -1.430572628 | 0.01065234 | 589.9410603 | 221.8122253 |
| Solyc09g075020.3 | ABC transporter C family member 4 (AHRD V3.3 *** A0A2G2ZW52_CAPAN) | NA | -1.430433975 | 0.001355432 | 24.343474 | 9.237120667 |
| Solyc09g018780.4 | Oligoribonuclease (AHRD V3.3 *-* A0A2G2ZEC5_CAPAN) | ORN | -1.429033931 | 4.11577E-07 | 7.614155333 | 2.849863 |
| Solyc08g082250.3 | endo-beta-1,4-D-glucanase (Cel8) | endoglucanase | -1.428169377 | 0.022879612 | 4.956781333 | 1.836528333 |
| Solyc09g042710.3 | Weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** A0A1P8AX38_ARATH) | NA | -1.427870174 | 0.005682412 | 2.468057667 | 0.917899667 |
| Solyc12g055840.2 | Glucan endo-1,3-beta-glucosidase 10 (AHRD V3.3 *** A0A1U8F6Q1_CAPAN) | NA | -1.421826218 | 0.017762483 | 2.814111667 | 1.070752667 |
| Solyc01g006430.3 | Fatty acid desaturase (AHRD V3.3 *** E7CCC0_9BRAS) | FAD2 | -1.419246687 | 2.01963E-05 | 146.6551233 | 55.77069867 |
| Solyc06g069190.4 | Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A2U1MGD4_ARTAN) | NA | -1.419244145 | 0.001770618 | 13.684475 | 5.202985 |
| Solyc11g071870.2 | Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A200R0U5_9MAGN) | UBE2H | -1.41788949 | 2.23462E-07 | 12.76049033 | 4.829035333 |
| Solyc03g113710.4 | Formin-like protein (AHRD V3.3 *** A0A2G3AWB8_CAPCH) | NA | -1.415487041 | 0.000317011 | 1.266564333 | 0.475308 |
| Solyc11g040120.3 | DNA helicase (AHRD V3.3 *** A0A2G2X978_CAPBA) | MCM2 | -1.41503536 | 4.34475E-07 | 31.15194033 | 11.76572633 |
| Solyc09g010550.4 | dentin sialophosphoprotein-like protein (AHRD V3.3 *-* AT5G02520.2) | NA | -1.414192716 | 8.80381E-06 | 2.957247667 | 1.118060667 |
| Solyc01g088600.4 | protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic (AHRD V3.3 *** A0A2I4EI43_9ROSI) | NA | -1.411250337 | 0.00664786 | 2.939663333 | 1.118778667 |
| Solyc07g056480.3 | glutathione S-transferase/peroxidase | GST | -1.408905605 | 0.001833511 | 9.747872667 | 3.706376667 |
| Solyc09g075180.3 | DNA photolyase (AHRD V3.3 *** A0A200PWN3_9MAGN) | NA | -1.408713571 | 5.17132E-08 | 186.1134133 | 70.44126633 |
| Solyc09g063130.3 | Photosystem I reaction center subunit IV (AHRD V3.3 *-* A0A2P6U4S6_CHLSO) | PSAE | -1.408354519 | 9.14699E-08 | 22.950311 | 8.635092333 |
| Solyc07g015860.3 | peptide deformylase AF271258 | PDF | -1.40745066 | 0.000103112 | 3.843503333 | 1.451028667 |
| Solyc12g100200.2 | UPF0061 protein (AHRD V3.3 *** A0A2G2XP25_CAPBA) | SELENOO | -1.406556416 | 1.1069E-08 | 7.715367 | 2.908215 |
| Solyc04g051860.3 | shikimate kinase precursor | AROK | -1.405642582 | 8.62864E-09 | 45.497428 | 17.15037233 |
| Solyc01g105520.3 | DNA helicase (AHRD V3.3 *** A0A2U1PZH1_ARTAN) | MCM9 | -1.404752531 | 1.58954E-06 | 1.636123667 | 0.620746333 |
| Solyc02g083980.3 | Endoglucanase (AHRD V3.3 *** A0A2G3D7Z9_CAPCH) | NA | -1.404571881 | 1.52903E-15 | 14.592328 | 5.537918333 |
| Solyc02g092530.4 | Acetamidase/Formamidase (AHRD V3.3 *** A0A200R348_9MAGN) | formamidase | -1.395984018 | 0.004194686 | 3.314121 | 1.276767 |
| Solyc01g091200.4 | UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** A0A1J3F7T2_NOCCA) | GAE | -1.394485154 | 0.000374227 | 1.645787667 | 0.633178 |

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|---|---|---|---|---|---|---|
| Solyc05g051200.1 | ethylene-responsive factor 1 | ERF1 | -1.393874639 | 0.004075831 | 4.153215 | 1.599791667 |
| Solyc06g005170.3 | mitogen-activated protein kinase 3 | MPK3 | -1.38861868 | 0.010999798 | 453.7619527 | 177.2124123 |
| Solyc09g020150.4 | hypothetical protein (AHRD V3.3 *** AT5G48340.4) | NA | -1.38837442 | 1.54725E-05 | 2.083074667 | 0.797211333 |
| Solyc01g005560.3 | Isocitrate dehydrogenase [NADP] (AHRD V3.3 *** A0A2G3BR90_CAPCH) | IDH1 | -1.385680132 | 3.28254E-06 | 273.545232 | 105.531792 |
| Solyc01g079880.3 | Aluminum induced protein with YGL and LRDR motifs (AHRD V3.3 *** Q94BR2_ARATH) | NA | -1.382685279 | 0.001172119 | 925.1929523 | 359.3046777 |
| Solyc06g048590.3 | Transmembrane receptor (AHRD V3.3 *** A0A200Q182_9MAGN) | NA | -1.380351886 | 2.95377E-07 | 2.57947 | 1.000539667 |
| Solyc09g075560.1 | Hexosyltransferase (AHRD V3.3 *** A0A2G3BWD5_CAPCH) | NA | -1.379251347 | 0.001145233 | 3.043174 | 1.183586667 |
| Solyc10g086570.3 | transmembrane protein (AHRD V3.3 *** AT5G02160.1) | NA | -1.3769474 | 0.002980238 | 6.343416 | 2.43051 |
| Solyc03g065340.3 | Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** A0A2G3CMG9_CAPCH) | PYG | -1.37556973 | 0.00019502 | 25.889538 | 10.12081067 |
| Solyc01g058320.4 | transmembrane protein (AHRD V3.3 *-* AT3G17120.5) | NA | -1.375122517 | 0.012570722 | 3.126604333 | 1.229714667 |
| Solyc03g078780.3 | UDP-glycosyltransferase 76C4-like (AHRD V3.3 *** A0A2I4EQP1_9ROSI) | NA | -1.370807854 | 0.000165205 | 4.771787667 | 1.862459333 |
| Solyc11g072820.3 | Kinesin (AHRD V3.3 *** A0A200R660_9MAGN) | KIF11 | -1.363626719 | 0.000862197 | 1.757472667 | 0.694702 |
| Solyc10g086190.3 | Adenosine kinase (AHRD V3.3 *** A0A1U8FGB1_CAPAN) | ADK | -1.359815169 | 0.032113745 | 5.269558333 | 2.10888 |
| Solyc01g107090.2 | beta-1%2C4-xylosidase (AHRD V3.3 *** AT3G19615.1) | NA | -1.359117183 | 0.018312496 | 39.31947233 | 15.77674667 |
| Solyc10g080970.2 | Bifunctional protein FolD 2 (AHRD V3.3 *** A0A1U8EB53_CAPAN) | NA | -1.35782693 | 0.000586838 | 18.42581267 | 7.318069333 |
| Solyc02g088390.4 | Lamin-like protein (AHRD V3.3 *** A0A2G2V9B8_CAPBA) | NA | -1.357585666 | 0.022753699 | 39.71524567 | 15.852915 |
| Solyc09g018760.2 | Oligoribonuclease (AHRD V3.3 *** A0A2G2ZEC5_CAPAN) | ORN | -1.35716726 | 1.70231E-06 | 7.136141 | 2.800806 |
| Solyc07g006050.3 | Histone-lysine N-methyltransferase ASHR3 (AHRD V3.3 *-* A0A2G2XZF7_CAPAN) | NA | -1.355743528 | 0.005750326 | 1.794966667 | 0.703916333 |
| Solyc09g005230.3 | Protein root UVB sensitive 5 (AHRD V3.3 *** A0A2G3BL77_CAPCH) | NA | -1.349421142 | 1.7759E-06 | 4.638623 | 1.822852667 |
| Solyc06g064430.1 | Longin domain-containing protein (AHRD V3.3 *** A0A1Q3BVJ4_CEPFO) | NA | -1.347009069 | 9.38631E-05 | 4.764781333 | 1.884128 |
| Solyc01g106380.2 | hypothetical protein (AHRD V3.3 *** AT5G64480.2) | NA | -1.346211709 | 0.001735441 | 5.044806667 | 1.985466 |
| Solyc09g018510.3 | Phytol kinase (AHRD V3.3 *** A0A2K3MZ75_TRIPR) | FOLK | -1.345951402 | 3.09143E-12 | 16.76052233 | 6.646862667 |
| Solyc07g005020.3 | DNA helicase (AHRD V3.3 *** A0A2G2Z086_CAPAN) | MCM5 | -1.34481794 | 4.28073E-05 | 25.02715167 | 9.891460333 |
| Solyc09g074410.4 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1L0Y3_ARTAN),Pfam:PF13561 | NA | -1.340736827 | 0.007397893 | 2.758599667 | 1.103164667 |
| Solyc09g057580.4 | DUF760 domain-containing protein (AHRD V3.3 *-* A0A1Q3CD93_CEPFO) | NA | -1.337441579 | 0.000151104 | 5.495882333 | 2.167551667 |
| Solyc12g008560.1 | Unknown protein | NA | -1.337009418 | 0.00128893 | 114.726135 | 45.70380533 |
| Solyc09g098130.3 | Spotted wilt resistance-5 | NA | -1.33616934 | 2.19411E-05 | 4.658402 | 1.845460333 |
| Solyc12g049390.2 | Transmembrane receptor (AHRD V3.3 *** A0A200Q182_9MAGN) | NA | -1.335969283 | 0.016083397 | 3.124121 | 1.251549333 |

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|---|---|---|---|---|---|---|
| Solyc06g075930.1 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | H4 | -1.332136885 | 4.09795E-05 | 14.39925367 | 5.731588 |
| Solyc06g005390.1 | Histone H2B (AHRD V3.3 *** A0A1U8GXA4_CAPAN) | H2B | -1.330899595 | 9.83936E-07 | 17.58323033 | 6.980798333 |
| Solyc05g005070.2 | Cysteine-rich receptor-like protein kinase 2 (AHRD V3.3 *** A0A1U8EWZ9_CAPAN) | NA | -1.329128861 | 0.037984095 | 1.519033667 | 0.616624333 |
| Solyc03g113480.1 | extensin-like protein (AHRD V3.3 *** AT1G77400.1) | NA | -1.326142688 | 4.02995E-10 | 23.92891067 | 9.630674333 |
| Solyc10g051030.2 | electron transporter%2C putative (Protein of unknown function%2C DUF547) (AHRD V3.3 *** AT5G66600.9) | NA | -1.324016667 | 0.003105732 | 5.135237 | 2.093881333 |
| Solyc05g007470.4 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A2U1QF48_ARTAN) | NA | -1.32327366 | 9.38631E-05 | 4.938080667 | 1.998145333 |
| Solyc12g014110.2 | Sodium/calcium exchanger family protein / calcium-binding EF hand family protein (AHRD V3.3 *** A0A2U1MZE4_ARTAN) | NA | -1.320444501 | 6.30796E-11 | 17.995423 | 7.292447 |
| Solyc04g080960.4 | pre-pro-cysteine proteinase | CTSF | -1.316540828 | 3.75423E-06 | 450.9701743 | 182.6023713 |
| Solyc11g068830.2 | Uridine 5'-monophosphate synthase (AHRD V3.3 *** A0A1U8EL35_CAPAN) | UMPS | -1.316261372 | 5.58962E-15 | 61.77665167 | 24.924579 |
| Solyc09g011770.3 | RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *-* B6SN54_MAIZE) | NA | -1.310941074 | 0.033423878 | 2.341102333 | 0.964169667 |
| Solyc09g060090.3 | Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** A0A178VMA9_ARATH) | NA | -1.308837643 | 6.99145E-09 | 5.154151667 | 2.09647 |
| Solyc03g119970.3 | ADP,ATP carrier protein (AHRD V3.3 *** A0A2G3D148_CAPCH) | TC.AAA | -1.308423269 | 9.55097E-05 | 4.039571 | 1.647443 |
| Solyc03g118860.3 | UDP-N-acetylglucosamine--N-acetylmuramyl-(Pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (AHRD V3.3 *** A0A1J3I8H5_NOCCA) | MURG | -1.306840012 | 5.63268E-08 | 18.251723 | 7.456552 |
| Solyc05g009010.1 | Protein kinase family protein (AHRD V3.3 *-* A0A2U1MH78_ARTAN) | NA | -1.305655267 | 0.01524458 | 17.65713967 | 7.292912667 |
| Solyc09g072590.3 | actin-depolymerizing factor (AHRD V3.3 *** A0A2I4EMY6_9ROSI) | CFL | -1.303334335 | 1.61772E-11 | 116.197492 | 47.65643567 |
| Solyc08g075940.4 | DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** A0A2G2XMC1_CAPBA) | NA | -1.297197213 | 1.18499E-06 | 6.763553 | 2.784705333 |
| Solyc12g056510.3 | Trihelix transcription factor GTL1 (AHRD V3.3 *** A0A2G3B3E4_CAPCH) | NA | -1.295841335 | 0.004804273 | 6.050774333 | 2.491731 |
| Solyc01g099190.4 | lipoxygenase B | LOX1_5 | -1.293460429 | 9.31049E-07 | 3902.90918 | 1605.607422 |
| Solyc04g064480.3 | Unknown protein | NA | -1.291969835 | 2.92595E-05 | 7.42401 | 3.036623667 |
| Solyc02g084450.4 | NBS-LRR resistance protein (AHRD V3.3 *** A0A2K3NU03_TRIPR) | NA | -1.290685694 | 1.65689E-06 | 4.009878 | 1.641553333 |
| Solyc07g051950.3 | S-type anion channel SLAH1 (AHRD V3.3 *** A0A2G2WD71_CAPBA) | NA | -1.290067866 | 6.97496E-12 | 186.6983287 | 76.91642 |
| Solyc06g051720.3 | GDSL esterase/lipase CPRD49 (AHRD V3.3 *** A0A2G2XS51_CAPBA) | IAH1 | -1.288391334 | 6.62038E-09 | 26.69807367 | 10.97768267 |
| Solyc01g111930.4 | Rop guanine nucleotide exchange factor 1 (AHRD V3.3 *** A0A2G2W9R1_CAPBA) | NA | -1.284488518 | 0.002491979 | 1.956627333 | 0.817796333 |
| Solyc05g054590.4 | UDP-glucuronic acid decarboxylase (AHRD V3.3 *-* G5DXR5_SILLA) | UXS1 | -1.274667851 | 0.019877603 | 7.261982333 | 3.060816 |
| Solyc12g005850.2 | Protein DETOXIFICATION (AHRD V3.3 *** A0A1J7GU23_LUPAN) | TC.MATE | -1.272788317 | 1.62277E-09 | 12.66158167 | 5.269821667 |
| Solyc10g080920.2 | Protein RADIALIS-like 2 (AHRD V3.3 *** A0A2G2VVI4_CAPBA) | NA | -1.272096002 | 0.019269302 | 8.501229667 | 3.520306667 |
| Solyc06g008220.4 | Multiple organellar RNA editing factor 2, chloroplastic (AHRD V3.3 *** A0A2G3C3Y9_CAPCH) | NA | -1.269345493 | 2.07021E-06 | 28.41766733 | 11.97301933 |

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|---|---|---|---|---|---|---|
| Solyc06g059740.4 | Alcohol dehydrogenase (AHRD V3.3 *** A0A2U1MN94_ARTAN) | ADH1 | -1.268523756 | 0.00013048 | 5015.030924 | 2089.326294 |
| Solyc02g079990.3 | Cysteine-rich receptor-like protein kinase 10 (AHRD V3.3 *** A0A2G3D6H0_CAPCH) | NA | -1.264402422 | 0.000435997 | 3.078604 | 1.301631667 |
| Solyc06g073970.3 | Core-2 i-branching beta-n-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A2K3MQ33_TRIPR) | NA | -1.263676221 | 1.26759E-07 | 13.72542 | 5.722643667 |
| Solyc11g066720.3 | UDP-apiose/UDP-xylose synthase (AHRD V3.3 *** A0A1B3TP38_SPIPO) | AXS | -1.263285877 | 0.01653334 | 5.738438 | 2.440548333 |
| Solyc01g099980.4 | Enolase (DUF1399) (AHRD V3.3 *-* F4I3L9_ARATH) | NA | -1.260119973 | 0.007309782 | 1.740208333 | 0.730511667 |
| Solyc02g082190.3 | CTP synthase (AHRD V3.3 *** A0A2G2XFG8_CAPBA) | PYRG | -1.257953076 | 2.48E-10 | 16.58436167 | 6.949141333 |
| Solyc09g010420.4 | Arginine biosynthesis bifunctional protein ArgJ, chloroplastic (AHRD V3.3 *** A0A2G2YQV3_CAPAN) | ARGJ | -1.256833822 | 2.15101E-09 | 33.55625 | 14.23924667 |
| Solyc11g005190.3 | WD40 repeat (AHRD V3.3 *** A0A200QUE5_9MAGN) | RFWD2 | -1.25415174 | 0.043409273 | 11.45913167 | 4.740769667 |
| Solyc09g064500.3 | Photosystem II reaction center Psb28 protein (AHRD V3.3 *** A0A1U8EF03_CAPAN) | PSB28 | -1.253555064 | 0.037843605 | 8.662497333 | 3.609384667 |
| Solyc02g085130.4 | Tubby-like F-box protein (AHRD V3.3 *** A0A2G3D7T8_CAPCH) | TUB | -1.251010666 | 0.026318369 | 1.442762667 | 0.616997 |
| Solyc02g085760.2 | Rhomboid domain-containing protein (AHRD V3.3 *** A0A1Q3C608_CEPFO) | NA | -1.250321951 | 0.007161983 | 5.021901 | 2.131921 |
| Solyc01g005250.4 | Aspartate-semialdehyde dehydrogenase (AHRD V3.3 *** A0A2G3AYJ3_CAPCH) | ASD | -1.245254865 | 4.17177E-12 | 58.384996 | 24.69585533 |
| Solyc01g088390.3 | Sister chromatid cohesion protein DCC1 (AHRD V3.3 *** A0A2K3PFF6_TRIPR) | DSCC1 | -1.243892291 | 0.033008766 | 2.741219667 | 1.158709333 |
| Solyc09g064440.4 | ABC transporter C family member 13 (AHRD V3.3 *** A0A2G2VCG3_CAPBA) | NA | -1.24314249 | 4.18074E-14 | 12.831739 | 5.464515333 |
| Solyc07g041970.4 | Subtilisin-like protease (AHRD V3.3 *** A0A1J3J113_NOCCA) | NA | -1.24241185 | 0.000112689 | 21.041819 | 9.055039333 |
| Solyc04g078950.1 | Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *-* A0A2G2ZRM3_CAPAN) | NA | -1.242348129 | 0.000456885 | 3.629078333 | 1.543299667 |
| Solyc05g050120.3 | cytosolic NADP-malic enzyme | MAEB | -1.241956301 | 5.89339E-10 | 197.0438947 | 83.67950433 |
| Solyc03g115500.3 | Heparanase-like protein 1 (AHRD V3.3 *** A0A2G3CZA9_CAPCH) | HPSE | -1.240939508 | 2.94244E-10 | 20.07691 | 8.549797333 |
| Solyc03g119690.3 | Eukaryotic aspartyl protease family protein (AHRD V3.3 *** Q9C6M0_ARATH) | APF2 | -1.239829029 | 4.31022E-05 | 11.27403167 | 4.829311333 |
| Solyc05g014980.4 | Adenylate kinase (AHRD V3.3 *** A0A200R495_9MAGN),Pfam:PF00406 | ADK | -1.239538661 | 2.48933E-08 | 28.27915767 | 12.08380567 |
| Solyc04g077780.3 | LIM domain-containing protein (AHRD V3.3 *** A0A1Q3ALK2_CEPFO) | CSRP | -1.237256726 | 0.002980238 | 26.60589233 | 11.453236 |
| Solyc10g007060.4 | Phenylalanine--tRNA ligase alpha subunit (AHRD V3.3 *** A0A2G2XXC1_CAPAN) | FARSA | -1.23692403 | 4.54651E-11 | 20.106782 | 8.622538667 |
| Solyc08g079430.3 | partialcopper-containing amine oxidase | AOC3 | -1.235718727 | 0.016849595 | 18.72086267 | 8.110541 |
| Solyc02g063420.3 | Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** A0A2U1M3E1_ARTAN) | NA | -1.234290638 | 0.007378062 | 44.986766 | 19.16044133 |
| Solyc08g061490.3 | MTD1 (AHRD V3.3 *** A0A2K3PL64_TRIPR) | NA | -1.233306297 | 0.003945106 | 5.773542667 | 2.474053 |
| Solyc10g079950.2 | Glycosyltransferase (AHRD V3.3 *** A0A288W8G2_GARJA) | CISZOG | -1.231791549 | 6.91098E-07 | 21.03472 | 8.978759667 |
| Solyc08g080780.4 | Myosin heavy chain-related protein (AHRD V3.3 *** Q9C8T4_ARATH) | NA | -1.23017513 | 2.25443E-05 | 3.590984 | 1.532605 |
| Solyc02g089760.3 | Protein kinase family protein (AHRD V3.3 *-* E5GBJ3_CUCME) | NA | -1.229565665 | 0.000557966 | 6.935618333 | 3.005356667 |

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| Solyc09g074880.4 | Protein LOW PSII ACCUMULATION 1, chloroplastic (AHRD V3.3 *** A0A2G2W035_CAPBA) | NA | -1.227093333 | 3.60546E-07 | 6.502473667 | 2.803851 |
| Solyc05g009470.4 | Glycoside hydrolase family 31 (AHRD V3.3 *** A0A2U1PBY7_ARTAN) | XYL1 | -1.226912679 | 1.06589E-06 | 15.58631567 | 6.687368333 |
| Solyc09g090700.1 | Succinate semialdehyde dehydrogenase (AHRD V3.3 *** A0A2U1MA81_ARTAN) | SSADH | -1.221208903 | 1.36524E-10 | 97.89026133 | 42.19082533 |
| Solyc09g091260.3 | Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** A0A2R6PXD2_ACTCH) | NA | -1.218182653 | 0.017741203 | 0.614969333 | 0.264569333 |
| Solyc06g051400.3 | omega-3 fatty acid desaturase | FAD3 | -1.214363566 | 0.000191752 | 27.989391 | 12.22306267 |
| Solyc07g042550.3 | sucrose synthase | SUS | -1.214061423 | 2.56806E-05 | 103.6787567 | 45.54784833 |
| Solyc02g063060.4 | Zinc-finger domain of monoamine-oxidase A repressor R1 (AHRD V3.3 *** A0A2U1N5J3_ARTAN) | NA | -1.212801542 | 5.91763E-05 | 2.535574667 | 1.096805667 |
| Solyc07g056500.4 | glutathione S-transferase T5 | GST | -1.203866395 | 3.12824E-07 | 57.10158533 | 25.14288333 |
| Solyc06g084060.3 | F-box/LRR-repeat protein 17 (AHRD V3.3 *** A0A2G2WN42_CAPBA) | NA | -1.203009852 | 1.87426E-08 | 10.78480467 | 4.706204333 |
| Solyc09g007850.3 | RNA-binding protein (AHRD V3.3 *** A0A2U1PI86_ARTAN) | NA | -1.202242871 | 7.37801E-10 | 139.674174 | 61.08928567 |
| Solyc06g071990.4 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* A0A2U1N2C4_ARTAN) | NA | -1.200822616 | 0.000587534 | 32.655547 | 14.27371567 |
| Solyc02g082420.3 | RING/U-box superfamily protein (AHRD V3.3 *** A0A2U1LI04_ARTAN) | NA | -1.199180896 | 0.002829358 | 25.608302 | 11.31184267 |
| Solyc02g092940.3 | Receptor protein kinase-like protein (AHRD V3.3 *** W9RY70_9ROSA) | NA | -1.198465017 | 1.59019E-05 | 3.843803667 | 1.684011 |
| Solyc11g068540.2 | beta-alanine synthase | AGUB | -1.197686295 | 7.49307E-13 | 80.14357267 | 35.29570133 |
| Solyc10g086580.2 | Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic (AHRD V3.3 *** RCA_SOLPN) | NA | -1.195516461 | 2.39889E-11 | 90.04227467 | 39.48913833 |
| Solyc09g009020.3 | enolase | ENO | -1.195347634 | 6.08588E-05 | 433.3317563 | 192.09227 |
| Solyc09g074280.1 | Ankyrin repeat-containing protein (AHRD V3.3 *** A0A2U1QG31_ARTAN) | NA | -1.195017832 | 0.037369794 | 9.460344667 | 4.206425667 |
| Solyc06g065950.4 | Vesicle-associated membrane protein (AHRD V3.3 *** A0A1U8GUV8_CAPAN) | VAMP7 | -1.194881651 | 0.000316 | 25.86870433 | 11.45128633 |
| Solyc03g114030.3 | PermeaseI-like protein | NA | -1.194532563 | 2.4442E-10 | 23.64334633 | 10.39699833 |
| Solyc05g012600.3 | hypothetical protein (AHRD V3.3 *** AT2G03420.1) | NA | -1.185257774 | 0.000546977 | 11.03710567 | 4.875349667 |
| Solyc03g031890.3 | Cold induced protein-like (AHRD V3.3 *-* Q94JH8_ORYSJ) | NA | -1.184086958 | 0.038988743 | 19.700606 | 8.611337 |
| Solyc08g081160.3 | DUF3741 domain-containing protein/DUF4378 domain-containing protein (AHRD V3.3 *-* A0A1Q3CNJ4_CEPFO) | NA | -1.183583423 | 0.003720312 | 6.633163 | 2.971607 |
| Solyc08g079280.3 | Cytochrome P450 (AHRD V3.3 *** A0A1U9X605_THAGA) | NA | -1.183052156 | 1.31899E-09 | 12.36742567 | 5.498820667 |
| Solyc10g047030.3 | LEXYL1 | XYL4 | -1.182015293 | 0.000934972 | 27.91786633 | 12.39605833 |
| Solyc05g055550.3 | vacuolar acid trehalase (AHRD V3.3 *** AT3G10405.1) | NA | -1.180613934 | 0.000716447 | 4.767387333 | 2.105349667 |
| Solyc01g100280.4 | RNA helicase DEAH-box4 | RECQL | -1.180529595 | 0.004499292 | 0.99395 | 0.440142333 |
| Solyc12g014180.2 | Malate dehydrogenase (AHRD V3.3 *** A0A2G2X2U9_CAPBA) | MDH2 | -1.179749414 | 0.000110271 | 4.066515667 | 1.805220667 |
| Solyc01g079520.3 | DNA mismatch repair protein MutS (AHRD V3.3 *** A0A200R263_9MAGN) | MSH6 | -1.178985948 | 0.000333195 | 1.217917 | 0.540369667 |

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| Solyc04g005160.3 | 6-phosphogluconate dehydrogenase, decarboxylating (AHRD V3.3 *** A0A1U8F1N4_CAPAN) | PGD | -1.176368577 | 0.00235098 | 176.0277147 | 79.37985233 |
| Solyc10g007120.4 | transmembrane protein (AHRD V3.3 *** AT3G15110.1) | NA | -1.175236817 | 0.001948348 | 3.299917333 | 1.472507 |
| Solyc09g098540.3 | Chitinase-like protein (AHRD V3.3 *** Q6JX03_GOSHI) | NA | -1.175128102 | 0.002985986 | 158.3030347 | 71.41459133 |
| Solyc02g081830.4 | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *** A0A2U1MTA1_ARTAN),Pfam:PF00702 | NA | -1.171282254 | 0.039921305 | 50.88878267 | 22.83203967 |
| Solyc10g084770.3 | Protein kinase APK1B, chloroplastic (AHRD V3.3 *** A0A1U8E7T5_CAPAN) | NA | -1.168694452 | 0.028317861 | 1.772008333 | 0.802108667 |
| Solyc03g122110.1 | Pre-mRNA-splicing factor CWC22-like protein (AHRD V3.3 *** A0A2G2ZS42_CAPAN) | CWC22 | -1.168278886 | 0.000371579 | 1.500899667 | 0.669611333 |
| Solyc02g092980.3 | cyclin D3.1 | CYCD3 | -1.167806555 | 6.39536E-05 | 3.085550333 | 1.374075667 |
| Solyc02g077770.3 | F-box domain-containing protein (AHRD V3.3 *** A0A2U1MSG2_ARTAN) | NA | -1.167782312 | 0.01792162 | 3.882204 | 1.728769 |
| Solyc09g009990.4 | GATA zinc finger protein (AHRD V3.3 *** AT3G52610.1) | NA | -1.167536427 | 6.81367E-05 | 5.360389 | 2.391106667 |
| Solyc06g051020.2 | Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (AHRD V3.3 *** A0A200PX65_9MAGN) | NA | -1.165565039 | 0.000272934 | 34.120375 | 15.456941 |
| Solyc10g005640.4 | Protein phosphatase 2C (AHRD V3.3 *** A0A2U1PF73_ARTAN) | NA | -1.165327634 | 0.00048458 | 1.744547 | 0.780847333 |
| Solyc04g054710.3 | Aminotransferase (AHRD V3.3 *** A0A200QW13_9MAGN) | PAT | -1.162284235 | 4.06135E-10 | 49.44183633 | 22.24319567 |
| Solyc08g077690.3 | SNF2-related (AHRD V3.3 *** A0A200QQJ8_9MAGN) | RAD54L | -1.161736811 | 2.91418E-07 | 7.697154333 | 3.452110667 |
| Solyc12g068070.2 | Filament-like plant protein 3 (AHRD V3.3 *** A0A314LEB5_NICAT) | NA | -1.161192851 | 0.001423207 | 17.814655 | 8.042360667 |
| Solyc11g072110.2 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1Q1F3_ARTAN) | F6H | -1.160296547 | 0.000141885 | 13.01330067 | 5.840450333 |
| Solyc06g066770.1 | F-box/kelch-repeat protein (AHRD V3.3 *** A0A1J3DG12_NOCCA) | NA | -1.159892032 | 0.01317715 | 14.38839333 | 6.545518667 |
| Solyc02g089750.4 | Proline-rich receptor-like protein kinase PERK9 (AHRD V3.3 *-* A0A2G3D983_CAPCH) | NA | -1.158696654 | 0.005426277 | 8.592451333 | 3.912454333 |
| Solyc01g105020.3 | Protein phosphatase 2C (PP2C)-like domain (AHRD V3.3 *-* A0A200PXZ2_9MAGN) | NA | -1.153851985 | 0.000930362 | 1.730556 | 0.787150667 |
| Solyc06g048820.1 | Wound-induced protein 1 (AHRD V3.3 *** A0A2G3C5E3_CAPCH) | NA | -1.153045399 | 0.01270641 | 23.561181 | 10.796891 |
| Solyc02g082260.3 | 3-hydroxy-3-methylglutaryl CoA reductase | HMGCR | -1.149917136 | 0.000763191 | 17.14682367 | 7.844747 |
| Solyc08g014130.3 | Isopropylmalate synthase (AHRD V3.3 *** K4CJ46_SOLLC) | LEUA | -1.148425493 | 0.016962291 | 764.077067 | 341.575104 |
| Solyc10g052510.2 | Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU) | PCBER1 | -1.147440883 | 0.005806732 | 2.840315333 | 1.28536 |
| Solyc08g080140.4 | 3,5-epimerase/4-reductase (AHRD V3.3 *** A0A1Z5KIY2_FISSO) | UER1 | -1.139900326 | 0.001924303 | 5.500901333 | 2.529383667 |
| Solyc02g083110.1 | DUF641 domain-containing protein (AHRD V3.3 *** A0A1Q3C2N9_CEPFO) | NA | -1.138072988 | 0.007837253 | 5.596217333 | 2.591596 |
| Solyc08g082990.3 | Oligopeptide transporter (AHRD V3.3 *** A0A200RD47_9MAGN) | NA | -1.137929179 | 0.008160048 | 48.588234 | 21.86188733 |
| Solyc10g075020.3 | Elongation factor P (AHRD V3.3 *** A0A2G2YL80_CAPAN) | EFP | -1.135236538 | 8.1591E-05 | 7.283866 | 3.354486333 |
| Solyc01g008160.4 | Protein SLOW GREEN 1, chloroplastic (AHRD V3.3 *** A0A2G2YVV0_CAPAN) | NA | -1.13201119 | 0.000125509 | 47.804751 | 21.96192333 |
| Solyc12g014440.2 | BNR/Asp-box repeat family protein (AHRD V3.3 *** A0A2U1NQE8_ARTAN) | NA | -1.131435658 | 1.08607E-10 | 15.512835 | 7.11144 |

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| Solyc12g017850.2 | DUF581 domain-containing protein (AHRD V3.3 *** A0A1Q3AVJ7_CEPFO) | NA | -1.130337361 | 1.93995E-10 | 26.46123067 | 12.16245767 |
| Solyc01g067750.3 | dehydroquinate dehydratase/shikimate:NADP oxidoreductase | ARODE | -1.128775611 | 8.02388E-05 | 37.44457733 | 17.255033 |
| Solyc06g063240.3 | O-fucosyltransferase family protein (AHRD V3.3 *** A0A061GA16_THECC) | NA | -1.126642341 | 7.49942E-06 | 26.02939667 | 12.06012033 |
| Solyc12g007230.2 | auxin-regulated IAA8 | IAA | -1.119639048 | 0.034562572 | 4.862951667 | 2.284633333 |
| Solyc06g053860.3 | alpha-1,2-Mannosidase (AHRD V3.3 *** A0A328D328_9ASTE) | EDEM2 | -1.118528146 | 1.23874E-08 | 12.262242 | 5.659544 |
| Solyc04g077230.1 | Unknown protein | NA | -1.118450776 | 0.026021953 | 109.0633343 | 51.290304 |
| Solyc09g010740.4 | Peptidylprolyl isomerase (AHRD V3.3 *-* A0A2G2YNK8_CAPAN) | NA | -1.117274589 | 8.07995E-09 | 25.74066733 | 11.976041 |
| Solyc09g007110.3 | Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** A0A0K9PPV4_ZOSMR) | NA | -1.113357364 | 5.32312E-05 | 1.489870667 | 0.692676333 |
| Solyc05g050970.4 | Transketolase (AHRD V3.3 *** A0A200R9X0_9MAGN) | TKTA | -1.111662029 | 1.47826E-05 | 94.23936967 | 43.827816 |
| Solyc12g056450.2 | 3-hydroxy-3-methylglutaryl coenzyme A synthase (AHRD V3.3 *** A0A1U8F7M5_CAPAN) | HMGCS | -1.110795469 | 0.000367996 | 4.672492667 | 2.181996667 |
| Solyc08g061630.3 | YGGT family protein (AHRD V3.3 *** F8WLD3_CITUN) | YGGT | -1.110547013 | 0.000593286 | 2.613994 | 1.211202333 |
| Solyc12g099930.2 | Serine--glyoxylate aminotransferase (AHRD V3.3 *** A0A2G2YAX9_CAPAN) | AGXT | -1.108452001 | 0.000260428 | 9.82418 | 4.583848 |
| Solyc06g074240.3 | Beta-carotene,Pfam:PF05834 | CCS1 | -1.106704794 | 0.006305072 | 11.73383967 | 5.560454667 |
| Solyc10g085030.1 | Heme-binding-like protein (AHRD V3.3 *** A0A2I0X8X3_9ASPA) | NA | -1.1039872 | 0.005862513 | 37.15507467 | 17.590906 |
| Solyc10g007700.3 | Rab family GTPase (AHRD V3.3 *** A0A1Y1I8A7_KLENI) | RAB2A | -1.103223415 | 7.25617E-05 | 32.16303833 | 15.12140267 |
| Solyc04g053130.4 | Stress enhanced protein 2, chloroplastic (AHRD V3.3 *** A0A1U8F0B2_CAPAN) | NA | -1.100849517 | 0.011685379 | 593.217265 | 274.2004143 |
| Solyc10g081440.2 | NADH-cytochrome b5 reductase (AHRD V3.3 *** K4D331_SOLLC) | cytochrome-b5 reductase | -1.099845482 | 4.07209E-07 | 120.59361 | 56.82098267 |
| Solyc05g005180.3 | 1,4-dihydroxy-2-naphthoyl-CoA synthase (AHRD V3.3 *** A0A2G2XZJ4_CAPAN) | MENB | -1.099446138 | 0.001332272 | 3.407581667 | 1.593492333 |
| Solyc01g109160.4 | CYP74C4 | AOS | -1.099415623 | 0.049136545 | 3.627787667 | 1.723014333 |
| Solyc08g023270.3 | myosin heavy chain-like protein (AHRD V3.3 *** AT4G03620.2) | NA | -1.097992454 | 0.010706064 | 4.058874333 | 1.929736333 |
| Solyc06g073260.3 | Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (AHRD V3.3 *** A0A2G3CAL3_CAPCH) | NA | -1.096531029 | 0.014975437 | 1.516443 | 0.714665667 |
| Solyc10g008400.1 | E3 ubiquitin-protein ligase RMA1H1 (AHRD V3.3 *** A0A2G3BCU0_CAPCH) | RNF5 | -1.09630032 | 3.23257E-06 | 235.214544 | 110.9414497 |
| Solyc09g011170.3 | Prf interactor 30137 | NA | -1.091108698 | 0.003085604 | 0.881877 | 0.417677667 |
| Solyc09g010940.4 | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *** A0A1P8BF18_ARATH) | K07025 | -1.089440145 | 0.004121763 | 29.02076933 | 13.861537 |
| Solyc06g005110.3 | 40S ribosomal protein S23 (AHRD V3.3 *** A0A2I4EYK6_9ROSI) | RP-S23E | -1.087563951 | 6.34999E-05 | 24.59430367 | 11.65292567 |
| Solyc04g081300.4 | Endoglucanase (AHRD V3.3 *** A0A2G3CQE2_CAPCH) | NA | -1.087465304 | 0.002180929 | 6.704233667 | 3.217476333 |
| Solyc08g078720.3 | 14.7 kDa heat shock protein (AHRD V3.3 *-* A0A1J3HSD8_NOCCA) | HSP20 | -1.086597126 | 6.00466E-06 | 21.81227433 | 10.35776133 |
| Solyc06g011350.3 | plasma membrane intrinsic protein 2.4 | PIP | -1.085438264 | 0.004272919 | 5.800096 | 2.732946 |

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| Solyc01g060070.3 | Outer envelope pore protein 16-2, chloroplastic (AHRD V3.3 *** A0A2G2XR36_CAPBA),Pfam:PF02466 | NA | -1.083190405 | 0.021892676 | 2.531037 | 1.202397333 |
| Solyc08g076670.3 | SNARE associated Golgi protein (AHRD V3.3 *** A0A200PXG4_9MAGN) | NA | -1.081842344 | 3.38162E-06 | 35.830631 | 17.01815233 |
| Solyc01g080220.3 | endo-1,31,4-beta-D-glucanase-like (AHRD V3.3 *** A0A2I4F2Y3_9ROSI) | carboxymethylenebut enolidase | -1.080998185 | 0.030245389 | 35.88977767 | 16.93457567 |
| Solyc01g088610.4 | 10 kDa chaperonin (AHRD V3.3 *** A0A2K3N899_TRIPR) | GROES | -1.080826522 | 3.63787E-09 | 238.5722607 | 113.4635647 |
| Solyc12g099270.2 | 4Fe-4S ferredoxin-iron-sulfur binding protein (AHRD V3.3 *** A0A2K3N1K7_TRIPR) | NA | -1.079799192 | 2.9479E-08 | 13.46073367 | 6.396364667 |
| Solyc07g032740.4 | Aspartate aminotransferase (AHRD V3.3 *** A0A0J8BGE0_BETVU) | GOT1 | -1.078688541 | 0.019824695 | 78.11685667 | 37.31281267 |
| Solyc08g029050.4 | TOPLESS 6 | NA | -1.078612645 | 0.012818152 | 4.163541333 | 2.008364333 |
| Solyc09g083120.3 | Acylamino-acid-releasing enzyme (AHRD V3.3 *** A0A1J3FLE9_NOCCA) | APEH | -1.075591922 | 6.25662E-05 | 2.694674667 | 1.289824667 |
| Solyc06g034120.4 | Quinone oxidoreductase (AHRD V3.3 *** A0A1J3DL74_NOCCA) | QOR | -1.075511241 | 4.28635E-07 | 21.88859033 | 10.52541833 |
| Solyc04g009530.4 | Glutathione S-transferase (AHRD V3.3 *** A0A200QHH9_9MAGN) | GST | -1.074685491 | 0.003596273 | 3.181958667 | 1.525027 |
| Solyc04g077970.4 | Adenine phosphoribosyltransferase 3 (AHRD V3.3 *** A0A2G3CPQ3_CAPCH) | APRT | -1.074281445 | 1.64402E-07 | 508.5004273 | 242.7426603 |
| Solyc09g074930.3 | REF/SRPP-like protein (AHRD V3.3 *** A0A2G3CTD5_CAPCH) | NA | -1.072812671 | 0.005208607 | 15.639899 | 7.560297333 |
| Solyc07g016180.3 | Auxin Response Factor 7A | NA | -1.071419751 | 0.002604639 | 2.482406667 | 1.195931333 |
| Solyc12g095850.2 | Tryptophan--tRNA ligase (AHRD V3.3 *** A0A2G2VHY5_CAPBA) | WARS | -1.069921685 | 0.006482643 | 1.832969667 | 0.871337667 |
| Solyc09g098110.4 | bHLH transcription factor 092 | NA | -1.06750696 | 0.042295049 | 10.07843933 | 4.895549667 |
| Solyc12g009270.1 | Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** A0A061GSW0_THECC) | NA | -1.067150455 | 1.70165E-06 | 29.44704433 | 14.10629033 |
| Solyc06g005140.3 | Pentatricopeptide repeat-containing protein, mitochondrial (AHRD V3.3 *** A0A2G3DBW2_CAPCH) | NA | -1.066181629 | 1.44308E-07 | 9.993159 | 4.793154667 |
| Solyc11g040040.2 | Phototropic-responsive NPH3 family protein (AHRD V3.3 *** A0A2U1NLD8_ARTAN) | NA | -1.062548011 | 0.004670221 | 2.996926 | 1.442258 |
| Solyc02g088330.2 | Protein kinase domain (AHRD V3.3 *** A0A200QSE8_9MAGN) | NA | -1.061117668 | 0.001256904 | 1.457266 | 0.703891667 |
| Solyc10g051120.3 | Mitochondrial pyruvate carrier (AHRD V3.3 *** A0A2G2WMA1_CAPBA) | MPC1 | -1.06041086 | 0.000393007 | 32.319894 | 15.54812733 |
| Solyc02g069110.4 | Cathepsin B-like cysteine proteinase (AHRD V3.3 *** Q40413_NICRU) | CTSB | -1.059757123 | 0.001760173 | 11.591885 | 5.668440667 |
| Solyc10g051373.1 | RNA-binding protein (AHRD V3.3 *-* O24106_NICGU) | CIRBP | -1.059317665 | 0.006324391 | 53.51856233 | 25.93614467 |
| Solyc09g059030.4 | Quinone-oxidoreductase chloroplastic-like (AHRD V3.3 *** A0A2K3P901_TRIPR) | CEQORH | -1.057616609 | 1.44559E-05 | 109.9900563 | 52.80090467 |
| Solyc01g111870.3 | Serine/threonine-protein kinase ATR (AHRD V3.3 *** A0A2G3BW62_CAPCH) | ATR | -1.057317725 | 0.001831495 | 0.31006 | 0.149451667 |
| Solyc04g076040.3 | cyclinD5_1 | CYCD1_2_4 | -1.056876858 | 5.61148E-05 | 4.828755333 | 2.340818 |
| Solyc05g054350.3 | Epoxide hydrolase (AHRD V3.3 *** Q41414_SOLTU) | NA | -1.055441008 | 9.55499E-05 | 87.61247233 | 42.56935233 |
| Solyc11g012290.2 | SWIB domain-containing protein (AHRD V3.3 *-* A0A1Q3D4Q9_CEPFO) | UAF30 | -1.054222044 | 0.003566505 | 6.654834333 | 3.226969667 |

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| Solyc04g076460.4 | LRR receptor-like serine/threonine-protein kinase GSO1 (AHRD V3.3 *** A0A1U8F0D9_CAPAN) | NA | -1.053749847 | 0.039256477 | 8.840367 | 4.295590667 |
| Solyc11g069430.2 | plasma membrane intrinsic protein 2.6 | PIP | -1.053467928 | 0.005379791 | 843.368062 | 407.9149373 |
| Solyc10g085430.3 | Saposin B (AHRD V3.3 *** A0A2U1NDA3_ARTAN) | PSAP | -1.052263351 | 1.77298E-08 | 166.000178 | 80.672193 |
| Solyc05g007260.3 | Ribulose-phosphate 3-epimerase (AHRD V3.3 *** A0A328DMM8_9ASTE) | RPE | -1.05189814 | 3.73134E-09 | 72.14657833 | 35.04353433 |
| Solyc06g060260.3 | Stromal ascorbate peroxidase (AHRD V3.3 *** Q9TNL9_TOBAC) | L-ascorbate peroxidase | -1.051463269 | 5.0636E-05 | 152.3648327 | 73.997963 |
| Solyc05g016330.3 | Cytochrome P450 (AHRD V3.3 *** A0A200QCI8_9MAGN) | CYP97B3 | -1.049439656 | 1.22443E-05 | 17.82861833 | 8.712423667 |
| Solyc06g076660.3 | proliferating cell nuclear antigen | PCNA | -1.048166943 | 0.002154341 | 7.209074667 | 3.541150667 |
| Solyc09g090050.4 | RNA-binding ASCH domain protein (AHRD V3.3 *** AT2G20410.2) | TRIP4 | -1.047692555 | 0.006428642 | 7.202046 | 3.515579333 |
| Solyc04g077220.3 | Homeobox-leucine zipper protein HAT22 (AHRD V3.3 *** A0A2G3CPE7_CAPCH) | HD-ZIP | -1.047272156 | 0.002840984 | 7.28317 | 3.571919 |
| Solyc01g057520.4 | ARM repeat superfamily protein (AHRD V3.3 *** F4J550_ARATH) | NA | -1.04589892 | 5.10194E-08 | 7.885261667 | 3.846232667 |
| Solyc11g008680.2 | Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A2G3B0E0_CAPCH) | FAB2 | -1.045165935 | 0.015847675 | 33.20168167 | 16.107918 |
| Solyc10g055390.2 | Major facilitator superfamily protein (AHRD V3.3 *** Q9SW40_ARATH) | NA | -1.042629257 | 0.000924575 | 12.330218 | 6.054414 |
| Solyc01g081390.4 | Xylulose 5-phosphate/phosphate translocator, chloroplastic (AHRD V3.3 *** A0A1U8EHP7_CAPAN) | SLC35E1 | -1.042373781 | 1.71671E-05 | 20.88229333 | 10.289155 |
| Solyc07g066600.3 | Phosphoglycerate kinase (AHRD V3.3 *** A0A2G3C3B1_CAPCH) | PGK | -1.041510431 | 4.30217E-05 | 390.055135 | 191.1332603 |
| Solyc11g011590.2 | GEM-like protein 6 (AHRD V3.3 *** A0A2G2ZGW1_CAPAN) | NA | -1.041007661 | 0.011093976 | 4.938625 | 2.399159333 |
| Solyc07g063000.4 | Phytosulfokine receptor 2 (AHRD V3.3 *** A0A2G3C1N9_CAPCH) | NA | -1.03948559 | 0.002056462 | 1.907643667 | 0.931914 |
| Solyc01g095590.3 | Extra-large G-like protein, putative (DUF3133) (AHRD V3.3 *** Q0WVG1_ARATH) | NA | -1.038542911 | 1.14416E-06 | 12.77409767 | 6.25776 |
| Solyc07g056490.4 | Glutathione S-transferase-like protein (AHRD V3.3 *** A0A2K3N2T5_TRIPR) | GST | -1.037861479 | 2.44348E-06 | 75.43745433 | 37.18496333 |
| Solyc02g086740.1 | 50S ribosomal protein L12, chloroplastic (AHRD V3.3 *** A0A2G3D9E1_CAPCH) | RP-L7 | -1.037397264 | 0.000159012 | 17.553213 | 8.621615 |
| Solyc09g075570.1 | hypothetical protein (AHRD V3.3 *** AT3G62650.2) | NA | -1.035387964 | 0.038593903 | 6.937420333 | 3.375217667 |
| Solyc10g081720.2 | Fasciclin-like arabinogalactan protein 17 (AHRD V3.3 *** A0A2G3AVK5_CAPCH) | NA | -1.034467063 | 7.28837E-07 | 140.8098093 | 69.58716967 |
| Solyc08g007800.3 | SPX domain-containing protein (AHRD V3.3 *** D7MDY2_ARALL) | NA | -1.033721997 | 3.90546E-06 | 13.23001 | 6.489901333 |
| Solyc10g049970.2 | Kynurenine formamidase (AHRD V3.3 *** A0A1J3JDK4_NOCCA) | NA | -1.032473843 | 2.92376E-05 | 15.59574867 | 7.731324333 |
| Solyc06g065310.3 | Biotin/lipoate A/B protein ligase family (AHRD V3.3 *** A0A2U1MSZ4_ARTAN) | NA | -1.030043718 | 0.020879476 | 3.101748333 | 1.541489667 |
| Solyc11g007160.2 | RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** A0A1I9LPX6_ARATH) | NA | -1.02844779 | 0.009209771 | 1.921692667 | 0.949494667 |
| Solyc09g064800.3 | Isoamylase 2, chloroplastic (AHRD V3.3 *** A0A2G3A6V3_CAPAN) | ISA | -1.028220968 | 1.06244E-05 | 13.32985333 | 6.537607 |
| Solyc02g094280.4 | Yellow stripe-like protein (AHRD V3.3 *** A0A2D1UXE7_ROSHC) | NA | -1.027874727 | 2.44667E-07 | 52.58259333 | 25.86524633 |
| Solyc11g072180.3 | THO complex subunit 7A (AHRD V3.3 *-* A0A1U8EMF0_CAPAN) | THOC7 | -1.02757638 | 0.000681715 | 10.92503733 | 5.392514667 |

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| Solyc04g008650.4 | Inactive leucine-rich repeat receptor-like serinethreonine-protein kinase (AHRD V3.3 *** A0A314KSQ6_NICAT) | NA | -1.026466466 | 0.010790284 | 5.00924 | 2.495686333 |
| Solyc10g083760.3 | chloroplast threonine deaminase 1 precursor | ILVA | -1.025846098 | 0.001956374 | 34.51071067 | 17.14583867 |
| Solyc01g099580.3 | Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *-* Q9ZUW8_ARATH) | NA | -1.025417158 | 0.037232193 | 1.666573333 | 0.811978333 |
| Solyc02g087190.1 | Peroxidase (AHRD V3.3 *** K4BBM6_SOLLC) | peroxidase | -1.025377866 | 0.00144772 | 29.71760067 | 14.810232 |
| Solyc06g062840.4 | Threonine synthase, chloroplastic (AHRD V3.3 *** A0A1U8H4Z2_CAPAN) | THRC | -1.025052046 | 0.002650396 | 4.679056667 | 2.337703333 |
| Solyc03g121850.3 | hypothetical protein (AHRD V3.3 *-* AT1G05950.4) | NA | -1.023052964 | 0.005496862 | 2.837988667 | 1.390792667 |
| Solyc06g007760.4 | Ycf54-like protein (AHRD V3.3 *** B4FED9_MAIZE) | NA | -1.020754565 | 0.000503456 | 35.377387 | 17.56249167 |
| Solyc04g015040.3 | Peptidylprolyl isomerase (AHRD V3.3 *** A0A2G2XYE0_CAPAN) | peptidylprolyl isomerase | -1.020434847 | 1.4211E-05 | 13.020985 | 6.448684333 |
| Solyc03g116870.3 | NAD(P)H dehydrogenase subunit 48 (AHRD V3.3 *** A0A0F7GZU3_9ROSI) | NA | -1.020075476 | 0.000129472 | 10.403594 | 5.186699333 |
| Solyc11g069450.1 | Senescence regulator S40 (AHRD V3.3 *** A0A200QID2_9MAGN) | NA | -1.019981477 | 0.000483284 | 38.42458867 | 19.01871367 |
| Solyc06g052060.3 | hypothetical protein (AHRD V3.3 *** AT4G10810.1) | NA | -1.019656816 | 0.020912819 | 6.404949 | 3.199879 |
| Solyc02g081070.4 | Kinase (AHRD V3.3 *** D7ME76_ARALL) | NA | -1.019162171 | 0.001748047 | 5.435851 | 2.727929333 |
| Solyc01g108660.4 | N-acetyl-gamma-glutamyl-phosphate reductase (AHRD V3.3 *** A0A1U8E8L1_CAPAN) | ARGC | -1.015954958 | 2.14383E-07 | 48.307307 | 24.18946 |
| Solyc08g081930.3 | Glucose-6-phosphate 1-epimerase (AHRD V3.3 *** A0A2G3DB64_CAPCH) | glucose-6-phosphate 1-epimerase | -1.015166317 | 8.5878E-05 | 13.07899433 | 6.464204667 |
| Solyc06g005380.3 | F-box protein (AHRD V3.3 *** A0A1U8H630_CAPAN) | FBXL2_20 | -1.015114667 | 0.000809171 | 6.629086333 | 3.272537667 |
| Solyc07g045350.4 | Acetyl-CoA C-acetyltransferase (AHRD V3.3 *** D9U856_BACMN) | ACAT | -1.014586491 | 0.001195162 | 7.615827 | 3.826246 |
| Solyc04g073990.3 | annexin p34 | ANNAT | -1.01223788 | 0.007310689 | 271.72081 | 137.3489533 |
| Solyc11g012450.2 | Inositol transporter 4 | SLC2A13 | -1.010015746 | 0.007637636 | 5.595508667 | 2.824716 |
| Solyc02g080300.3 | Beta-glucosidase 46 (AHRD V3.3 *** A0A1U8FUJ5_CAPAN) | BGLB | -1.007399037 | 0.04446507 | 2.370737333 | 1.202603 |
| Solyc09g015370.1 | Pentatricopeptide repeat (AHRD V3.3 *** A0A200R528_9MAGN) | NA | -1.001996502 | 0.022646796 | 1.563215333 | 0.774585667 |
| Solyc07g061930.1 | Unknown protein | NA | -1.00192912 | 0.032588584 | 23.423163 | 11.72568 |
| Solyc06g068450.3 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G2WLA4_CAPBA) | NA | -1.001247885 | 0.020761012 | 46.10214667 | 23.28920867 |
| Solyc11g033288.1 | Transaldolase (AHRD V3.3 *** Q7XJH9_SOLLC) | TALA | -1.000641536 | 2.15186E-06 | 149.279663 | 75.15563433 |
| Solyc05g015470.1 | Chaperone protein dnaJ-like protein (AHRD V3.3 *** Q94CB5_ARATH) | NA | -0.998199544 | 1.12164E-05 | 43.33085767 | 21.875875 |
| Solyc07g049280.3 | Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (AHRD V3.3 *** A0A2G2Z2T1_CAPAN) | PFP | -0.99606349 | 0.00656508 | 2.483707333 | 1.262044667 |
| Solyc02g092090.3 | basic leucine zipper 43-like (AHRD V3.3 *** A0A2I4G035_9ROSI) | NA | -0.995661681 | 0.044882893 | 12.39836967 | 6.291517 |
| Solyc09g031970.3 | Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** A0A1U8E418_CAPAN) | PYG | -0.991985192 | 7.13932E-07 | 14.92865033 | 7.516926 |

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| Solyc06g082190.3 | Protein kinase like protein (AHRD V3.3 *** Q0WN89_ARATH) | NA | -0.990046869 | 0.000260407 | 5.338250667 | 2.703483 |
| Solyc04g082580.3 | F-box/kelch-repeat protein (AHRD V3.3 *** A0A2G2X1H4_CAPBA) | NA | -0.987471771 | 3.95431E-05 | 3.276162333 | 1.662891333 |
| Solyc11g068430.3 | Ferredoxin (AHRD V3.3 *** K4DA01_SOLLC) | PETF | -0.987074395 | 0.002481708 | 666.4462077 | 339.0161237 |
| Solyc03g065250.4 | Fatty acid hydroxylase superfamily (AHRD V3.3 *** A0A2U1L8N4_ARTAN) | K15404 | -0.98531086 | 0.008026402 | 4.512575 | 2.261007667 |
| Solyc08g079630.3 | AT-hook motif nuclear-localized protein 1 (AHRD V3.3 *** A0A2G3AEB8_CAPAN) | NA | -0.985003206 | 0.044925052 | 2.496785667 | 1.260545333 |
| Solyc01g103580.3 | DUF679 domain-containing protein (AHRD V3.3 *** A0A1Q3DCM8_CEPFO) | NA | -0.984604498 | 0.043083914 | 13.135012 | 6.728671667 |
| Solyc06g069120.3 | BnaA05g33450D protein (AHRD V3.3 *** A0A078J4B8_BRANA) | NA | -0.984416907 | 0.049975583 | 196.9029287 | 99.86508167 |
| Solyc06g051510.2 | Protein kinase superfamily protein (AHRD V3.3 *** A0A2U1KT12_ARTAN) | NA | -0.983159918 | 0.006454198 | 6.574532 | 3.3452 |
| Solyc07g009473.1 | Unknown protein | NA | -0.98245763 | 0.031353822 | 124.5075913 | 64.25023533 |
| Solyc11g069460.2 | Double-stranded RNA-binding protein 2 (AHRD V3.3 *** A0A2G2VQC6_CAPBA) | NA | -0.981305468 | 0.048137953 | 1.821535667 | 0.937399333 |
| Solyc09g064470.3 | Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *** A0A1U8E641_CAPAN) | MUR3 | -0.98086634 | 0.049429306 | 10.946708 | 5.669872333 |
| Solyc03g005330.1 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G2WWB5_CAPBA) | SNF1 | -0.979179693 | 0.002609443 | 4.554652333 | 2.330549333 |
| Solyc06g060250.3 | Aldehyde dehydrogenase (AHRD V3.3 *** A0A2G2WJP7_CAPBA) | ALDH | -0.978878068 | 6.70937E-08 | 19.08513667 | 9.759941 |
| Solyc06g005360.3 | Actin-depolymerizing factor (AHRD V3.3 *** D9I9X9_HEVBR) | CFL | -0.977556854 | 4.07209E-07 | 804.9199017 | 411.837372 |
| Solyc09g007640.4 | Serine carboxypeptidase-like 50 (AHRD V3.3 *** A0A2G2YQA0_CAPAN) | CPVL | -0.975134096 | 0.023367598 | 1.392021 | 0.712745 |
| Solyc02g086260.1 | 50S ribosomal-like protein (AHRD V3.3 *** Q9C618_ARATH) | NA | -0.973955855 | 0.0050381 | 15.32253067 | 7.846753667 |
| Solyc05g023900.1 | Pentatricopeptide repeat (AHRD V3.3 *** A0A200R3X1_9MAGN) | NA | -0.973688257 | 0.001637637 | 1.560384 | 0.79586 |
| Solyc06g050170.4 | Potassium transporter (AHRD V3.3 *** A0A1Q3B385_CEPFO) | KUP | -0.973431159 | 0.003431127 | 7.082978667 | 3.667098 |
| Solyc12g009880.1 | Serine-rich protein (AHRD V3.3 *** E5GCC5_CUCME) | NA | -0.973430155 | 0.012251303 | 7.084918 | 3.632964667 |
| Solyc06g060675.1 | Unknown protein | NA | -0.972594332 | 0.019269302 | 8.523861667 | 4.323471333 |
| Solyc09g082780.3 | Aluminum induced protein with YGL and LRDR motifs (AHRD V3.3 *** Q9LIL3_ARATH) | NA | -0.972577173 | 0.014449689 | 43.10546367 | 22.261589 |
| Solyc02g082760.3 | ethylene-responsive catalase | KATE | -0.971642668 | 0.002371642 | 17.963105 | 9.125683 |
| Solyc01g095530.2 | hypothetical protein (AHRD V3.3 *-* AT5G41761.1) | NA | -0.971126944 | 0.002602404 | 21.60373633 | 11.121227 |
| Solyc03g121720.2 | Glyoxylate reductase 2 (AHRD V3.3 *** A0A1P8AS42_ARATH) | GLYR | -0.969424976 | 0.027914076 | 2.077513333 | 1.06212 |
| Solyc03g114020.3 | D-ribose-binding periplasmic protein (AHRD V3.3 *** A0A2P5CJ45_PARAD) | NA | -0.969216204 | 0.038130377 | 7.397682 | 3.822391667 |
| Solyc06g005370.3 | Cofactor-independent phosphoglycerate mutase (AHRD V3.3 *** A0A2K3PS83_TRIPR) | NA | -0.968490351 | 1.62202E-08 | 22.284623 | 11.441207 |
| Solyc01g111120.4 | Triosephosphate isomerase (AHRD V3.3 *** A0A200Q3A8_9MAGN) | TPI | -0.967133719 | 1.66909E-07 | 145.2806703 | 74.78988167 |
| Solyc11g008270.2 | DUF4050 domain-containing protein (AHRD V3.3 *** A0A1Q3AYV9_CEPFO) | NA | -0.966037852 | 6.62565E-07 | 48.03659567 | 24.763849 |
| Solyc02g088130.1 | transmembrane protein (AHRD V3.3 *** AT3G29034.1) | NA | -0.965121156 | 0.000167017 | 110.79598 | 57.19431067 |

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| Solyc09g090340.3 | Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G14310.1) | NA | -0.963895297 | 0.00800772 | 0.778898 | 0.400746333 |
| Solyc07g063520.3 | Organic solute transporter ostalpha protein (DUF300) (AHRD V3.3 *** O65422_ARATH) | NA | -0.963646857 | 4.52707E-07 | 96.91356433 | 50.26663067 |
| Solyc01g087980.4 | DUF793 domain-containing protein (AHRD V3.3 *** A0A1Q3CNG5_CEPFO) | NA | -0.962306749 | 0.001357677 | 128.2595953 | 67.001475 |
| Solyc06g068270.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** Q9XIA5_ARATH) | NA | -0.961666263 | 0.000151702 | 42.93034767 | 22.336561 |
| Solyc02g071450.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** Q9SB33_ARATH) | NA | -0.959742786 | 0.005082928 | 11.223073 | 5.86915 |
| Solyc07g005060.3 | Defective in cullin neddylation protein (AHRD V3.3 *** A0A2G2WAX8_CAPBA) | DCUN1D4_5 | -0.959544157 | 5.05115E-05 | 16.63259867 | 8.588725 |
| Solyc04g005540.3 | Pvr4 (AHRD V3.3 *** A0A1D5AHY8_CAPAN) | NA | -0.954702918 | 0.040932372 | 5.005177333 | 2.640827667 |
| Solyc12g098150.2 | Voltage-dependent potassium channel, beta subunit (AHRD V3.3 *** A0A2H5RZM1_RHIID) | NA | -0.952949856 | 1.29916E-06 | 70.52530167 | 36.87303467 |
| Solyc10g078340.2 | Stomatal closure-related actin-binding protein 2 (AHRD V3.3 *** A0A1U8EKT6_CAPAN) | NA | -0.952561907 | 0.019742801 | 8.758491 | 4.577096333 |
| Solyc12g044850.2 | WAS/WASL-interacting family protein (AHRD V3.3 *** AT1G55160.1) | NA | -0.950525077 | 0.000349766 | 54.78061933 | 28.56411933 |
| Solyc04g007650.4 | 1-phosphatidylinositol-3-phosphate 5-kinase-like protein (AHRD V3.3 *** A0A2K3P1Y5_TRIPR) | PIKFYVE | -0.946446468 | 0.000183803 | 3.282494 | 1.72104 |
| Solyc06g009020.2 | Glutathione S-transferase (AHRD V3.3 *** A0A2G3C3Q3_CAPCH) | GST | -0.945470632 | 0.002933185 | 679.1758627 | 354.282837 |
| Solyc12g098370.2 | Myb family transcription factor APL (AHRD V3.3 *** A0A1U8F7R6_CAPAN) | NA | -0.944825961 | 0.019829094 | 6.511001 | 3.427262667 |
| Solyc09g064480.1 | Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *-* A0A1U8E641_CAPAN) | MUR3 | -0.942644038 | 0.012818152 | 12.12139267 | 6.374336333 |
| Solyc08g080940.3 | glutathione peroxidase  like encoding 1 | GPX | -0.942543192 | 2.81048E-06 | 609.8592123 | 319.150187 |
| Solyc09g083030.1 | inactive protein RESTRICTED TEV MOVEMENT 1-like (AHRD V3.3 *** A0A1S3ZEZ8_TOBAC) | NA | -0.94094668 | 0.005379791 | 121.4128647 | 64.564692 |
| Solyc04g015020.3 | Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* B3H4A8_ARATH) | NA | -0.93988402 | 2.94676E-05 | 94.09200767 | 49.55509067 |
| Solyc01g059880.3 | Citrate synthase-like (AHRD V3.3 *** A0A200R252_9MAGN) | ACLY | -0.93933514 | 0.023503751 | 21.06169567 | 11.059455 |
| Solyc12g013820.3 | Ubiquitin-conjugating enzyme (AHRD V3.3 *-* A0A200QWS6_9MAGN) | UBE2O | -0.93587753 | 0.001735441 | 6.955327667 | 3.666775333 |
| Solyc12g095870.3 | Aurora kinase A-A (AHRD V3.3 *** A0A1U8F0D3_CAPAN) | AURKX | -0.934796131 | 0.018601628 | 1.988806333 | 1.049247667 |
| Solyc09g075460.3 | Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A2U1PV10_ARTAN) | NA | -0.934719734 | 0.002427789 | 24.03776467 | 12.61243233 |
| Solyc05g010260.4 | 6-phosphogluconate dehydrogenase, decarboxylating (AHRD V3.3 *** A0A1U8F1N4_CAPAN) | PGD | -0.932391306 | 0.000386321 | 32.36440233 | 17.09821833 |
| Solyc08g005150.3 | RBR-type E3 ubiquitin transferase (AHRD V3.3 *** A0A2G2XWS5_CAPAN) | RNF14 | -0.932163092 | 0.025139276 | 11.82026333 | 6.172869333 |
| Solyc03g096730.3 | pollen-specific kinase partner protein | GMPP | -0.929276929 | 8.6405E-07 | 26.286272 | 13.936833 |
| Solyc07g053220.2 | G-type lectin S-receptor-like serine/threonine-protein kinase (AHRD V3.3 *** A0A2G2WDS9_CAPBA) | NA | -0.928151054 | 0.043406845 | 21.84837733 | 11.68153367 |
| Solyc12g096120.2 | Ubiquitin-fold modifier 1 (AHRD V3.3 *** A0A2G3B4L7_CAPCH) | UFM1 | -0.927925016 | 8.77019E-07 | 91.785347 | 48.81323 |
| Solyc05g053310.3 | Stress responsive A/B Barrel domain containing protein (AHRD V3.3 *** A0A1Y1IK97_KLENI) | NA | -0.927130132 | 0.00785656 | 11.31821 | 5.982542333 |
| Solyc06g053600.4 | Aldo/keto reductase (AHRD V3.3 *** A0A200QWT0_9MAGN) | NA | -0.926292627 | 0.000106612 | 7.98382 | 4.227928667 |

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| Solyc11g067300.2 | ABC transporter B family member (AHRD V3.3 *** A0A2K3NLX3_TRIPR) | ABCB1 | -0.92614228 | 0.010643208 | 1.067692 | 0.560549333 |
| Solyc04g079110.1 | BRI1 kinase inhibitor 1-like (AHRD V3.3 *** A0A2I4E9L6_9ROSI) | BKI1 | -0.925259112 | 0.033574499 | 3.425038667 | 1.822044333 |
| Solyc04g007420.4 | RNAse P, Rpr2/Rpp21 subunit (AHRD V3.3 *-* A0A2U1KVN4_ARTAN) | NA | -0.922215938 | 0.045285108 | 1.571979 | 0.842519 |
| Solyc07g007600.3 | vacuolar-type H+-pyrophosphatase | AVP | -0.921989564 | 0.022253575 | 60.32816433 | 32.11109567 |
| Solyc08g006820.4 | Transmembrane 9 superfamily member (AHRD V3.3 *** A0A2G3BR15_CAPCH) | TM9SF2_4 | -0.920832834 | 0.00054946 | 11.555709 | 6.202614 |
| Solyc08g077530.3 | Beta-amylase (AHRD V3.3 *** Q94EU9_SOLTU) | beta-amylase | -0.920262901 | 0.000828341 | 41.825622 | 22.20771667 |
| Solyc02g080810.3 | Aminomethyltransferase (AHRD V3.3 *** A0A2G2VBG4_CAPBA) | GCVT | -0.918381588 | 3.46071E-05 | 34.813228 | 18.53050733 |
| Solyc10g005180.3 | Ycf3-interacting protein 1, chloroplastic (AHRD V3.3 *** Y3IP1_TOBAC) | NA | -0.918107879 | 0.002519554 | 44.47043867 | 23.91643567 |
| Solyc11g010380.2 | Protein DETOXIFICATION (AHRD V3.3 *** A0A328DDG5_9ASTE) | TC.MATE | -0.915444311 | 0.00053228 | 32.57152867 | 17.39945967 |
| Solyc01g112280.3 | partialaminoacylase-1 | ACY1 | -0.914840945 | 2.96955E-05 | 41.60319 | 22.285874 |
| Solyc01g111970.4 | L-ascorbate oxidase-like protein (AHRD V3.3 *** A0A1U8DYA0_CAPAN) | NA | -0.911074868 | 0.030758306 | 52.536871 | 28.184304 |
| Solyc11g030600.3 | cytosine-5 DNA methyltransferase | DNMT1 | -0.910946019 | 1.37082E-05 | 5.115180667 | 2.752928 |
| Solyc06g084260.3 | Fatty-acid-binding protein 1 (AHRD V3.3 *** A0A1U8HAC4_CAPAN) | NA | -0.910882622 | 0.000245301 | 7.587323667 | 4.078458667 |
| Solyc08g005570.4 | Root UVB sensitive family (AHRD V3.3 *** A0A2U1QLM3_ARTAN) | NA | -0.909876107 | 0.000168981 | 5.580177333 | 2.986396 |
| Solyc04g072810.4 | Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** B6T8I8_MAIZE) | NA | -0.908639607 | 0.004543292 | 3.528705 | 1.899264 |
| Solyc06g005450.1 | Unknown protein | NA | -0.908402615 | 0.00259225 | 9.093964667 | 4.877477333 |
| Solyc02g089980.3 | electron transporter%2C putative (Protein of unknown function%2C DUF547) (AHRD V3.3 *** AT5G66600.9) | NA | -0.907809184 | 2.62924E-06 | 6.628992667 | 3.557466 |
| Solyc02g084990.3 | Mannan endo-1,4-beta-mannosidase (AHRD V3.3 *** A0A2K3NB99_TRIPR) | MAN | -0.907065325 | 0.013259186 | 13.291648 | 7.043153667 |
| Solyc03g083900.4 | monocopper oxidase-like protein SKU5 (AHRD V3.3 *** A0A2I4GW38_9ROSI) | NA | -0.90605739 | 0.016543708 | 26.38223833 | 14.356474 |
| Solyc06g065570.3 | N-alpha-acetyltransferase 50 (AHRD V3.3 *** A0A1U8GUI6_CAPAN) | NAA50 | -0.905369945 | 0.000578742 | 156.612953 | 84.28187833 |
| Solyc03g063730.4 | Protein DETOXIFICATION (AHRD V3.3 *** A0A191UP89_GLYSO) | TC.MATE | -0.900439197 | 0.00140132 | 6.060272 | 3.261607667 |
| Solyc06g005200.3 | Ribonuclease P protein subunit p30 (AHRD V3.3 *-* A0A1J3CKF4_NOCCA) | RPP1 | -0.900133907 | 0.000106894 | 9.714141333 | 5.248128667 |
| Solyc03g019880.3 | UPF0426 protein, chloroplastic (AHRD V3.3 *** A0A2G3AW71_CAPCH) | NA | -0.899794207 | 0.000187991 | 81.611473 | 43.96522 |
| Solyc04g011510.4 | Triosephosphate isomerase (AHRD V3.3 *** S8E0E9_9LAMI) | TPI | -0.898383644 | 0.000262465 | 201.9839477 | 109.4120583 |
| Solyc11g044230.3 | Costars family protein (AHRD V3.3 *-* A0A1U8F9R1_CAPAN) | NA | -0.897066124 | 1.02932E-05 | 66.77093767 | 36.12364833 |
| Solyc09g011730.4 | Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *** A0A178VFU5_ARATH) | NA | -0.896813661 | 2.22918E-06 | 23.686275 | 12.78128733 |
| Solyc08g076530.3 | binding partner of ACD11 1-like (AHRD V3.3 *** A0A1U8FBL9_CAPAN) | NA | -0.894739395 | 0.039388113 | 4.816671667 | 2.642601 |
| Solyc02g093290.3 | Nicotinate phosphoribosyltransferase (AHRD V3.3 *** A0A2G3D572_CAPCH) | PNCB | -0.893898429 | 0.032362297 | 62.839213 | 33.90896 |

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|---|---|---|---|---|---|---|
| Solyc10g076360.1 | PRA1 family protein (AHRD V3.3 *** A0A2G3BEF0_CAPCH) | RABAC1 | -0.893599 | 0.012478617 | 61.324168 | 33.623916 |
| Solyc11g013170.2 | Aminotransferase (AHRD V3.3 *** A0A200QIS8_9MAGN) | GTK | -0.8919863 | 0.000245096 | 41.064195 | 22.286331 |
| Solyc08g006890.3 | Tubulin alpha chain (AHRD V3.3 *** A0A1U8GD16_CAPAN) | TUBA | -0.889449851 | 0.002980238 | 167.9376017 | 92.18800233 |
| Solyc10g085550.3 | Enolase (AHRD V3.3 *** A0A200Q2G1_9MAGN) | ENO | -0.888786346 | 0.038712626 | 15.83283767 | 8.680007333 |
| Solyc01g006150.3 | Cation efflux protein (AHRD V3.3 *** A0A200PY73_9MAGN) | NA | -0.88873044 | 0.000377992 | 14.087017 | 7.704154 |
| Solyc03g007760.3 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** F4JKF8_ARATH) | NA | -0.8882432 | 0.016296311 | 6.80427 | 3.744526667 |
| Solyc08g007225.1 | Phospholipase A1-Ibeta2, chloroplastic (AHRD V3.3 *** A0A2G3BPM7_CAPCH) | NA | -0.886379741 | 0.020851562 | 1.451467333 | 0.785670667 |
| Solyc09g010800.5.1 | Metallothionein-like protein type 2 (AHRD V3.3 *** A0A2G2VXD7_CAPBA) | NA | -0.885217995 | 8.53238E-05 | 3430.467855 | 1865.139933 |
| Solyc03g111000.3 | Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** A0A2G2X869_CAPBA) | GAPDH | -0.884429198 | 0.001637637 | 5.888374 | 3.206146667 |
| Solyc11g066840.3 | Histone deacetylase HDT1 (AHRD V3.3 *** A0A2G2VQ39_CAPBA) | NA | -0.884419413 | 0.022879612 | 78.32953767 | 42.89877467 |
| Solyc04g076220.3 | AT-hook motif nuclear-localized protein (AHRD V3.3 *** A0A1U8GD78_CAPAN) | NA | -0.883655235 | 0.000657018 | 20.248355 | 11.11990933 |
| Solyc06g073090.3 | chloroplast-specific ribosomal protein chloroplast-specific ribosomal protein | NA | -0.883255914 | 0.000260407 | 31.088785 | 16.83502367 |
| Solyc06g074510.4 | Phosphoglycerate/bisphosphoglycerate mutase family protein (AHRD V3.3 *** A0A1P8BB43_ARATH) | 2-carboxy-D-arabinitol-1-phosphatase | -0.881977315 | 0.00441056 | 3.092943667 | 1.698599333 |
| Solyc07g041900.3 | cysteine proteinase | CTSH | -0.881233783 | 0.000165254 | 311.1786197 | 170.170644 |
| Solyc12g007070.2 | Heat shock transcription factor (AHRD V3.3 *-* A0A1Y1I763_KLENI) | HSFF | -0.878839597 | 0.000369623 | 24.89887933 | 13.55385767 |
| Solyc09g098100.4 | NB-LRR tospovirus immune receptor (AHRD V3.3 *** A0A221IWV2_SOLPN) | NA | -0.878792715 | 0.022227926 | 10.11604767 | 5.598978667 |
| Solyc02g030225.1 | UDP-glucose 4-epimerase (AHRD V3.3 *** A0A1Y1ITM0_KLENI) | UXE | -0.878592597 | 0.000215322 | 14.43663667 | 7.912381667 |
| Solyc06g005230.3 | Receptor-like protein kinase THESEUS 1 (AHRD V3.3 *** A0A2G2WHH2_CAPBA) | NA | -0.877829585 | 0.000167017 | 20.94228033 | 11.551502 |
| Solyc02g084031.1 | Ribonuclease H (AHRD V3.3 *-* A0A2K3NTL9_TRIPR) | NA | -0.877603034 | 0.02045226 | 2.348345 | 1.280507333 |
| Solyc07g065410.1 | hypothetical protein (AHRD V3.3 *** AT5G41761.1) | NA | -0.875968077 | 0.049429306 | 364.279846 | 202.9522883 |
| Solyc11g008870.2 | Methylenetetrahydrofolate reductase (AHRD V3.3 *** A0A1U8F633_CAPAN) | METF | -0.875744901 | 1.19623E-05 | 46.16381067 | 25.37120967 |
| Solyc05g055260.4 | Small nuclear ribonucleoprotein G (AHRD V3.3 *** A0A2G3CIT2_CAPCH) | SNRPG | -0.875074376 | 0.004834825 | 123.274732 | 68.25153733 |
| Solyc02g089930.4 | Protein DA1 (AHRD V3.3 *** A0A2G3D8V7_CAPCH) | NA | -0.874857194 | 2.72359E-05 | 13.94155233 | 7.683918 |
| Solyc11g067140.2 | DNA polymerase epsilon catalytic subunit (AHRD V3.3 *** A0A2G2VQQ6_CAPBA) | POLE | -0.874687136 | 0.002831451 | 2.233117 | 1.226444667 |
| Solyc09g055910.3 | D-amino acid dehydrogenase (AHRD V3.3 *** A0A1J3CZD8_NOCCA) | NA | -0.873596753 | 2.08684E-05 | 10.479771 | 5.766240667 |
| Solyc01g107800.4 | glucuronoxylan 4-O-methyltransferase 1-like (AHRD V3.3 *** A0A2I4H011_9ROSI) | NA | -0.873064347 | 0.001332522 | 6.781291667 | 3.722572667 |
| Solyc05g053810.3 | Serine hydroxymethyltransferase (AHRD V3.3 *** A0A2G3CI35_CAPCH) | GLYA | -0.87286851 | 0.000799106 | 53.116755 | 29.44966767 |

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|---|---|---|---|---|---|---|
| Solyc02g077720.4 | Unknown protein | NA | -0.871761081 | 0.003220051 | 7.269200333 | 3.977744333 |
| Solyc03g064030.3 | Alpha/beta hydrolase family protein (AHRD V3.3 *** Q8RWA3_ARATH) | NA | -0.871733949 | 0.006396489 | 32.266282 | 17.709898 |
| Solyc02g075610.4 | Golgin candidate 6 (AHRD V3.3 *-* A0A2G2XK18_CAPBA) | NA | -0.870871527 | 3.31512E-06 | 34.13326533 | 18.73847267 |
| Solyc10g009030.4 | sphingolipid delta 4 desaturase | DEGS | -0.87086267 | 0.010593603 | 4.081463667 | 2.246379667 |
| Solyc09g065540.3 | biotin-binding protein | 3-methylcrotonyl-CoA carboxylase alpha subunit | -0.867935423 | 0.000679329 | 44.390317 | 24.37895067 |
| Solyc12g043040.1 | Sulfate transporter (AHRD V3.3 *** A1YKF8_BRASY) | SULTR3 | -0.864760989 | 0.026527201 | 3.116421 | 1.701155333 |
| Solyc03g006330.4 | Leucine-rich repeat receptor-like serine/threonine-protein kinase (AHRD V3.3 *** A0A0A7LUM7_ALBBR) | NA | -0.864679372 | 5.94372E-06 | 17.03606433 | 9.442444667 |
| Solyc06g071070.1 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1L921_ARTAN),Pfam:PF13561 | FABG | -0.86464574 | 0.026331481 | 6.349720667 | 3.520414 |
| Solyc08g081060.3 | DUF3527 domain-containing protein (AHRD V3.3 *** A0A1Q3AQL6_CEPFO) | NA | -0.863703033 | 0.013187278 | 1.005997333 | 0.556515 |
| Solyc12g005730.2 | DUF604 domain-containing protein (AHRD V3.3 *** A0A1Q3CI87_CEPFO) | NA | -0.862041716 | 0.008447104 | 7.591918667 | 4.173807667 |
| Solyc02g084480.3 | golgin candidate 6-like isoform X2 (AHRD V3.3 *-* XP_025885295.1) | NA | -0.862010904 | 0.000317686 | 29.79531433 | 16.46302667 |
| Solyc05g025680.3 | Respiratory burst oxidase homolog (AHRD V3.3 *** Q84KK8_NICBE) | RBOH | -0.860336554 | 0.000186459 | 4.679774333 | 2.601964 |
| Solyc05g005860.3 | WAT1-related protein (AHRD V3.3 *** K4BWB3_SOLLC) | NA | -0.859671364 | 0.011395167 | 4.354622667 | 2.404712667 |
| Solyc09g072880.3 | Protein FLUORESCENT IN BLUE LIGHT, chloroplastic (AHRD V3.3 *** A0A1U8GA42_CAPAN) | NA | -0.859652423 | 0.009157198 | 1.566254667 | 0.861816667 |
| Solyc06g073060.3 | IAA-amino acid hydrolase ILR1-like 4 (AHRD V3.3 *** A0A1U8H3P8_CAPAN) | ILR1 | -0.859434056 | 9.02168E-06 | 80.02507767 | 44.469611 |
| Solyc01g005220.3 | MACPF domain-containing protein (AHRD V3.3 *** A0A2G3AYJ5_CAPCH) | NA | -0.85919522 | 0.001677786 | 22.48886967 | 12.550653 |
| Solyc03g116150.4 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** A0A2U1LK68_ARTAN) | NA | -0.856906385 | 0.001852635 | 5.099383333 | 2.851283667 |
| Solyc08g066750.3 | Major facilitator superfamily protein (AHRD V3.3 *** A0A2U1QCK3_ARTAN) | MFSD5 | -0.856516602 | 0.000923363 | 7.835255 | 4.383747 |
| Solyc10g086565.2 | S-acyltransferase (AHRD V3.3 *** A0A2G2VTM9_CAPBA) | ZDHHC3_7_25 | -0.855325462 | 0.028205443 | 1.56318 | 0.861727667 |
| Solyc02g082430.4 | MLO-like protein (AHRD V3.3 *** K4BAB3_SOLLC) | MLO | -0.854303463 | 1.02996E-05 | 31.044011 | 17.31347033 |
| Solyc10g081510.2 | ethylene-responsive methionine synthase | METE | -0.852334433 | 0.002368535 | 186.197581 | 104.3733977 |
| Solyc05g047550.4 | Protein kinase domain (AHRD V3.3 *** A0A200QZ79_9MAGN) | NA | -0.850660279 | 0.047000878 | 1.725354 | 0.960985 |
| Solyc07g054490.3 | Secretory carrier-associated membrane protein (AHRD V3.3 *** A0A2G2Z3L9_CAPAN) | SCAMP | -0.850017311 | 0.003529153 | 10.520037 | 5.930503333 |
| Solyc12g096830.2 | Glycosyltransferase (AHRD V3.3 *** A0A2I4H5B3_9ROSI) | NA | -0.84799355 | 0.002759341 | 10.62062367 | 5.957564333 |
| Solyc02g079190.3 | Protein AUXIN SIGNALING F-BOX 3 (AHRD V3.3 *** A0A2G3D604_CAPCH) | TIR1 | -0.843324987 | 0.013117796 | 7.232683333 | 4.054976333 |
| Solyc09g008790.4 | SRSF protein kinase 1 (AHRD V3.3 *** A0A1U8EHQ6_CAPAN) | SRPK3 | -0.842014452 | 0.007064395 | 6.105362 | 3.432924667 |
| Solyc07g061935.1 | C2 domain-containing protein (AHRD V3.3 *-* A0A2G2Z4M9_CAPAN) | NA | -0.837742301 | 0.022648356 | 16.32976867 | 9.204754667 |

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| Solyc05g023770.4 | Coiled-coil domain-containing protein SCD2 (AHRD V3.3 *** A0A2G2VN50_CAPBA) | NA | -0.836971544 | 0.021617161 | 2.790986667 | 1.581374333 |
| Solyc02g089065.1 | Protein SPIRAL1 (AHRD V3.3 *** A0A1U8FPZ4_CAPAN) | SPR1 | -0.836450919 | 0.008300105 | 170.0160727 | 96.01312533 |
| Solyc11g009080.2 | DAHP synthase 1 precursor | AROF | -0.836140377 | 0.001172119 | 107.3884 | 60.02342867 |
| Solyc02g084490.1 | Golgin candidate 6 (AHRD V3.3 *** A0A2G2XK18_CAPBA) | NA | -0.836072923 | 5.50468E-06 | 32.19264933 | 18.10761367 |
| Solyc02g085830.4 | Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 *-* Q9FX63_ARATH) | NA | -0.832460455 | 0.017876488 | 73.475792 | 41.91655333 |
| Solyc04g081440.3 | beta-fructofuranosidase | NA | -0.83010146 | 4.23352E-05 | 85.27998367 | 48.25893533 |
| Solyc08g065220.3 | glycine decarboxylase p-protein | GLDC | -0.829489133 | 0.000386321 | 40.09179167 | 22.70639767 |
| Solyc03g005220.4 | Histone H2A (AHRD V3.3 *** A0A1U8G3K0_CAPAN) | H2A | -0.828826421 | 0.003548208 | 29.41618367 | 16.827721 |
| Solyc01g091340.3 | Peptidylprolyl isomerase (AHRD V3.3 *** A0A2G3AH66_CAPAN) | FPR3_4 | -0.827818378 | 0.001596133 | 6.346152667 | 3.609298 |
| Solyc10g083380.2 | Basic-leucine zipper (BZIP) transcription factor family protein (AHRD V3.3 *-* Q8L5Y2_ARATH) | NA | -0.827116942 | 0.008172851 | 16.86829667 | 9.551974 |
| Solyc10g079470.3 | gldhL-galactono-1,4-lactone dehydrogenase | GLDH | -0.825314723 | 0.014272801 | 6.143719667 | 3.519843333 |
| Solyc06g007680.1 | F-box/LRR-repeat protein 12 (AHRD V3.3 *** A0A2G2WHC5_CAPBA) | FBXL2_20 | -0.824334104 | 0.010010476 | 3.073037 | 1.744776333 |
| Solyc08g061800.3 | hypothetical protein (AHRD V3.3 *-* AT2G26340.2) | NA | -0.82394099 | 0.009973667 | 8.903962 | 5.045211333 |
| Solyc11g008670.2 | Chromatin assembly factor 1 subunit FAS1 (AHRD V3.3 *** A0A2G2VEF8_CAPBA) | CHAF1A | -0.821549543 | 0.00373895 | 2.541162667 | 1.456543667 |
| Solyc09g055755.1 | Myosin heavy chain-related protein (AHRD V3.3 *** A0A2U1LV14_ARTAN) | NA | -0.816538821 | 4.92509E-06 | 23.53684333 | 13.42395833 |
| Solyc03g005000.4 | Peptidase M48 (AHRD V3.3 *-* A0A200R452_9MAGN) | NA | -0.816347621 | 0.006027347 | 20.10378067 | 11.45962233 |
| Solyc10g083960.2 | Phosphoadenosine phosphosulfate (PAPS) reductase family protein (AHRD V3.3 *** Q9LZE4_ARATH) | NA | -0.813323333 | 0.036383862 | 2.101269333 | 1.198 |
| Solyc05g013380.3 | Alanine aminotransferase 2 (AHRD V3.3 *** B6TXZ8_MAIZE) | GGAT | -0.813043906 | 0.033847475 | 9.576531333 | 5.558789333 |
| Solyc09g082210.4 | DUF581 domain-containing protein (AHRD V3.3 *** A0A1Q3DCU3_CEPFO) | NA | -0.81295209 | 0.008108974 | 34.739962 | 19.86524333 |
| Solyc05g050740.3 | dentin sialophosphoprotein isoform X2 (AHRD V3.3 *-* XP_023890879.1) | NA | -0.810483433 | 0.005862513 | 3.700809 | 2.123109333 |
| Solyc09g083380.4 | Histone H1 (AHRD V3.3 *-* A0A2G3CST5_CAPCH) | H1_5 | -0.810252812 | 0.003713056 | 27.988235 | 16.05430067 |
| Solyc12g014600.2 | RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** F4JFN7_ARATH) | MSI | -0.809933887 | 0.034267968 | 11.753499 | 6.838989667 |
| Solyc11g005620.1 | Acetylglutamate kinase (AHRD V3.3 *** A0A1U8EW67_CAPAN) | ARGB | -0.809535767 | 0.00482626 | 16.054555 | 9.227349 |
| Solyc05g013240.4 | DUF538 family protein%2C putative (Protein of unknown function%2C DUF538) (AHRD V3.3 *** AT1G55265.1) | NA | -0.808903773 | 0.00026701 | 69.271314 | 39.98206867 |
| Solyc06g005190.4 | RNA binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** Q9M1E4_ARATH) | CNOT4 | -0.808375405 | 1.78047E-05 | 34.818176 | 19.98030267 |
| Solyc10g006960.3 | E3 ubiquitin-protein ligase rma1h1-like protein (AHRD V3.3 *** A0A2K3P2S4_TRIPR) | RNF5 | -0.806938714 | 0.021161547 | 6.958411667 | 4.014161667 |
| Solyc11g013500.1 | myotubularin-like protein (AHRD V3.3 *** AT1G36940.1) | NA | -0.806644022 | 0.02932361 | 4.721062 | 2.708597333 |
| Solyc11g072690.2 | LES294902 3-desoxy-D-manno octulosonic acid-8-phosphate synthase | KDSA | -0.805104297 | 0.018860536 | 7.511424667 | 4.364282 |

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|---|---|---|---|---|---|---|
| Solyc01g087040.2 | Photosystem II PsbP (AHRD V3.3 *** A0A200Q959_9MAGN) | NA | -0.804287166 | 0.010110665 | 9.876218667 | 5.663697333 |
| Solyc05g006520.4 | dehydrogenase AF209924 | PDHA | -0.803245303 | 0.000245077 | 58.69339767 | 34.101099 |
| Solyc09g007410.3 | SUN-like protein 25 | NA | -0.801537729 | 0.000501439 | 10.33438767 | 5.957024333 |
| Solyc12g014390.3 | 50S ribosomal protein L13 (AHRD V3.3 *** A0A1U8E5A8_CAPAN) | RP-L13 | -0.800996402 | 0.000776666 | 53.88013333 | 31.077746 |
| Solyc08g082480.3 | Phosphatidylinositol 4-kinase gamma 2 (AHRD V3.3 *** A0A2G3ADD9_CAPAN) | NA | -0.800104672 | 0.019748007 | 3.071142667 | 1.767431333 |
| Solyc03g116800.4 | homoserine O-acetyltransferase (AHRD V3.3 *-* AT3G15900.1) | NA | -0.798706779 | 0.008348595 | 10.666088 | 6.171109667 |
| Solyc10g084600.2 | Plant protein 1589 of Uncharacterized protein function (AHRD V3.3 *-* A0A061EZD3_THECC) | NA | -0.79865275 | 0.000779269 | 165.9159547 | 95.42179333 |
| Solyc10g083920.2 | Serine/threonine protein phosphatase 2A regulatory subunit (AHRD V3.3 *** A0A2G2VUQ8_CAPBA) | PPP2R5 | -0.798493994 | 0.000374324 | 11.4883 | 6.619980333 |
| Solyc11g066340.2 | actin protein 2/3 complex subunit-like protein (AHRD V3.3 *** AT2G28130.1) | NA | -0.79600016 | 0.040212788 | 2.19129 | 1.276122333 |
| Solyc11g071280.2 | 4-amino-4-deoxychorismate lyase | ADCL | -0.795082946 | 0.005657781 | 36.569315 | 21.351168 |
| Solyc07g044840.3 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (AHRD V3.3 *** A0A2G2WBT5_CAPBA) | GPMI | -0.794983198 | 0.000204741 | 245.7025093 | 142.3815053 |
| Solyc03g083440.4 | Glutamate synthase (AHRD V3.3 *** A0A2U1PKW7_ARTAN) | GLT1 | -0.794480881 | 0.014134629 | 4.804327667 | 2.81237 |
| Solyc11g006910.3 | Ferredoxin (AHRD V3.3 *** K4D4V2_SOLLC) | PETF | -0.794386135 | 0.001344247 | 38.46179067 | 22.244832 |
| Solyc07g042250.3 | chaperonin 21 precursor | GROES | -0.793466752 | 0.000625731 | 652.7784833 | 378.0120237 |
| Solyc08g013760.1 | F-box family protein (AHRD V3.3 *-* A0A2K3MZH1_TRIPR) | NA | -0.792819203 | 0.001158197 | 7.752247667 | 4.507222333 |
| Solyc09g091430.4 | Pectate lyase (AHRD V3.3 *** A0A2G2W1U1_CAPBA) | PEL | -0.792471139 | 9.90696E-05 | 14.26913833 | 8.321312333 |
| Solyc12g041880.2 | hypothetical protein (AHRD V3.3 *** AT1G28100.6) | NA | -0.791251379 | 0.002509087 | 7.630336667 | 4.418516667 |
| Solyc01g067730.3 | Acyl carrier protein (AHRD V3.3 *** A0A1U8EET6_CAPAN) | NA | -0.789666513 | 0.000127898 | 288.354604 | 168.7592823 |
| Solyc09g057630.3 | Glucan endo-1,3-beta-glucosidase 3-like protein (AHRD V3.3 *** A0A2K3MT62_TRIPR) | NA | -0.78731493 | 0.044559464 | 3.378458667 | 1.987806333 |
| Solyc02g070580.1 | sterol 22-desaturase | CYP710A | -0.786288227 | 0.012361985 | 25.94869867 | 15.06966433 |
| Solyc07g062030.3 | Chalcone-flavonone isomerase family protein (AHRD V3.3 *** A0A2G2WEX9_CAPBA) | NA | -0.785924516 | 0.002831545 | 11.05042133 | 6.457865333 |
| Solyc05g008105.1 | hydroxyproline-rich glycoprotein family protein (AHRD V3.3 --* AT1G23040.3) | NA | -0.784805943 | 0.002724981 | 305.9393513 | 178.9631347 |
| Solyc03g078370.1 | Receptor-like protein kinase (AHRD V3.3 *** A0A2U1PPA0_ARTAN) | NA | -0.784794586 | 0.015078439 | 13.48638933 | 7.918265333 |
| Solyc01g108020.3 | Thioredoxin M3, chloroplastic (AHRD V3.3 *** A0A1U8E6Y3_CAPAN) | TRXA | -0.780498618 | 0.000663339 | 26.50320433 | 15.55741267 |
| Solyc06g076790.1 | Thylakoid soluble phosphoprotein TSP9 (AHRD V3.3 *-* A0A200Q7Q2_9MAGN) | NA | -0.780243946 | 0.04783959 | 30.403405 | 17.66154133 |
| Solyc10g006310.3 | Protein FATTY ACID EXPORT 6 (AHRD V3.3 *** A0A1U8EPM9_CAPAN) | NA | -0.779119168 | 0.012432412 | 9.532477333 | 5.634398 |
| Solyc05g012110.4 | 6-phosphogluconolactonase (AHRD V3.3 *** B6U0H2_MAIZE) | PGLS | -0.774405164 | 0.000292681 | 19.01333233 | 11.16719967 |
| Solyc03g082580.3 | 6-phosphogluconolactonase (AHRD V3.3 *** B6UAK0_MAIZE) | PGLS | -0.772669291 | 1.40939E-05 | 29.13873733 | 17.21454967 |

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|---|---|---|---|---|---|---|
| Solyc11g068550.1 | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** Q9M287_ARATH) | NA | -0.772506464 | 0.001090303 | 23.256874 | 13.70095267 |
| Solyc01g102300.3 | bHLH transcription factor 006 | PIF3 | -0.771608877 | 0.048859211 | 14.575467 | 8.508712667 |
| Solyc11g012060.2 | hypothetical protein (AHRD V3.3 *-* AT1G12020.1) | NA | -0.771572319 | 0.006969573 | 7.519069333 | 4.418128 |
| Solyc02g071730.4 | Tomato AGAMOUS 1 | K09264 | -0.769976851 | 0.002060495 | 72.379336 | 42.99790933 |
| Solyc07g064740.3 | Rab3 GTPase-activating protein catalytic subunit (AHRD V3.3 *** A0A200QG39_9MAGN) | RAB3GAP1 | -0.769029762 | 0.03826893 | 2.390028667 | 1.412294667 |
| Solyc09g007100.3 | DUF632 domain-containing protein/DUF630 domain-containing protein (AHRD V3.3 *** A0A1Q3BWV7_CEPFO) | NA | -0.766118692 | 0.000122411 | 15.360814 | 9.099314333 |
| Solyc11g011010.1 | B-cell receptor-associated-like protein (AHRD V3.3 *** Q9FFJ0_ARATH) | NA | -0.764648456 | 0.043083914 | 8.110603333 | 4.839196 |
| Solyc09g005280.3 | Transposase, Ptta/En/Spm, plant (AHRD V3.3 *-* A0A1R3I9M9_9ROSI) | NA | -0.762671034 | 0.000791382 | 7.08441 | 4.208851 |
| Solyc09g020110.3 | T2-type RNase (AHRD V3.3 *** A0AQW5_SOLLC) | RNASET2 | -0.762090542 | 0.000190917 | 74.510465 | 44.085963 |
| Solyc09g090220.3 | Pentatricopeptide repeat (AHRD V3.3 *** A0A200QEC4_9MAGN) | NA | -0.761282641 | 0.042681626 | 0.927057 | 0.545722333 |
| Solyc04g076790.3 | Serine hydroxymethyltransferase (AHRD V3.3 *** A0A2G2ZR28_CAPAN) | GLYA | -0.759852254 | 0.001803919 | 81.61141967 | 48.55003867 |
| Solyc05g008800.4 | lipid phosphate phosphatase 2-like (AHRD V3.3 *** A0A1S4AJT8_TOBAC) | DPP1 | -0.7579863 | 0.000755752 | 8.731674667 | 5.212232 |
| Solyc09g090540.3 | hypothetical protein (AHRD V3.3 *** AT2G33390.1) | NA | -0.757931418 | 0.042127182 | 7.307573667 | 4.328478333 |
| Solyc06g082750.3 | 50S ribosomal protein L17 (AHRD V3.3 *** A0A1U8H2A3_CAPAN) | RP-L17 | -0.753773764 | 0.004638239 | 52.83737567 | 31.508642 |
| Solyc10g083720.3 | Pyruvate kinase (AHRD V3.3 *** A0A1U8EAH7_CAPAN) | PK | -0.753505414 | 0.028897277 | 232.7890423 | 138.850759 |
| Solyc12g044910.2 | copz2 nonclathrin coat protein zeta2-COP | COPZ | -0.753213011 | 0.000626994 | 19.17983433 | 11.49456633 |
| Solyc03g116910.3 | cinnamoyl-CoA reductase 2 | CCR | -0.753072588 | 0.045017507 | 2.161747333 | 1.299716667 |
| Solyc08g081140.4 | bHLH transcription factor 090 | NA | -0.751494557 | 0.038395854 | 5.488346333 | 3.281991333 |
| Solyc09g092450.3 | Long-chain acyl-CoA synthetase (AHRD V3.3 *** A0A1Z5KCI0_FISSO) | ACSL | -0.749501655 | 0.038498905 | 3.962677667 | 2.393251667 |
| Solyc03g007470.4 | Ubiquitin conjugating enzyme (AHRD V3.3 *** B3TLN8_ELAGV) | UBE2D | -0.747610161 | 0.008857618 | 108.9797133 | 65.35714867 |
| Solyc11g011760.3 | voltage-dependent L-type calcium channel subunit (AHRD V3.3 *** AT5G16550.1) | NA | -0.746968443 | 2.32371E-05 | 44.71587133 | 26.74720767 |
| Solyc03g113340.3 | Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A2U1M3G7_ARTAN) | NA | -0.742481648 | 0.049137269 | 12.682684 | 7.627053333 |
| Solyc07g062670.1 | Unknown protein | NA | -0.742281195 | 0.032588584 | 149.7834477 | 89.40257733 |
| Solyc11g011960.2 | UTP--glucose-1-phosphate uridylyltransferase (AHRD V3.3 *** Q5F1U6_SOLTU) | UGP2 | -0.740644845 | 0.000372126 | 104.1426697 | 63.05850833 |
| Solyc05g017760.4 | Acetyl-CoA C-acetyltransferase (AHRD V3.3 *** D9U856_BACMN) | ACAT | -0.739928957 | 5.08868E-05 | 53.47305567 | 32.30651167 |
| Solyc10g074870.2 | KH domain-containing protein (AHRD V3.3 *** A0A2G2VT48_CAPBA) | QKI | -0.739775059 | 0.000635801 | 33.529696 | 20.34915 |
| Solyc07g056390.4 | Endoplasmic reticulum oxidoreductin-1 (AHRD V3.3 *** A0A2G2WEL6_CAPBA) | ERO1L | -0.739224151 | 0.016734182 | 14.39614767 | 8.718121 |
| Solyc03g083580.3 | Peptidase_M3 domain-containing protein (AHRD V3.3 *** A0A1Q3BAD5_CEPFO) | MIPEP | -0.7387299 | 0.021128005 | 2.226543333 | 1.341445 |

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|---|---|---|---|---|---|---|
| Solyc04g015210.4 | Disease resistance protein (AHRD V3.3 *** A0A2U1N8H9_ARTAN) | NA | -0.738551125 | 0.005745162 | 1.734341333 | 1.047682 |
| Solyc12g089110.1 | Unknown protein | NA | -0.738211384 | 0.006215667 | 116.297231 | 69.711498 |
| Solyc05g008860.4 | Receptor protein kinase-like protein (AHRD V3.3 *** A0A2R6P9S7_ACTCH) | NA | -0.737082691 | 0.022031957 | 1.613124333 | 0.972668333 |
| Solyc03g119480.4 | hypothetical protein (AHRD V3.3 *** AT3G02555.2) | NA | -0.736935372 | 0.035029179 | 5.207300667 | 3.158984 |
| Solyc01g102410.3 | Glutamine--tRNA ligase (AHRD V3.3 *** A0A2I0WQV3_9ASPA) | EARS | -0.735109473 | 0.01215436 | 68.95115 | 41.89830067 |
| Solyc05g054430.4 | DNA replication complex GINS protein PSF2 (AHRD V3.3 *** A0A1U8GTG0_CAPAN) | GINS2 | -0.733401253 | 0.041851016 | 3.015796 | 1.825837667 |
| Solyc02g077480.1 | Histone H3 (AHRD V3.3 *** B3TM40_ELAGV) | H3 | -0.732783324 | 0.037910799 | 25.99598533 | 15.56326733 |
| Solyc12g005180.2 | Chloroplast lipocalin (AHRD V3.3 *** Q38JB4_SOLTU) | NA | -0.727484821 | 0.000965237 | 28.86680367 | 17.49157667 |
| Solyc03g013240.4 | lysine-tRNA ligase (AHRD V3.3 *** AT3G01060.1) | NA | -0.727461848 | 0.039921305 | 10.16484567 | 6.166641 |
| Solyc03g098750.3 | Unknown protein | NA | -0.726099834 | 0.030005235 | 39.07920767 | 23.98663467 |
| Solyc02g092840.1 | Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *** A0A2K3L4H3_TRIPR) | NA | -0.723970939 | 0.045682884 | 10.72466933 | 6.589668667 |
| Solyc09g011380.3 | BEL1-like homeodomain protein 9 (AHRD V3.3 *** A0A2G2VXF9_CAPBA) | NA | -0.722623085 | 0.002662945 | 7.291207333 | 4.446971667 |
| Solyc02g085670.3 | Major facilitator superfamily protein (AHRD V3.3 *** A0A2U1P386_ARTAN) | NA | -0.721298376 | 0.0104622 | 6.015379333 | 3.680808 |
| Solyc08g066160.3 | Early nodulin-93 (AHRD V3.3 *** A0A1U8DU22_CAPAN) | NA | -0.72076388 | 0.008408648 | 59.88570567 | 36.622478 |
| Solyc01g079350.3 | HIT zinc finger and PAPA-1-like domain-containing protein (AHRD V3.3 *-* F4I548_ARATH) | NA | -0.719455839 | 0.013788773 | 19.313045 | 11.82220667 |
| Solyc02g091890.3 | myb-like protein X (AHRD V3.3 *-* A0A2I4FW88_9ROSI) | NA | -0.718284207 | 0.019269302 | 1.708750667 | 1.042739333 |
| Solyc05g051770.3 | transmembrane protein (AHRD V3.3 *** AT5G09995.2) | NA | -0.717234348 | 0.018601628 | 7.177783667 | 4.392044333 |
| Solyc05g007020.4 | LOV/LOV protein (AHRD V3.3 *** E3WH16_SOLLC) | NA | -0.715021272 | 0.021039412 | 39.63611233 | 24.25759167 |
| Solyc01g102580.3 | endo-1,4-beta-glucanase (Cel3) | endoglucanase | -0.714381535 | 0.042032606 | 76.04867833 | 47.056689 |
| Solyc02g089150.4 | PI-PLC X domain-containing protein (AHRD V3.3 *** A0A1U8FSV1_CAPAN) | NA | -0.714215733 | 0.005368238 | 7.404334333 | 4.561146667 |
| Solyc09g008730.3 | GTP-binding protein (AHRD V3.3 *** A0A2G2YPQ8_CAPAN) | ENGB | -0.713986633 | 0.019120804 | 9.526835667 | 5.855182667 |
| Solyc08g081150.4 | GMP synthase [glutamine-hydrolyzing] (AHRD V3.3 *** A0A2G3DAK4_CAPCH) | GUAA | -0.713086494 | 0.036516144 | 5.424746333 | 3.364835 |
| Solyc03g117310.1 | Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** Q9M8M0_ARATH) | NA | -0.711683166 | 0.002598323 | 25.56005733 | 15.728528 |
| Solyc07g020860.3 | Peroxiredoxin (AHRD V3.3 *** Q8S3L0_POPPZ) | PRXII | -0.711584563 | 0.000260095 | 331.897176 | 204.3241983 |
| Solyc03g116590.3 | Embryo-specific protein (AHRD V3.3 *** A0A2K3LFD9_TRIPR) | NA | -0.711305784 | 0.019017557 | 175.7140707 | 109.1470667 |
| Solyc01g005910.3 | Acid phosphatase/vanadium-dependent haloperoxidase-related protein (AHRD V3.3 *** A0A2U1NM03_ARTAN) | NA | -0.711210074 | 0.001463167 | 9.690619 | 5.968826667 |
| Solyc08g081010.3 | gamma-glutamylcysteine synthetase 1 | GSHA | -0.709217104 | 0.009873887 | 416.5333963 | 255.5520933 |
| Solyc07g066080.3 | Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A200QCU7_9MAGN) | UBE2D | -0.708319079 | 0.021437923 | 53.92003767 | 33.55646767 |
| Solyc08g068390.3 | Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a (AHRD V3.3 *** | MFP2 | -0.708232164 | 0.04079826 | 2.605471667 | 1.60925 |

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|---|---|---|---|---|---|---|
| | A0A2G2YXE3_CAPAN) | | | | | |
| Solyc03g118640.3 | Ketose-bisphosphate aldolase class-II family protein (AHRD V3.3 *** Q8VYC5_ARATH) | NA | -0.707374516 | 0.002694538 | 15.66057667 | 9.717105 |
| Solyc08g083330.2 | Polyketide cyclase/dehydrase and lipid transport superfamily protein (AHRD V3.3 *** Q9XIR9_ARATH) | NA | -0.70630447 | 0.007425367 | 99.85968767 | 61.54634333 |
| Solyc07g063190.3 | Thioredoxin (AHRD V3.3 *** A0A200PQX5_9MAGN) | TRXA | -0.704284366 | 0.001304663 | 102.2621917 | 62.987015 |
| Solyc05g052690.4 | Eukaryotic translation initiation factor 3 subunit F (AHRD V3.3 *** A0A1U8GMA9_CAPAN) | EIF3F | -0.704177605 | 0.001228575 | 11.113041 | 6.884411667 |
| Solyc07g063390.3 | Beta-glucosidase 16 (AHRD V3.3 *** A0A2G2WEV4_CAPBA) | BGLB | -0.703183746 | 7.40605E-05 | 27.66018567 | 17.05540633 |
| Solyc02g094520.3 | histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4-like (AHRD V3.3 *** A0A1S3YJW9_TOBAC) | EHMT | -0.701763445 | 0.013818144 | 3.463794 | 2.149542333 |
| Solyc04g009330.4 | Serine/threonine-protein kinase Aurora-3 (AHRD V3.3 *** A0A2G2ZF68_CAPAN) | AURKX | -0.701374578 | 0.032982196 | 3.650612 | 2.260961667 |
| Solyc06g069220.1 | Eukaryotic aspartyl protease family protein (AHRD V3.3 *** Q9C6M0_ARATH) | APF2 | -0.699706056 | 0.041228157 | 2.003833 | 1.239263333 |
| Solyc01g111510.3 | Ascorbate peroxidase (AHRD V3.3 *** Q8W4V7_CAPAN) | L-ascorbate peroxidase | -0.6971881 | 0.000126276 | 114.1121217 | 70.899602 |
| Solyc06g076510.3 | Phosphoserine phosphatase, chloroplastic (AHRD V3.3 *** A0A2G3CBM8_CAPCH),Pfam:PF00702 | SERB | -0.695626371 | 0.014353622 | 7.481357333 | 4.670437333 |
| Solyc03g111010.4 | Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** A0A0F7JIC2_NICBE) | GAPDH | -0.694908524 | 0.001603612 | 238.9750213 | 148.6071373 |
| Solyc02g079960.3 | Thioredoxin (AHRD V3.3 *** A0A2G3D6G6_CAPCH) | TRXA | -0.694821655 | 0.001385036 | 95.068324 | 59.109849 |
| Solyc10g017850.3 | Peroxisomal membrane protein 11C (AHRD V3.3 *** A0A2G3BDG9_CAPCH) | NA | -0.694301137 | 0.003593531 | 11.092002 | 6.913515667 |
| Solyc12g013910.2 | PRA1 family protein (AHRD V3.3 *** A0A2G2X2T8_CAPBA) | NA | -0.692925188 | 0.020599016 | 7.300193667 | 4.565586 |
| Solyc01g096460.2 | RING-type E3 ubiquitin transferase (AHRD V3.3 *-* T1R384_DATGL) | NA | -0.690194482 | 0.026663729 | 11.71236367 | 7.296663333 |
| Solyc03g007170.3 | Peptidylprolyl isomerase (AHRD V3.3 *** A0A2G2X6E0_CAPBA) | FPR3_4 | -0.68942101 | 0.043940915 | 5.066443 | 3.189781 |
| Solyc08g082820.4 | TOMBIPGRBC Tomato BiP (binding protein)/grp78 | HSPA5 | -0.68920635 | 0.025341732 | 43.21873367 | 27.11668467 |
| Solyc01g110290.3 | Squalene synthase (AHRD V3.3 *** Q9XJ31_SOLTU),Pfam:PF00494 | FDFT1 | -0.688341943 | 0.003747345 | 21.10919633 | 13.25526467 |
| Solyc02g062780.4 | ATP-dependent DNA helicase DDM1 (AHRD V3.3 *** A0A2G3D1Z5_CAPCH) | HELLS | -0.686215723 | 0.04408589 | 2.770740333 | 1.748751667 |
| Solyc04g080460.3 | Sugar facilitator protein 4 | ERD6 | -0.683468726 | 0.048166975 | 7.430383 | 4.685836667 |
| Solyc10g083350.2 | Heme-binding-like protein, chloroplastic (AHRD V3.3 *** A0A1U8EAT6_CAPAN) | NA | -0.683285019 | 0.014366079 | 11.67074867 | 7.280503 |
| Solyc01g079590.3 | Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 *** F4IYB7_ARATH) | NA | -0.682543573 | 0.002910046 | 160.7482097 | 100.520327 |
| Solyc08g069000.4 | Mg2+ transporter protein, CorA-like/Zinc transport protein ZntB (AHRD V3.3 *-* A0A2U1Q3X4_ARTAN) | NA | -0.682493244 | 0.023497525 | 7.623321667 | 4.789865 |
| Solyc02g063270.4 | Protein DETOXIFICATION (AHRD V3.3 *** A0A328DLR5_9ASTE) | TC.MATE | -0.681951963 | 0.034532313 | 53.40124133 | 33.62463 |
| Solyc07g014670.3 | Cytochrome P450 (AHRD V3.3 *-* A0A200QZM5_9MAGN) | NA | -0.681588775 | 0.026312446 | 9.179589667 | 5.799426333 |
| Solyc06g073240.3 | Carbohydrate esterase, putative (DUF303) (AHRD V3.3 *** Q0WNN6_ARATH) | NA | -0.680365218 | 0.03012965 | 7.539532667 | 4.768075667 |
| Solyc01g006980.4 | Malonyl CoA-acyl carrier protein transacylase containing protein, expressed (AHRD V3.3 *** | FABD | -0.678984836 | 0.001032703 | 16.03873567 | 10.06696067 |

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| | Q10MS3_ORYSJ) | | | | | |
| Solyc09g018790.3 | Succinic semialdehyde reductase isofom1 | GLYR | -0.67842232 | 0.000611183 | 85.76264433 | 53.902879 |
| Solyc11g071790.2 | Succinate dehydrogenase subunit 6, mitochondrial (AHRD V3.3 *** A0A2G2XX03_CAPAN) | NA | -0.678397366 | 0.000142137 | 43.40195833 | 27.31770433 |
| Solyc02g081160.3 | Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (AHRD V3.3 *** A0A1U8FN75_CAPAN) | PFP | -0.676756006 | 0.000545311 | 106.863312 | 67.46009567 |
| Solyc03g005470.3 | HR-like lesion-inducing protein-related (AHRD V3.3 *** B6SJ11_MAIZE) | NA | -0.675605849 | 0.000162815 | 112.3961843 | 70.808721 |
| Solyc02g084720.3 | beta-galactosidase 6 | NA | -0.67555551 | 0.005997644 | 5.652017 | 3.557095 |
| Solyc07g005730.4 | Low temperature and salt responsive protein (AHRD V3.3 *** A0A2K3ML14_TRIPR) | NA | -0.675317708 | 0.014612322 | 92.37522133 | 58.488069 |
| Solyc11g072440.2 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** Q9SF34_ARATH) | NA | -0.67430526 | 0.002309341 | 10.65662433 | 6.702797333 |
| Solyc01g079400.3 | Protein trichome birefringence-like 6 (AHRD V3.3 *** A0A2G3AKU6_CAPAN) | NA | -0.671785688 | 0.01001427 | 5.781859333 | 3.646589 |
| Solyc10g039270.2 | Peptidylprolyl isomerase (AHRD V3.3 *** A0A1U8FL13_CAPAN) | NA | -0.671009726 | 0.006092122 | 9.102474333 | 5.751195 |
| Solyc02g093830.4 | Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** F2Z9R1_NICBE) | G6PD | -0.671004405 | 0.000768925 | 94.32628633 | 59.652003 |
| Solyc04g015740.3 | transmembrane protein%2C putative (DUF288) (AHRD V3.3 *** AT2G41770.1) | NA | -0.669713648 | 0.036392411 | 3.398508667 | 2.163212333 |
| Solyc03g025800.3 | Heavy metal-associated isoprenylated plant protein (AHRD V3.3 *-* A0A2R6RWA7_ACTCH) | NA | -0.669641127 | 0.000855477 | 103.519732 | 65.36211167 |
| Solyc10g076600.2 | Acyl-CoA oxidase/dehydrogenase (AHRD V3.3 *** A0A200PWV2_9MAGN) | ACOX1 | -0.668955736 | 0.009404883 | 62.14671067 | 39.28494133 |
| Solyc05g007130.4 | SUN-like protein 15 | NA | -0.663203605 | 0.025341732 | 2.375817333 | 1.512901333 |
| Solyc08g005420.3 | cell division cycle 20.2, cofactor of APC complex-like (AHRD V3.3 *** A0A2I4FBA0_9ROSI) | CDC20 | -0.662790259 | 0.026010576 | 5.342264667 | 3.408059 |
| Solyc07g047960.3 | WRKY transcription factor 1 | WRKY1 | -0.662682668 | 0.043514804 | 6.295423667 | 3.990397667 |
| Solyc02g083810.4 | Ferredoxin--NADP reductase, chloroplastic (AHRD V3.3 *** K4BAP9_SOLLC) | PETH | -0.661921223 | 0.008092427 | 65.316012 | 41.304728 |
| Solyc06g051360.3 | gibberellin 2-beta-dioxygenase 8 (AHRD V3.3 *** A0A2I4EQW7_9ROSI) | NA | -0.661753617 | 0.048226811 | 11.91380233 | 7.548828 |
| Solyc03g097190.3 | WEB family protein, chloroplastic (AHRD V3.3 *** A0A2G2VB89_CAPBA) | NA | -0.661061376 | 0.041293034 | 11.89670867 | 7.666280667 |
| Solyc10g005100.3 | Plasma membrane-associated cation-binding protein 1 (AHRD V3.3 *** A0A2G2YJZ6_CAPAN) | NA | -0.65738182 | 0.004401501 | 406.999237 | 259.5102387 |
| Solyc10g079260.2 | Protein FATTY ACID EXPORT 1, chloroplastic (AHRD V3.3 *** A0A1U8E9B3_CAPAN) | NA | -0.657247331 | 0.000260377 | 38.26494233 | 24.48330633 |
| Solyc12g095800.2 | Chaperone protein dnaJ 10 (AHRD V3.3 *** A0A2G2YA74_CAPAN) | NA | -0.655453244 | 0.015118872 | 23.64014867 | 15.06998867 |
| Solyc03g111670.3 | Protein kinase (AHRD V3.3 *** D6N3G3_MALDO) | NA | -0.654921386 | 0.015230772 | 3.589811333 | 2.297501667 |
| Solyc09g018280.1 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G3DDH8_CAPCH) | NA | -0.653421105 | 0.00128014 | 141.7642543 | 90.746063 |
| Solyc01g102730.3 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** Q9ZVQ2_ARATH) | NA | -0.652986954 | 0.005272117 | 8.644545667 | 5.533247333 |
| Solyc03g098640.4 | Peroxisomal membrane MPV17/PMP22-like protein (AHRD V3.3 *-* A8J1X1_CHLRE) | PXMP2 | -0.652383741 | 0.021148005 | 7.551421 | 4.828272667 |
| Solyc05g054730.3 | Metal tolerance protein 11 (AHRD V3.3 *** A0A2G2WUE3_CAPBA) | NA | -0.650268854 | 0.006863104 | 21.94801967 | 14.130398 |
| Solyc05g005000.4 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* F4I5X3_ARATH) | NA | -0.649255851 | 0.00596873 | 9.521390333 | 6.142541 |

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| Solyc12g055740.2 | Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** A8MQN4_ARATH) | MPPE1 | -0.648622393 | 0.036835823 | 6.431204 | 4.158905 |
| Solyc10g079970.2 | Transmembrane protein 19 (AHRD V3.3 *** A0A1J3EWI5_NOCCA) | NA | -0.648069175 | 0.01376519 | 18.44534633 | 11.80547067 |
| Solyc12g005220.2 | Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** F4JIR5_ARATH) | NA | -0.64761011 | 0.002345649 | 34.77975467 | 22.26173433 |
| Solyc04g009030.3 | Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** A0A0A8IBT8_NICBE) | GAPA | -0.647194753 | 0.038235294 | 19.07415 | 12.201257 |
| Solyc08g077050.3 | Ferredoxin (AHRD V3.3 *** A0A1U8GXA1_CAPAN) | PETF | -0.647194751 | 0.007658295 | 58.65334067 | 37.45901867 |
| Solyc09g065630.3 | Tify domain-containing protein/CCT_2 domain-containing protein (AHRD V3.3 *** A0A1Q3D4M6_CEPFO) | NA | -0.646806938 | 0.015847675 | 4.045963 | 2.605392333 |
| Solyc11g030720.2 | 2-alkenal reductase (NADP(+)-dependent) (AHRD V3.3 *** A0A2G2ZP98_CAPAN) | DBR | -0.645807416 | 0.012432412 | 6.485535333 | 4.181078333 |
| Solyc11g068460.2 | Calcium-binding EF-hand family protein (AHRD V3.3 *** A0A2U1NS17_ARTAN) | CML | -0.64540829 | 0.000512358 | 35.04916633 | 22.52405167 |
| Solyc10g083460.1 | Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *** V5PZR5_9CARY) | NA | -0.642917619 | 0.046945933 | 15.079848 | 9.748124 |
| Solyc02g067840.3 | altered inheritance of mitochondria protein 32-like (AHRD V3.3 *** A0A2I4HUQ2_9ROSI) | NA | -0.64208496 | 0.006411224 | 77.47712967 | 49.92352433 |
| Solyc08g065480.3 | Ferrochelatase (AHRD V3.3 *** A0A2G3BRU7_CAPCH) | HEMH | -0.641196138 | 0.005813518 | 30.60302167 | 19.749789 |
| Solyc09g018160.3 | PAP/OAS1 substrate-binding domain superfamily (AHRD V3.3 *** F4J4G2_ARATH) | NA | -0.641010454 | 0.003774647 | 7.564161 | 4.866373 |
| Solyc11g067080.3 | Serine/threonine-protein kinase D6PKL2 (AHRD V3.3 *** A0A2G2YHG1_CAPAN) | protein-serine/ threonine kinase | -0.639840459 | 0.012570722 | 10.53722333 | 6.839660667 |
| Solyc05g014470.3 | glyceraldehyde 3-phosphate dehydrogenase | GAPDH | -0.639373818 | 0.010278565 | 598.7705283 | 389.1118977 |
| Solyc09g075290.3 | 60S ribosomal protein L18 (AHRD V3.3 *** B6SJC8_MAIZE) | RP-L18E | -0.638688917 | 0.001489758 | 140.9727327 | 91.12236533 |
| Solyc05g008930.3 | Protein kinase family protein (AHRD V3.3 *** A0A1P8BDK9_ARATH) | NA | -0.637996979 | 0.017295832 | 3.849914 | 2.493251 |
| Solyc12g099440.3 | Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a (AHRD V3.3 *** A0A2G2VJQ0_CAPBA) | MFP2 | -0.635736218 | 0.003327134 | 184.0901693 | 119.0234577 |
| Solyc09g014400.3 | Phosphoglucan, water dikinase, chloroplastic (AHRD V3.3 *-* A0A1J3J5B0_NOCCA) | NA | -0.63432781 | 0.03180639 | 5.397935333 | 3.492397 |
| Solyc09g059040.3 | Oxidoreductase, zinc-binding dehydrogenase family protein (AHRD V3.3 *** A0A2U1PT68_ARTAN) | CEQORH | -0.633423928 | 0.001784985 | 203.0286407 | 131.5340783 |
| Solyc06g084310.4 | Small nuclear ribonucleoprotein Sm D1 (AHRD V3.3 *** A0A2U1M5R8_ARTAN) | SNRPD1 | -0.633219486 | 0.022997863 | 34.41105567 | 22.41824467 |
| Solyc02g087150.3 | Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G14910.2) | NA | -0.630902517 | 0.005592901 | 26.778743 | 17.32502133 |
| Solyc12g009250.3 | 10 kDa chaperonin (AHRD V3.3 *** A0A1U8HGQ0_CAPAN) | GROES | -0.630452285 | 0.037984095 | 133.885343 | 87.13855233 |
| Solyc12g087890.3 | transcription factor bHLH143-like (AHRD V3.3 *** A0A2I4FQB9_9ROSI) | NA | -0.630352509 | 0.023931034 | 7.417847 | 4.826938333 |
| Solyc01g028810.3 | Beta chaperonin 60 (AHRD V3.3 *** Q0W9E2_SOLCO) | GROEL | -0.630321432 | 0.01317715 | 687.7634077 | 445.8011067 |
| Solyc08g006150.3 | Gamma-glutamylcyclotransferase (AHRD V3.3 *** A0A2G2W469_CAPBA) | GGCT | -0.628907914 | 0.023122483 | 10.62110233 | 6.867807333 |
| Solyc07g008530.1 | Tyrosine--tRNA ligase (AHRD V3.3 *** A0A1U8H9E5_CAPAN) | YARS | -0.628412535 | 0.008347771 | 14.709598 | 9.555367667 |
| Solyc10g006010.3 | Two pore potassium channel a (AHRD V3.3 *** A0A2G2VRA3_CAPBA) | KCNKF | -0.62834602 | 0.022387412 | 5.782469667 | 3.785295 |

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| Solyc08g078390.4 | peroxisomal acyl-CoA oxidase 1A | ACOX1 | -0.627556607 | 0.008342266 | 37.621156 | 24.64790333 |
| Solyc07g007310.3 | Methyltransferase-like (AHRD V3.3 *** Q67W64_ORYSJ) | NA | -0.62642004 | 0.00532113 | 19.12327567 | 12.45342767 |
| Solyc06g048730.3 | Uroporphyrinogen decarboxylase (AHRD V3.3 *** A0A2G3CAB7_CAPCH) | HEME | -0.62423663 | 0.005346485 | 38.78373967 | 25.29268967 |
| Solyc09g011620.2 | Glutathione S-transferase-like protein (AHRD V3.3 *** A8DUB0_SOLLC) | GST | -0.623856707 | 0.034318663 | 7.689213 | 5.011262 |
| Solyc11g010480.2 | Protein CURVATURE THYLAKOID 1A, chloroplastic (AHRD V3.3 *** A0A2G3B0C6_CAPCH) | NA | -0.621054224 | 0.013534904 | 30.507611 | 19.86027467 |
| Solyc08g066850.3 | Lactoylglutathione lyase (AHRD V3.3 *** A0A1U8DS55_CAPAN) | GLO1 | -0.620255075 | 0.029408529 | 2.205290333 | 1.438813667 |
| Solyc09g082710.3 | Histone H2A (AHRD V3.3 *** A0A1U8G3K0_CAPAN) | H2A | -0.619747124 | 0.004698232 | 57.320614 | 37.375805 |
| Solyc08g060940.1 | Nucleotide-sugar transporter family protein (AHRD V3.3 *** A0A2U1NGQ1_ARTAN) | NA | -0.617479894 | 0.003460961 | 42.71321767 | 28.11978567 |
| Solyc01g104020.2 | Embryo-specific protein (AHRD V3.3 *** A0A2K3LK15_TRIPR) | NA | -0.616988302 | 0.040212469 | 22.59867933 | 14.948409 |
| Solyc09g009390.3 | Monodehydroascorbate reductase (AHRD V3.3 *** A0A2G2VWV8_CAPBA) | monodehydroascorbate reductase (NADH) | -0.616930727 | 0.002784737 | 227.1594493 | 148.8858743 |
| Solyc02g091000.4 | Late embryogenesis abundant protein (AHRD V3.3 *** A0A200QZD5_9MAGN) | NA | -0.616694389 | 0.03093489 | 18.18992367 | 12.02907233 |
| Solyc12g098890.2 | 50S ribosomal protein L18 (AHRD V3.3 *** A0A1U8F639_CAPAN) | RP-L18 | -0.615513236 | 0.017189896 | 25.465168 | 16.66816233 |
| Solyc08g080910.3 | Glutathione S-transferase (AHRD V3.3 *** A0A200QUC6_9MAGN) | GST | -0.615402783 | 0.006107522 | 11.35471767 | 7.447978333 |
| Solyc11g006370.2 | Calcium-dependent protein kinase (AHRD V3.3 *** A0A060N6D3_SOLTU) | CPK | -0.615390014 | 0.009039768 | 50.11996467 | 32.75090133 |
| Solyc01g006450.4 | Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic (AHRD V3.3 *** A0A2G3DE80_CAPCH) | FABI | -0.615049004 | 0.008145446 | 48.05198167 | 31.480496 |
| Solyc06g075810.3 | NADH-ubiquinone oxidoreductase subunit (AHRD V3.3 *** A0A166XFE7_9PEZI) | NDUFA2 | -0.615026048 | 0.000590611 | 186.0418803 | 122.3862507 |
| Solyc03g080050.3 | Stomatin family protein (SPFH domain/Band 7 family protein) (AHRD V3.3 *** A0A166USA6_9PEZI) | NA | -0.614416434 | 0.001839049 | 28.40677967 | 18.67781133 |
| Solyc01g067010.3 | F-box protein (AHRD V3.3 *** A0A2K3P6V3_TRIPR) | NA | -0.614034525 | 0.039185034 | 22.97158067 | 15.12690733 |
| Solyc09g082970.3 | Pyruvate kinase (AHRD V3.3 *** A0A2G2W137_CAPBA) | PK | -0.612284362 | 0.011663708 | 82.14754467 | 53.921617 |
| Solyc11g012070.3 | Phospholipase/carboxylesterase/thioesterase (AHRD V3.3 *** A0A200RBD1_9MAGN) | NA | -0.610758978 | 0.046386075 | 11.806975 | 7.824363333 |
| Solyc11g045330.2 | GPI-anchored protein (AHRD V3.3 *** Q8RWE3_ARATH) | NA | -0.610710422 | 0.019196307 | 9.676891333 | 6.337915333 |
| Solyc09g090430.3 | Cyanate hydratase (AHRD V3.3 *** A0A1U8G4F5_CAPAN) | CYNS | -0.610254258 | 0.012396765 | 21.02315933 | 13.89361967 |
| Solyc02g068900.3 | Glutathione S-transferase (AHRD V3.3 *** A0A200QN08_9MAGN) | ECM4 | -0.610201308 | 0.000488164 | 33.64721267 | 22.22024733 |
| Solyc10g008740.3 | Mg-protoporphyrin IX chelatase (AHRD V3.3 *** A0A2G2YJA3_CAPAN) | CHLI | -0.609204698 | 0.010121386 | 24.92349 | 16.43924533 |
| Solyc04g078610.4 | Kinesin (AHRD V3.3 *** A0A200QZN6_9MAGN) | NA | -0.60617072 | 0.00076934 | 19.12643967 | 12.661172 |
| Solyc01g006630.3 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1KNW2_ARTAN) | NA | -0.605313289 | 0.023191695 | 6.390081 | 4.230104333 |
| Solyc02g014360.3 | Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A1U8FF53_CAPAN) | NA | -0.601646359 | 0.048848394 | 2.700512667 | 1.79282 |
| Solyc01g110550.3 | Ribosome-binding factor A (AHRD V3.3 *** A0A200QQX5_9MAGN) | RBFA | -0.599801707 | 0.034980257 | 8.788069333 | 5.859983667 |

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| Solyc06g068980.4 | MAP kinase kinase kinase 39 | NA | -0.598874674 | 0.049319935 | 5.698485 | 3.796029 |
| Solyc02g094220.2 | Transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** Q9SMN3_ARATH) | NA | -0.5987371 | 0.012349342 | 122.838435 | 81.58956433 |
| Solyc12g094430.1 | Glutathione S-transferase (AHRD V3.3 *** A0A200QZS2_9MAGN) | GST | -0.598616775 | 0.037386768 | 60.01804333 | 39.75059667 |
| Solyc01g102820.4 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (AHRD V3.3 *** A9ZN09_HEVBR) | ISPD | -0.595457737 | 0.007221857 | 14.73196633 | 9.797284667 |
| Solyc04g076870.4 | Glutamyl-tRNA reductase (AHRD V3.3 *** A6Q0F0_TOBAC) | HEMA | -0.595132519 | 0.010790284 | 34.289515 | 22.73773267 |
| Solyc03g113780.3 | NAD(P)H-hydrate epimerase (AHRD V3.3 *** A0A2G2VFG5_CAPBA) | PPOX | -0.59354396 | 0.001210504 | 17.64985 | 11.78949933 |
| Solyc10g081820.3 | Expp1 protein (AHRD V3.3 *** Q8VZ18_ARATH) | NA | -0.592151813 | 0.008665522 | 29.61550267 | 19.89011633 |
| Solyc06g066440.3 | hexokinase 2 | HK | -0.591985285 | 0.042387711 | 5.776594333 | 3.871760667 |
| Solyc03g117580.3 | GAG1At protein (AHRD V3.3 *** AT1G16000.1) | NA | -0.589961479 | 0.009476613 | 47.24062367 | 31.707921 |
| Solyc02g077460.3 | Octanoyltransferase (AHRD V3.3 *** A0A2G3AER8_CAPAN) | LIPT2 | -0.589812272 | 0.047621232 | 16.31594133 | 10.90726967 |
| Solyc12g010040.2 | leucine aminopeptidase A | CARP | -0.588801864 | 0.004453731 | 198.6525013 | 132.9584223 |
| Solyc08g077880.3 | Chlorophyll A-B binding protein (AHRD V3.3 *** A0A200RAS0_9MAGN) | NA | -0.588205335 | 0.008957338 | 45.912403 | 30.66113967 |
| Solyc08g015960.3 | Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 (AHRD V3.3 *** A0A2G3BRQ1_CAPCH) | NA | -0.587440171 | 0.003840872 | 22.02180733 | 14.781125 |
| Solyc04g007640.3 | RING-type E3 ubiquitin transferase (AHRD V3.3 *** A0A2G2WRT2_CAPBA) | NA | -0.586670346 | 0.008681813 | 12.184296 | 8.192043 |
| Solyc06g069390.4 | D-aminoacyl-tRNA deacylase (AHRD V3.3 *** A0A2G2WLT1_CAPBA) | DTDA | -0.586054502 | 0.0253919 | 7.180529 | 4.820385 |
| Solyc02g087620.3 | Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (AHRD V3.3 *** A0A2G3ACA5_CAPAN) | PPIP5K | -0.585498214 | 0.002384504 | 14.721607 | 9.873520667 |
| Solyc01g108130.4 | B3 domain-containing protein (AHRD V3.3 *-* A0A2G2W9Y8_CAPBA) | NA | -0.583497812 | 0.006997034 | 14.03954367 | 9.449832333 |
| Solyc05g051030.3 | Protein cornichon-like protein 4 (AHRD V3.3 *** A0A2G2WSR4_CAPBA) | CNIH | -0.580757678 | 0.041020264 | 29.66566133 | 19.98567633 |
| Solyc01g098650.2 | GDSL esterase/lipase (AHRD V3.3 *** A0A2G3BUB9_CAPCH) | NA | -0.580197231 | 0.025890961 | 31.50173267 | 21.267711 |
| Solyc12g006180.2 | RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** F4JFN7_ARATH) | MSI | -0.579144768 | 0.001256904 | 25.67331367 | 17.338459 |
| Solyc04g076380.4 | NADPH--cytochrome P450 reductase (AHRD V3.3 *** A0A2G3CP38_CAPCH) | POR | -0.578809845 | 0.007952421 | 47.04450467 | 31.68862533 |
| Solyc08g079240.4 | dimethylallyl%2C adenosine tRNA methylthiotransferase (AHRD V3.3 *** AT1G62780.1) | NA | -0.57781851 | 0.028077228 | 13.633501 | 9.161978667 |
| Solyc03g033620.3 | Serine carboxypeptidase S28 family protein (AHRD V3.3 *** A0A2U1LKS7_ARTAN) | NA | -0.576787672 | 0.0027852 | 21.156776 | 14.32042167 |
| Solyc03g062940.3 | peroxisomal targeting signal type 2 receptor | PEX7 | -0.575727824 | 0.027330092 | 98.306722 | 66.103832 |
| Solyc06g066030.4 | Protein WVD2-like 1 (AHRD V3.3 *** A0A2G3C7U3_CAPCH) | NA | -0.574279218 | 0.027121521 | 11.02415433 | 7.474892 |
| Solyc06g035970.3 | Tubulin beta chain (AHRD V3.3 *** A0A2G3C5Z8_CAPCH) | TUBB | -0.573432772 | 0.013657175 | 148.5707703 | 100.8472243 |
| Solyc01g006900.3 | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein (AHRD V3.3 *** A0A2U1NF61_ARTAN) | NA | -0.573258921 | 0.010110665 | 136.2518973 | 92.634702 |
| Solyc09g089670.3 | HR-like lesion-inducing protein-related (AHRD V3.3 *** B6SJ11_MAIZE) | NA | -0.572353137 | 0.044576643 | 15.400393 | 10.50236067 |

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|---|---|---|---|---|---|---|
| Solyc01g105160.4 | Copper-transporting ATPase PAA1, chloroplastic (AHRD V3.3 *** A0A2G2X1Z0_CAPBA) | COPA | -0.569874427 | 0.021617161 | 17.67946333 | 11.98045533 |
| Solyc04g054400.3 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1NLW3_ARTAN) | NA | -0.569528741 | 0.004833688 | 19.15284667 | 12.980839 |
| Solyc06g066310.3 | Phosphomevalonate kinase (AHRD V3.3 *** A0A2L0V4K1_9APIA) | MVAK2 | -0.568402175 | 0.015626433 | 8.028812 | 5.455393333 |
| Solyc04g076810.4 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G3CPB2_CAPCH) | NA | -0.566822687 | 0.001529297 | 22.42353433 | 15.258084 |
| Solyc02g068090.3 | 30S ribosomal protein S21 (AHRD V3.3 *** A0A2G2XI83_CAPBA) | NA | -0.561576032 | 0.014016282 | 63.627471 | 43.26249433 |
| Solyc02g091520.3 | Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** A0A2U1LMA8_ARTAN) | NA | -0.561212651 | 0.019627302 | 30.88417667 | 20.99575233 |
| Solyc12g096190.2 | Tryptophan synthase beta chain (AHRD V3.3 *** Q9FFW8_ARATH) | TRPB | -0.559335574 | 0.005618768 | 61.56963733 | 42.014257 |
| Solyc12g015780.2 | DNA-directed RNA polymerase (AHRD V3.3 *** A0A200Q9V0_9MAGN) | RPC40 | -0.557268919 | 0.036235301 | 16.75571767 | 11.540386 |
| Solyc03g116170.3 | Nucleosome assembly protein family (AHRD V3.3 *** A9RDK1_PHYPA) | SET | -0.557026913 | 0.043767113 | 24.52091033 | 16.873222 |
| Solyc06g051810.4 | XH/XS domain protein (AHRD V3.3 *** A0A2K3NHW6_TRIPR) | NA | -0.556656373 | 0.049792876 | 58.384201 | 39.69766767 |
| Solyc09g018730.4 | Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** A0A1U8E1K2_CAPAN) | UCHL5 | -0.555063725 | 0.002424892 | 36.596624 | 25.07162733 |
| Solyc01g105560.3 | GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase | RIBBA | -0.553626613 | 0.027425156 | 119.9827347 | 82.65524267 |
| Solyc06g064810.3 | zinc finger/BTB domain protein (AHRD V3.3 *** AT1G33810.1) | NA | -0.551508225 | 0.040409992 | 27.11971867 | 18.61391067 |
| Solyc03g112910.3 | Pantothenate kinase 2 (AHRD V3.3 *** A0A0K9S3P1_SPIOL) | PANK4 | -0.546963103 | 0.001784985 | 24.31839433 | 16.75842467 |
| Solyc04g082700.3 | Tonoplast monosaccharide transporter 2 | NA | -0.546077642 | 0.02080307 | 20.14664 | 13.91462833 |
| Solyc03g058860.3 | 3-dehydroquinate synthase (AHRD V3.3 *** A0A200QS88_9MAGN) | NA | -0.545938502 | 0.005953131 | 24.168368 | 16.66936867 |
| Solyc09g009940.3 | Signal recognition particle protein (AHRD V3.3 *** A0A1U8EGH6_CAPAN) | SRP54 | -0.54520018 | 0.002843594 | 41.159307 | 28.346212 |
| Solyc03g112770.3 | Glutaredoxin (AHRD V3.3 *** I2FJT7_SOLTU) | GRXC | -0.544540081 | 0.019729335 | 26.03202433 | 17.995201 |
| Solyc07g007970.3 | Keratin-associated protein, putative (DUF819) (AHRD V3.3 *** Q9LTG3_ARATH) | NA | -0.544192819 | 0.0219403 | 10.30531667 | 7.088373 |
| Solyc08g077780.3 | Protein kinase (AHRD V3.3 *** O65765_CRAPL) | SNRK2 | -0.543530901 | 0.009995341 | 31.93866167 | 22.141674 |
| Solyc12g098680.3 | Unknown protein | NA | -0.542715808 | 0.042901678 | 76.71152233 | 52.91439833 |
| Solyc02g065380.3 | Cold-regulated plasma membrane protein 2 (AHRD V3.3 *** A0A1U8FJM9_CAPAN) | NA | -0.539421709 | 0.0026429 | 55.499873 | 38.46358 |
| Solyc07g066430.3 | Ribosome-binding ATPase YchF (AHRD V3.3 *** A0A1J3HW77_NOCCA) | OLA1 | -0.538098742 | 0.006563225 | 18.89670633 | 13.13781967 |
| Solyc07g042180.4 | oligouridylate-binding protein 1-like (AHRD V3.3 *** A0A2I4E5R0_9ROSI) | TIA1 | -0.536690018 | 0.032153104 | 66.344663 | 45.86504233 |
| Solyc11g007020.2 | mevalonate disphosphate decarboxylase | MVD | -0.534389639 | 0.03831489 | 16.530007 | 11.53757 |
| Solyc02g078920.4 | Endonuclease 3 (AHRD V3.3 *** A0A2G3D5Y1_CAPCH) | NUCS | -0.53331738 | 0.032362297 | 15.20287933 | 10.609138 |
| Solyc12g042950.2 | ADP,ATP carrier protein (AHRD V3.3 *** A0A2G2Y8J4_CAPAN) | TC.AAA | -0.532575335 | 0.022014762 | 48.16605633 | 33.574323 |
| Solyc08g048550.3 | Protease Do-like 5, chloroplastic (AHRD V3.3 *** A0A1U8DTN0_CAPAN) | NA | -0.531761796 | 0.012056567 | 17.11009 | 11.900807 |

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|---|---|---|---|---|---|---|
| Solyc01g009990.3 | Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A2G3DGA1_CAPCH) | PPIB | -0.53112216 | 0.017956366 | 127.2393773 | 88.433558 |
| Solyc02g082340.3 | RNA polymerase I-specific transcription initiation factor RRN3 (AHRD V3.3 *** A0A2I4H2G7_9ROSI) | RRN3 | -0.530008228 | 0.048842035 | 52.006677 | 36.18536267 |
| Solyc01g100360.4 | Dihydrolipoyl dehydrogenase (AHRD V3.3 *** A0A2U1LTA9_ARTAN) | DLD | -0.52931476 | 0.015172181 | 59.25911333 | 41.45519633 |
| Solyc12g098830.2 | 5-nucleotidase (AHRD V3.3 *** B6SV15_MAIZE) | NA | -0.528833117 | 0.004285037 | 34.397564 | 24.029674 |
| Solyc12g099810.2 | CRT (Chloroquine-resistance transporter)-like transporter (AHRD V3.3 *** A0A1Y1I3N1_KLENI) | NA | -0.52675998 | 0.039388113 | 26.24947533 | 18.22347 |
| Solyc02g021000.3 | protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB3, chloroplastic (AHRD V3.3 *** A0A2I4G7H0_9ROSI) | NA | -0.523011701 | 0.048842035 | 12.92886667 | 9.062945 |
| Solyc06g053920.4 | hypothetical protein (AHRD V3.3 *** AT3G55760.3) | NA | -0.522790291 | 0.034709852 | 7.697681333 | 5.398186 |
| Solyc08g069030.4 | aminolevulinic acid dehydratase | HEMB | -0.52211356 | 0.029518799 | 105.0874607 | 73.355161 |
| Solyc08g081570.3 | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (AHRD V3.3 *** A0A2G3DAU7_CAPCH) | ISPF | -0.521233699 | 0.007131945 | 33.241435 | 23.33875167 |
| Solyc02g086730.3 | Ribosomal protein L7/L12 (AHRD V3.3 *** A0A200R2P7_9MAGN) | RP-L7 | -0.518155895 | 0.022296577 | 90.774803 | 63.55068333 |
| Solyc01g108280.3 | Protein kinase (AHRD V3.3 *** O65765_CRAPL) | SNRK2 | -0.516046146 | 0.00486623 | 26.36657633 | 18.573249 |
| Solyc02g065680.3 | Amino acid transporter (AHRD V3.3 *** A0A200QY84_9MAGN) | SLC38A2 | -0.512708343 | 0.01314529 | 16.21264467 | 11.469539 |
| Solyc12g100160.3 | 50S ribosomal protein L6 (AHRD V3.3 *** A0A2G2YBF1_CAPAN) | RP-L6 | -0.511035512 | 0.035391204 | 31.88739267 | 22.46705867 |
| Solyc04g082640.3 | inner membrane localized protein (AHRD V3.3 *-* AT1G42960.1) | NA | -0.508339707 | 0.005215596 | 60.240447 | 42.668082 |
| Solyc10g006030.3 | 30S ribosomal protein S10, chloroplastic (AHRD V3.3 *** A0A2G2VQX8_CAPBA) | RP-S10 | -0.507832825 | 0.044380363 | 30.282838 | 21.35547267 |
| Solyc07g063010.3 | 3-hydroxybutyryl-CoA dehydrogenase (AHRD V3.3 *** A0A2G2WF04_CAPBA) | PAAH | -0.505350603 | 0.036392411 | 40.440299 | 28.68537367 |
| Solyc04g082310.3 | hypothetical protein (AHRD V3.3 *** AT1G63610.1) | NA | -0.504314805 | 0.019543094 | 19.290335 | 13.72182233 |
| Solyc08g078250.4 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* A0A2U1MCE4_ARTAN) | PPT | -0.502812812 | 0.043906642 | 32.49094833 | 23.14349167 |
| Solyc11g020060.2 | D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** A0A1J3DFK2_NOCCA) | NA | -0.499178953 | 0.047234873 | 24.53195833 | 17.384669 |
| Solyc08g006000.3 | keratin-associated protein (DUF1218) (AHRD V3.3 *** AT4G31130.1) | NA | -0.499005698 | 0.006648119 | 75.08853667 | 53.423616 |
| Solyc04g009200.3 | glutamate 1-semialdehyde 2,1-aminomutase | HEML | -0.494878413 | 0.005884548 | 43.44769033 | 31.023353 |
| Solyc09g020130.3 | 60S ribosomal protein L5-like (AHRD V3.3 *** A0A2I4G950_9ROSI) | RP-L5E | -0.493813522 | 0.018560427 | 100.0621823 | 71.58525367 |
| Solyc11g040110.2 | Cobalt ion binding (AHRD V3.3 *** B6SJF4_MAIZE) | NA | -0.493006609 | 0.009563973 | 55.68924333 | 39.80939733 |
| Solyc06g074430.4 | 60S acidic ribosomal protein P2 (AHRD V3.3 *** A0A2G2ZDK5_CAPAN),Pfam:PF00428 | RP-LP2 | -0.491524476 | 0.023713975 | 241.8219097 | 173.6729173 |
| Solyc06g065390.4 | 50S ribosomal protein L21, chloroplastic (AHRD V3.3 *** A0A1U8GUE9_CAPAN) | RP-L21 | -0.489887292 | 0.043659963 | 52.441045 | 37.47681833 |
| Solyc06g069860.4 | 60S ribosomal protein L34 (AHRD V3.3 *** A0A1U8HB42_CAPAN) | RP-L34E | -0.487278362 | 0.048678786 | 135.6209103 | 97.83440667 |
| Solyc01g098610.4 | glutathione synthetase 2 | GSS | -0.4852617 | 0.031803643 | 9.361351333 | 6.735975 |
| Solyc10g080320.3 | Adenylosuccinate synthetase (AHRD V3.3 *** S8CIB7_9LAMI) | PURA | -0.482155768 | 0.020531288 | 42.896225 | 30.939059 |

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|---|---|---|---|---|---|---|
| Solyc08g081200.3 | Short-chain dehydrogenase TIC 32, chloroplastic (AHRD V3.3 *** A0A2G2XJP0_CAPBA) | NA | -0.481143015 | 0.045631551 | 18.61843467 | 13.48050667 |
| Solyc04g078850.4 | defective chloroplasts and leaves | NA | -0.48071262 | 0.031462832 | 18.422861 | 13.28316833 |
| Solyc01g073740.4 | Citrate synthase (AHRD V3.3 *** A0A2G3ALM4_CAPAN) | CS | -0.475549876 | 0.011799381 | 36.18839 | 26.23530633 |
| Solyc08g074750.2 | Zinc finger, C2H2 (AHRD V3.3 *** A0A2U1KGD1_ARTAN) | NA | -0.474710157 | 0.01966516 | 153.9208223 | 111.4438833 |
| Solyc06g072580.3 | Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** A0A2G3CA95_CAPCH) | PDHB | -0.471995644 | 0.034562572 | 19.74747833 | 14.37001267 |
| Solyc05g008600.3 | ripening regulated protein (DDTFR6/A) | ALDO | -0.47078649 | 0.042032606 | 232.3731897 | 169.0826057 |
| Solyc03g118020.3 | Nuclease domain-containing protein 1-like (AHRD V3.3 *** A0A2K3NZ95_TRIPR) | SND1 | -0.468860899 | 0.048767567 | 57.45250467 | 41.88227833 |
| Solyc09g090110.3 | Actin-depolymerizing factor (AHRD V3.3 *** A0A1U8GD07_CAPAN) | CFL | -0.468268972 | 0.042803982 | 21.588922 | 15.75654667 |
| Solyc12g055830.2 | Soluble inorganic pyrophosphatase (AHRD V3.3 *** A0A2G2VH82_CAPBA) | PPA | -0.464659138 | 0.049078022 | 84.08532233 | 61.68176533 |
| Solyc05g015710.3 | transmembrane protein (AHRD V3.3 *** AT1G27290.2) | NA | -0.460123827 | 0.025154195 | 37.97647333 | 27.72891533 |
| Solyc11g012470.2 | RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* F4JFN7_ARATH) | MSI | -0.458214926 | 0.026423887 | 24.45407867 | 17.97527933 |
| Solyc11g011250.3 | dehydroascorbate reductase 2 | DHAR | -0.455671472 | 0.045514318 | 48.815324 | 35.677732 |
| Solyc01g049960.4 | chromosome-associated kinesin (AHRD V3.3 *** AT4G26410.1) | NA | -0.453477913 | 0.015940415 | 52.627201 | 38.726677 |
| Solyc08g079820.3 | Nudix hydrolase 14, chloroplastic (AHRD V3.3 *** A0A2G3AE90_CAPAN) | NUDX14 | -0.452759482 | 0.019011702 | 24.63467333 | 18.134324 |
| Solyc03g118170.3 | Glycine--tRNA ligase (AHRD V3.3 *** A0A2G3A2W4_CAPAN) | GARS | -0.450911909 | 0.016832326 | 34.93320467 | 25.771597 |
| Solyc05g055440.1 | Histone H2B (AHRD V3.3 *** A0A1U8HBK7_CAPAN) | H2B | -0.449812939 | 0.049959906 | 251.659841 | 184.926778 |
| Solyc10g008560.3 | Protein root UVB sensitive 6 (AHRD V3.3 *** A0A2G2VRX7_CAPBA) | NA | -0.447917462 | 0.015555487 | 28.411046 | 20.95959667 |
| Solyc04g014270.3 | ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** A0A2G2XA03_CAPBA) | PFKA | -0.440332537 | 0.039154637 | 11.82929633 | 8.758776 |
| Solyc03g111850.3 | Indole-3-glycerol phosphate synthase (AHRD V3.3 *** A0A2G3CCR7_CAPCH) | TRPC | -0.437658301 | 0.020189177 | 35.29620133 | 26.22218567 |
| Solyc12g056740.2 | RNA helicase DEAD39 | NA | -0.437514905 | 0.049959906 | 30.00114533 | 22.25177267 |
| Solyc06g068880.3 | Carboxypeptidase (AHRD V3.3 *** A0A2G2ZBY4_CAPAN) | SCPL-II | -0.436621788 | 0.037232193 | 19.82506733 | 14.730172 |
| Solyc01g106320.2 | Phox/Bem1p (AHRD V3.3 *** A0A200QI01_9MAGN) | NA | -0.436538866 | 0.044019621 | 78.77842967 | 58.719097 |
| Solyc08g014470.4 | Amidohydrolase family (AHRD V3.3 *** A0A2U1PLT8_ARTAN) | NA | -0.435500922 | 0.031389121 | 26.453498 | 19.700868 |
| Solyc02g068640.3 | Pyrroline-5-carboxylate reductase (AHRD V3.3 *** A0A328DV79_9ASTE) | PROC | -0.434366504 | 0.019264864 | 37.21037167 | 27.73718433 |
| Solyc04g049180.3 | rhomboid-like protein 19 (AHRD V3.3 *** A0A2I4FB13_9ROSI) | NA | -0.428198321 | 0.047434411 | 33.41753267 | 25.088233 |
| Solyc04g014250.3 | GLABRA2 expression modulator (AHRD V3.3 *** A0A2G3CDH1_CAPCH) | NA | -0.413815715 | 0.043069064 | 44.81287367 | 33.80702467 |
| Solyc02g091580.4 | Oligopeptidase A (AHRD V3.3 *** A0A2U1NZK4_ARTAN) | PRLC | -0.412130432 | 0.045290917 | 45.59224067 | 34.52526533 |
| Solyc01g079820.3 | Peroxiredoxin (AHRD V3.3 *** H6VUU5_9FABA) | NA | -0.410427985 | 0.03711183 | 53.09180433 | 40.24201933 |
| Solyc05g007970.4 | Phytanoyl-CoA dioxygenase (AHRD V3.3 *** A0A2G2VK26_CAPBA) | PHYH | -0.408712932 | 0.042032606 | 31.59498233 | 23.942871 |

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| Solyc01g098380.4 | 4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic-like (AHRD V3.3 *** A0A1U8FAN3_CAPAN) | DAPB | -0.403224915 | 0.048577533 | 30.40946133 | 23.13556933 |
| Solyc05g052140.3 | ATP synthase subunit delta', mitochondrial (AHRD V3.3 *** A0A2G2WIK8_CAPBA) | ATPEF1D | -0.40101313 | 0.04232182 | 125.4406817 | 95.80148067 |
| Solyc07g017750.4 | Adagio-like protein 1 (AHRD V3.3 *** A0A1U8H9V5_CAPAN) | ZTL | 0.403349344 | 0.044740892 | 22.37710833 | 29.747782 |
| Solyc03g031790.1 | Oligosaccharyltransferase complex/magnesium transporter family protein (AHRD V3.3 *** AT1G61790.2) | OST3 | 0.405714057 | 0.047610933 | 40.37490333 | 54.00876133 |
| Solyc03g095290.3 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A1I9LRX3_ARATH) | NA | 0.407604339 | 0.049216117 | 8.085395667 | 10.79323667 |
| Solyc07g056370.3 | peroxisomal and mitochondrial division factor 2-like (AHRD V3.3 *-* A0A2I4EX70_9ROSI) | NA | 0.417581647 | 0.037271694 | 23.500575 | 31.61054267 |
| Solyc04g014810.3 | RING-type E3 ubiquitin transferase (AHRD V3.3 *-* A0A2I0XD88_9ASPA) | NA | 0.421352803 | 0.041651776 | 20.31364333 | 27.45138233 |
| Solyc01g104080.4 | Senescence associated gene 18 (AHRD V3.3 *** F4I8F7_ARATH) | NA | 0.425201627 | 0.026114533 | 26.65540367 | 36.01751067 |
| Solyc09g063030.4 | CLIP-associated protein (AHRD V3.3 *** A0A2G2WGM7_CAPBA) | CLASP1_2 | 0.427042175 | 0.029853293 | 11.760076 | 15.93339533 |
| Solyc06g071490.3 | serine/threonine-protein kinase ATM (AHRD V3.3 *-* A0A2I4DQU2_9ROSI) | NA | 0.43499117 | 0.029916683 | 13.244949 | 18.07044 |
| Solyc12g037980.2 | actin-related protein 4-like (AHRD V3.3 *** A0A2I4G8E9_9ROSI) | ACTL6A | 0.435005602 | 0.025934238 | 26.280246 | 35.79703667 |
| Solyc01g110520.3 | Amidophosphoribosyltransferase (AHRD V3.3 *** A0A2G3BW41_CAPCH) | PURF | 0.438876988 | 0.028554814 | 28.75640733 | 39.36493833 |
| Solyc03g006000.3 | Heat shock transcription factor (AHRD V3.3 *** Q9M597_MEDSA) | HSFF | 0.440606184 | 0.028003255 | 13.97575 | 19.075787 |
| Solyc01g105780.4 | DnaJ domain-containing protein (AHRD V3.3 *-* A0A2U1PVJ7_ARTAN) | NA | 0.445189098 | 0.04079826 | 7.358216 | 10.06472067 |
| Solyc03g120730.3 | Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** A0A2U1KY14_ARTAN) | NA | 0.45045368 | 0.017600058 | 25.25212833 | 34.70181633 |
| Solyc04g082620.3 | Serine/threonine-protein kinase/endoribonuclease IRE1a (AHRD V3.3 *** A0A1U8GAT1_CAPAN) | ERN1 | 0.450699524 | 0.039861037 | 4.589886 | 6.308375667 |
| Solyc01g073960.4 | Protein EMSY-LIKE 3 (AHRD V3.3 *** A0A2G3DHH9_CAPCH) | NA | 0.451163077 | 0.039388113 | 14.99701933 | 20.638637 |
| Solyc08g076100.4 | GBF9G-box binding | GBF | 0.452414416 | 0.030184784 | 11.32919733 | 15.56735433 |
| Solyc04g078490.1 | F-box protein (AHRD V3.3 *** A0A2G2XGV7_CAPBA) | NA | 0.45581794 | 0.020234488 | 15.494971 | 21.40490433 |
| Solyc01g006990.4 | F-box family protein (AHRD V3.3 *** E5GBH4_CUCME) | FBXO7 | 0.457273011 | 0.030659064 | 11.665141 | 16.11241467 |
| Solyc06g007120.3 | PI-phospholipase C4 | PLCD | 0.458687676 | 0.034029416 | 8.834157333 | 12.192708 |
| Solyc02g092780.3 | Suppressor of RPS4-RLD 1 (AHRD V3.3 *** A0A2G3D548_CAPCH) | NA | 0.459839098 | 0.012744871 | 16.59188133 | 22.99062333 |
| Solyc05g013730.3 | O-fucosyltransferase (AHRD V3.3 *** A0A2P5FMT7_TREOI) | NA | 0.460789382 | 0.042032606 | 6.331672 | 8.793258667 |
| Solyc09g064430.4 | Tyrosine decarboxylase 1 (AHRD V3.3 *** A0A2G2YS53_CAPAN) | DDC | 0.461316384 | 0.040668739 | 6.024156 | 8.362283667 |
| Solyc03g007610.4 | DnaJ protein ERDJ2A (AHRD V3.3 *** A0A2G3CWQ2_CAPCH) | SEC63 | 0.461347541 | 0.042523259 | 10.79706867 | 14.95984933 |
| Solyc01g044270.3 | DnaJ domain (AHRD V3.3 *** A0A200QGM0_9MAGN) | NA | 0.46184331 | 0.042165937 | 5.388715 | 7.495428333 |
| Solyc08g077510.4 | Poly(U)-specific endoribonuclease-B-like protein (AHRD V3.3 *** A0A2K3PLY2_TRIPR) | ENDOU | 0.463247565 | 0.04420628 | 23.64030833 | 32.90585133 |
| Solyc08g080520.4 | DUF810 domain-containing protein (AHRD V3.3 *** A0A1Q3BM37_CEPFO),Pfam:PF05664 | NA | 0.466827294 | 0.038719086 | 5.797297667 | 8.032380333 |

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|---|---|---|---|---|---|---|
| Solyc04g049120.4 | Nuclear receptor corepressor 1 (AHRD V3.3 *-* A0A1J3EKK6_NOCCA) | NA | 0.467563463 | 0.022597665 | 10.49416833 | 14.62621733 |
| Solyc09g090420.4 | U2 snRNP auxiliary factor large subunit (AHRD V3.3 *-* A0A1I7S9N1_BURXY) | U2AF2 | 0.468549555 | 0.033678355 | 5.384412667 | 7.501220333 |
| Solyc03g063220.2 | RNA helicase DEAH-box8 | NA | 0.47447128 | 0.048804161 | 3.321163 | 4.633560333 |
| Solyc11g033284.1 | Peptidylprolyl isomerase (AHRD V3.3 *** A0A2G3CEL0_CAPCH) | NA | 0.474631747 | 0.042142179 | 26.26823633 | 36.643312 |
| Solyc05g053835.2 | Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** A0A2U1Q1B2_ARTAN) | OGT | 0.475664184 | 0.044019621 | 42.54595567 | 59.65219233 |
| Solyc07g062970.3 | protein phosphatase 2C | PPM1L | 0.476336259 | 0.031634577 | 116.2390823 | 163.2405853 |
| Solyc10g076870.2 | RNA binding protein (AHRD V3.3 *-* A0A2K3MUE2_TRIPR) | NA | 0.476520719 | 0.023367598 | 14.224145 | 19.970342 |
| Solyc08g076930.1 | jasmonic acid 3 | MYC2 | 0.478453673 | 0.034051113 | 107.664098 | 150.9200643 |
| Solyc03g123520.3 | Phosphoinositide phosphatase SAC2 (AHRD V3.3 *** A0A2G3D1F1_CAPCH) | FIG4 | 0.482158234 | 0.046999442 | 8.483282 | 11.96841533 |
| Solyc09g091100.4 | 7-hydroxymethyl chlorophyll a reductase, chloroplastic (AHRD V3.3 *** A0A2G2VZY5_CAPBA) | HCAR | 0.483445515 | 0.033201798 | 6.459123 | 9.098214 |
| Solyc03g121400.1 | Dof zinc finger protein14 | NA | 0.485292528 | 0.013315074 | 42.376897 | 59.81782133 |
| Solyc11g013530.3 | PHD finger family protein (AHRD V3.3 *** A0A1P8APU9_ARATH) | NA | 0.485713014 | 0.02516313 | 8.274555667 | 11.62537633 |
| Solyc01g058670.3 | Transcription factor (AHRD V3.3 *** A0A2G3DG53_CAPCH) | NA | 0.485851854 | 0.012874409 | 34.72700033 | 48.96598167 |
| Solyc10g085300.2 | hypothetical protein (Protein of unknown function%2C DUF538) (AHRD V3.3 *** AT3G08890.2) | NA | 0.487489307 | 0.017586326 | 26.14500933 | 37.038525 |
| Solyc01g103780.4 | TCP transcription factor 11 | NA | 0.490461309 | 0.009963535 | 35.04038867 | 49.542333 |
| Solyc07g007370.3 | Ubiquitin-associated (UBA)/TS-N domain-containing protein (AHRD V3.3 *** A0A2U1MD44_ARTAN) | NA | 0.490465446 | 0.010581642 | 11.89019867 | 16.820363 |
| Solyc01g096110.3 | Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** A0A2U1M7G0_ARTAN) | DMXL | 0.490739335 | 0.04783959 | 5.977719667 | 8.411059667 |
| Solyc01g080660.3 | serine/arginine-rich SC35-like splicing factor SCL28 (AHRD V3.3 *-* A0A2I4G9K3_9ROSI) | SRSF10 | 0.491986943 | 0.04173084 | 4.859462 | 6.883349667 |
| Solyc11g067260.3 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A2U1LHG4_ARTAN) | NA | 0.492021391 | 0.021368715 | 34.40479233 | 48.55064933 |
| Solyc12g042070.3 | Auxin Response Factor 2B | NA | 0.492539389 | 0.019936483 | 7.989496667 | 11.289137 |
| Solyc01g005440.4 | Jasmonate ZIM-domain protein 2 (AHRD V3.3 *** B3Y562_TOBAC) | JAZ | 0.494615198 | 0.034603197 | 20.42205633 | 29.131908 |
| Solyc06g069310.3 | Nuclear factor Y, subunit B13 (AHRD V3.3 *** F4KBG0_ARATH) | DR1 | 0.495069099 | 0.043083914 | 23.35147967 | 33.20806167 |
| Solyc09g042750.3 | Acyl-coenzyme A thioesterase 9, mitochondrial (AHRD V3.3 *** A0A1J3CD94_NOCCA) | ACOT9 | 0.495535201 | 0.00808376 | 26.14320967 | 37.183141 |
| Solyc06g062850.3 | PHD finger protein ALFIN-LIKE 5 (AHRD V3.3 *** A0A2G3C8F0_CAPCH) | NA | 0.49652448 | 0.036080969 | 10.23645467 | 14.51088633 |
| Solyc03g098210.4 | Cyclic nucleotide gated channel (AHRD V3.3 *** A0A1Y1HP60_KLENI) | CNGC | 0.496675705 | 0.040668739 | 12.08023933 | 17.21680267 |
| Solyc02g069940.4 | WPP domain associated protein | NA | 0.499372614 | 0.018706002 | 6.731129333 | 9.556042667 |
| Solyc08g006940.4 | F-box protein SKIP19-like (AHRD V3.3 *** A0A2I4GUY1_9ROSI) | NA | 0.500092759 | 0.019842414 | 14.13496367 | 20.11867167 |
| Solyc03g044430.3 | Nicotinate phosphoribosyltransferase (AHRD V3.3 *** A0A1U8GGJ3_CAPAN) | PNCB | 0.502052148 | 0.022031957 | 6.818395 | 9.735673333 |

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|---|---|---|---|---|---|---|
| Solyc11g072470.3 | LOB domain-containing protein (AHRD V3.3 *** A0A2K3PP50_TRIPR) | NA | 0.502111205 | 0.030330822 | 94.81548833 | 135.0028433 |
| Solyc08g077430.3 | ephrin type-B receptor (AHRD V3.3 *** AT5G11700.2) | NA | 0.503184868 | 0.024246987 | 9.467050667 | 13.54691233 |
| Solyc07g022910.3 | Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *** A0A2G2VC40_CAPBA) | NA | 0.503930867 | 0.015860026 | 34.59865033 | 49.38166667 |
| Solyc01g104660.3 | Plant/F1M20-13 protein (AHRD V3.3 *** A0A072UZK1_MEDTR) | NA | 0.504047967 | 0.042523259 | 25.75911533 | 36.60661567 |
| Solyc02g087730.3 | F-box domain, cyclin-like protein (AHRD V3.3 *** A0A2U1KDV5_ARTAN) | NA | 0.506897187 | 0.029008617 | 11.17347133 | 16.000041 |
| Solyc12g056590.2 | Ethylene Response Factor D.2 | NA | 0.50786346 | 0.026021953 | 13.91351733 | 19.91634867 |
| Solyc05g009740.1 | Disease resistance protein (AHRD V3.3 *** A0A2U1Q201_ARTAN) | NA | 0.508021788 | 0.042523259 | 5.912619 | 8.467573333 |
| Solyc01g102760.3 | PHD finger protein ALFIN-LIKE 8 (AHRD V3.3 *** A0A1U8DXM3_CAPAN) | NA | 0.508159739 | 0.029397914 | 18.76510433 | 26.80267767 |
| Solyc09g007190.3 | Thioredoxin-like protein AAED1, chloroplastic (AHRD V3.3 *** A0A1U8E5E4_CAPAN) | NA | 0.509800326 | 0.040668739 | 12.81796733 | 18.30503433 |
| Solyc01g107170.2 | Zinc finger protein (AHRD V3.3 *** A0T3Q5_SOLTU) | NA | 0.509801503 | 0.043279666 | 263.8487347 | 379.1173603 |
| Solyc06g065720.1 | Cytochrome, and DOMON domain-containing protein (AHRD V3.3 *** A0A2G2WKK0_CAPBA) | NA | 0.509821688 | 0.012283807 | 14.22598867 | 20.44129833 |
| Solyc09g011840.1 | Lectin_legB domain-containing protein (AHRD V3.3 *** A0A1Q3BCE3_CEPFO) | NA | 0.509941682 | 0.008031163 | 49.16680933 | 70.513598 |
| Solyc01g065580.4 | Pumilio-like protein 24 (AHRD V3.3 *** A0A2G2XR42_CAPBA) | PUF6 | 0.511763966 | 0.030088014 | 8.040091333 | 11.55392367 |
| Solyc03g007260.3 | Cyclic nucleotide-gated ion channel 1 (AHRD V3.3 *** A0A2G2X7E9_CAPBA) | CNGC | 0.514032213 | 0.038949346 | 10.34578033 | 14.84132 |
| Solyc04g082760.3 | SWI/SNF complex subunit SWI3B (AHRD V3.3 *** A0A2G3CFP4_CAPCH) | SMARCC | 0.514251229 | 0.017625108 | 11.102127 | 15.944908 |
| Solyc01g005930.3 | Lipase/lipooxygenase%2C PLAT/LH2 family protein (AHRD V3.3 *** AT1G55280.2) | NA | 0.515131064 | 0.047538649 | 9.133874 | 13.133233 |
| Solyc02g062370.4 | Zinc finger CCCH domain-containing protein 19 (AHRD V3.3 *** A0A2G2XGC4_CAPBA) | NA | 0.515239804 | 0.04295361 | 9.009791667 | 12.982901 |
| Solyc11g011130.3 | THO complex subunit 4D (AHRD V3.3 *-* A0A2G2Y4P8_CAPAN) | THOC4 | 0.517705507 | 0.03469439 | 110.5712637 | 158.8338117 |
| Solyc09g055310.3 | Ethylene-overproduction protein 1 (AHRD V3.3 *** A0A2G3BLY9_CAPCH) | NA | 0.518207608 | 0.00613011 | 11.593613 | 16.70187067 |
| Solyc07g017510.3 | 1-phosphatidylinositol-3-phosphate 5-kinase FAB1B (AHRD V3.3 *** A0A2G2WC08_CAPBA) | PIKFYVE | 0.521112083 | 0.045256767 | 46.07022733 | 66.26483 |
| Solyc04g082210.3 | NADH-ubiquinone oxidoreductase chain (AHRD V3.3 *** AT1G76185.1) | NA | 0.522515885 | 0.008892463 | 12.62758267 | 18.241973 |
| Solyc03g094090.3 | Polyadenylate-binding protein (AHRD V3.3 *-* G5DWR4_SILLA) | NA | 0.523300394 | 0.008408648 | 69.381148 | 100.1564687 |
| Solyc06g060940.2 | GATA transcription factor 26 (AHRD V3.3 *** A0A2G3DC77_CAPCH) | NA | 0.525790621 | 0.026331481 | 5.314330333 | 7.696781667 |
| Solyc12g009640.1 | zinc finger BED domain-containing protein DAYSLEEPER-like (AHRD V3.3 *** A0A2I4F531_9ROSI) | NA | 0.526373432 | 0.008483934 | 10.27578433 | 14.84817333 |
| Solyc11g007120.2 | NifU-like protein (AHRD V3.3 *** A0A2K3MYY9_TRIPR) | NFU1 | 0.526875498 | 0.021368715 | 22.950744 | 33.37048333 |
| Solyc01g079690.4 | Snf2 chromatin remodeling protein (AHRD V3.3 *-* A0A1T3CE02_9HYPO) | NA | 0.527166678 | 0.015795593 | 3.813486667 | 5.529731 |
| Solyc08g007470.2 | HAT transposon superfamily (AHRD V3.3 *** A0A2U1Q846_ARTAN) | NA | 0.527942735 | 0.045157518 | 3.654458667 | 5.301774 |
| Solyc01g086810.2 | disease resistance protein RPM1-like (AHRD V3.3 *** A0A2I4DV93_9ROSI) | RPM1 | 0.529144162 | 0.015614573 | 3.320938 | 4.833087333 |

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|---|---|---|---|---|---|---|
| Solyc01g073985.1 | Disease resistance protein (AHRD V3.3 *** A0A200RBM1_9MAGN) | RPM1 | 0.530733572 | 0.043475057 | 2.469785333 | 3.591152667 |
| Solyc09g098310.3 | Unknown protein | NA | 0.532763283 | 0.027256278 | 198.2418773 | 290.1862993 |
| Solyc05g013580.4 | Beta-1,4-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A2U1NH94_ARTAN) | MGAT3 | 0.535807688 | 0.00853828 | 23.71910033 | 34.73337367 |
| Solyc01g096160.4 | L-fucokinase/GDP-L-fucose pyrophosphorylase (AHRD V3.3 *** A0A2U1NSI7_ARTAN) | FKGP | 0.542083979 | 0.03067525 | 3.723429667 | 5.441534667 |
| Solyc06g008340.4 | Adaptin ear-binding coat-associated protein (AHRD V3.3 *** A0A2K3NQR5_TRIPR) | NECAP1_2 | 0.543474684 | 0.006200288 | 20.36484067 | 29.84406667 |
| Solyc04g072640.3 | Membrane-anchored ubiquitin-fold protein (AHRD V3.3 *** A0A1U8GDC5_CAPAN) | NA | 0.545120544 | 0.013459953 | 12.857639 | 18.948909 |
| Solyc04g015970.3 | ABC transporter A family member 1 (AHRD V3.3 *** A0A2G3CCY6_CAPCH) | ABCA3 | 0.546768238 | 0.030782533 | 5.180479667 | 7.590520333 |
| Solyc01g086740.3 | Chaperone protein dnaJ (AHRD V3.3 *** B6TA99_MAIZE) | DNAJ | 0.546933967 | 0.042534211 | 23.488118 | 34.53922633 |
| Solyc11g008320.3 | Lysine-specific histone demethylase 1-like protein 3 (AHRD V3.3 *** A0A1U8F4Y3_CAPAN) | NA | 0.549346334 | 0.009473089 | 4.909732667 | 7.233749667 |
| Solyc07g041210.3 | Phospholipid:diacylglycerol acyltransferase (AHRD V3.3 *** A0A2U1KQW5_ARTAN) | phospholipid:diacylglycerol acyltransferase | 0.552182886 | 0.038130377 | 5.566485667 | 8.203172 |
| Solyc07g056260.4 | Callose synthase 3 (AHRD V3.3 *** A0A1U8HKF3_CAPAN) | CALS | 0.552871958 | 0.01976389 | 5.834014 | 8.671176333 |
| Solyc05g013970.4 | RNA recognition motif domain (AHRD V3.3 *-* A0A200R4F7_9MAGN) | CPSF6_7 | 0.553811519 | 0.028727033 | 5.927156333 | 8.731549 |
| Solyc08g008490.4 | Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A2U1PGZ8_ARTAN) | NA | 0.554131533 | 0.008640036 | 10.62468233 | 15.708657 |
| Solyc05g012400.4 | Chromatin modification-related protein Eaf7/MRGBP (AHRD V3.3 *** A0A2U1PNN2_ARTAN) | NA | 0.558612481 | 0.011395167 | 14.396625 | 21.31185267 |
| Solyc12g014280.2 | RNA-binding CRS1 / YhbY (CRM) domain protein (AHRD V3.3 *** A0A2U1NZ44_ARTAN) | NA | 0.561039042 | 0.041369954 | 3.614067667 | 5.376016333 |
| Solyc12g010400.2 | hypothetical protein (AHRD V3.3 *-* AT2G46490.1) | NA | 0.561170432 | 0.016083135 | 86.35288767 | 128.0136083 |
| Solyc02g082130.2 | Surfeit locus protein 6 (AHRD V3.3 *** A0A2U1QM59_ARTAN) | NA | 0.562601158 | 0.001637529 | 32.65261433 | 48.66383867 |
| Solyc01g091350.4 | ATP-dependent DNA helicase 2 subunit KU80 (AHRD V3.3 *** A0A2G3AH96_CAPAN) | XRCC5 | 0.562619676 | 0.035771346 | 4.302373 | 6.355716333 |
| Solyc07g032480.3 | cyclinT1_2 | CCNT | 0.564318169 | 0.020761012 | 9.632242 | 14.27118667 |
| Solyc06g051210.3 | Bromodomain-containing protein (AHRD V3.3 *-* A0A2U1N3G4_ARTAN) | BRD9 | 0.56447477 | 0.020934734 | 3.353857 | 5.01121 |
| Solyc09g074660.3 | spermatogenesis-associated protein 20 (AHRD V3.3 *** A0A2I4GIU1_9ROSI) | NA | 0.565454055 | 0.026123411 | 24.64326 | 36.545241 |
| Solyc10g006130.1 | EAR motif SlERF36 | EREBP | 0.566809211 | 0.010655939 | 273.8510337 | 409.8983253 |
| Solyc01g008850.3 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G2XP60_CAPBA) | NA | 0.569669042 | 0.043731106 | 110.786326 | 166.4463097 |
| Solyc11g007780.2 | SEC12-like protein 1 (AHRD V3.3 *** A0A2I4HBY6_9ROSI) | PREB | 0.570875849 | 0.006200288 | 24.65890633 | 36.936389 |
| Solyc04g076850.3 | entire | IAA | 0.57128376 | 0.007984224 | 136.0977683 | 203.6535593 |
| Solyc10g084650.3 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 *** F4IQY0_ARATH) | NA | 0.572007722 | 0.003819676 | 10.65483933 | 15.90945267 |
| Solyc02g083290.4 | Protein kinase domain (AHRD V3.3 *** A0A200QZU4_9MAGN) | NA | 0.57274259 | 0.002304184 | 10.69970433 | 16.02724767 |
| Solyc07g064940.3 | Thioredoxin-like protein, chloroplastic (AHRD V3.3 *** A0A2G2WFU8_CAPBA) | NA | 0.57396221 | 0.008145446 | 10.52026467 | 15.75215767 |

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| Solyc03g112560.4 | Pentatricopeptide repeat-containing protein, mitochondrial (AHRD V3.3 *** A0A2G3A1G4_CAPAN) | NA | 0.574428873 | 0.034379429 | 2.537351667 | 3.802712333 |
| Solyc08g083020.2 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A2U1LUP2_ARTAN) | ATAD1 | 0.575058638 | 0.011685379 | 7.385302333 | 11.08720967 |
| Solyc03g119440.3 | C2 domain-containing protein (AHRD V3.3 *** A0A1Q3BN33_CEPFO) | NA | 0.575076605 | 0.018579713 | 6.362807667 | 9.530742667 |
| Solyc11g045180.3 | DEAD-box ATP-dependent RNA helicase 50 (AHRD V3.3 *-* A0A1U8EMF9_CAPAN) | DDX18 | 0.582149542 | 0.049703615 | 8.794643333 | 13.190556 |
| Solyc11g005660.2 | Serine/threonine-protein kinase (AHRD V3.3 *** A0A0K0XQY4_TOBAC) | NA | 0.58281254 | 0.02302912 | 11.26456767 | 17.010219 |
| Solyc07g150147.1 | Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10 (AHRD V3.3 *** A0A2G3C166_CAPCH) | NA | 0.583588919 | 0.008075198 | 23.263457 | 35.12994367 |
| Solyc09g059520.3 | Heat stress transcription factor A-8 (AHRD V3.3 *** A0A2G3BLA4_CAPCH) | HSFF | 0.583998954 | 0.025928462 | 8.810760667 | 13.34459933 |
| Solyc03g005030.3 | hypothetical protein (AHRD V3.3 *-* AT3G01860.1) | NA | 0.584164158 | 0.017754815 | 16.24303867 | 24.550396 |
| Solyc11g005900.2 | Guanylate kinase-like (AHRD V3.3 *** A0A200PUL8_9MAGN) | GMK | 0.586856116 | 0.027349402 | 6.481477333 | 9.752596 |
| Solyc09g008520.4 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 *** Q8RWG0_ARATH) | NA | 0.587734257 | 0.022407902 | 3.647115667 | 5.525491333 |
| Solyc01g066430.3 | RING-H2 finger protein ATL2-like (AHRD V3.3 *** A0A2I4E8K9_9ROSI) | NA | 0.588206396 | 0.012115773 | 210.97112 | 320.693339 |
| Solyc04g051310.4 | transmembrane protein (AHRD V3.3 *** AT5G16520.1) | NA | 0.588571426 | 0.047026927 | 9.371525 | 14.22184333 |
| Solyc12g006370.3 | Polyamine oxidase-like protein (AHRD V3.3 *** A0A2K3NN16_TRIPR) | PAO4 | 0.590057791 | 0.03640456 | 28.00114467 | 42.59069433 |
| Solyc12g087960.2 | hypothetical protein (AHRD V3.3 *-* AT4G38060.4) | NA | 0.590572552 | 0.003612627 | 27.51338133 | 41.873442 |
| Solyc03g118820.4 | Ras-related protein RABA6a (AHRD V3.3 *** A0A1U8FCD3_CAPAN) | NA | 0.591663976 | 0.006428642 | 33.21277067 | 50.40150333 |
| Solyc09g090200.4 | Serine/threonine-protein kinase (AHRD V3.3 *** A0A2I0WHR6_9ASPA) | STK38 | 0.592980453 | 0.011608969 | 31.26961833 | 47.71999467 |
| Solyc09g064920.3 | transcription factor UNE12-like (AHRD V3.3 *** A0A2I4DEZ5_9ROSI) | NA | 0.594638752 | 0.033757477 | 5.781960333 | 8.820308667 |
| Solyc06g050980.3 | Ferritin (AHRD V3.3 *** A0A2G2WIC5_CAPBA) | FTH1 | 0.597428506 | 0.012135413 | 129.1002047 | 196.7770337 |
| Solyc03g112900.3 | Iron-sulfur cluster assembly scaffold protein IscU (AHRD V3.3 *** A0A2G7TDU8_9FLAO) | ISCU | 0.597604283 | 0.007970778 | 98.385844 | 149.3065493 |
| Solyc03g121360.1 | Charged multivesicular body protein 1-like (AHRD V3.3 *** A0A2K3LIZ7_TRIPR) | CHMP1 | 0.59914687 | 0.033395394 | 222.2759147 | 341.194224 |
| Solyc03g117890.3 | ACT domain-containing protein (AHRD V3.3 *** A0A2U1QDU0_ARTAN) | NA | 0.599634521 | 0.029574911 | 49.16077167 | 74.49621833 |
| Solyc02g091330.4 | AAR2 protein family (AHRD V3.3 *** A0A2U1KD81_ARTAN) | AAR2 | 0.601599098 | 0.005206352 | 15.03119067 | 22.91143867 |
| Solyc09g042770.4 | Rhodanese-like domain-containing protein 4A, chloroplastic (AHRD V3.3 *** A0A2G2X1L1_CAPBA) | NA | 0.602961464 | 0.00928212 | 13.80147567 | 21.00825567 |
| Solyc02g088720.4 | RNA-binding family protein (AHRD V3.3 *-* A0A1Y1HPM2_KLENI) | NA | 0.60368404 | 0.004617229 | 12.58081467 | 19.23680633 |
| Solyc01g103540.3 | Evolutionarily conserved C-terminal region 2 (AHRD V3.3 *-* F4JDC2_ARATH) | YTHDF | 0.604628587 | 0.035613649 | 227.948303 | 347.497823 |
| Solyc09g064540.3 | Vacuolar protein sorting-associated protein 62 (AHRD V3.3 *** A0A200PVW2_9MAGN) | NA | 0.606316089 | 0.0111118 | 3.37278 | 5.155964667 |
| Solyc03g121650.3 | Duf724 domain-containing protein 7 (AHRD V3.3 *** A0A314KGX7_NICAT) | NA | 0.606364904 | 0.028136054 | 5.256507667 | 8.04328 |

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| Solyc11g010230.2 | Histone H3 (AHRD V3.3 *** A0A2K1J132_PHYPA) | H3 | 0.606759428 | 0.002715463 | 280.7921243 | 429.7855837 |
| Solyc08g006480.3 | flocculation protein (AHRD V3.3 *-* AT4G31430.3) | NA | 0.607271284 | 0.023055753 | 4.005557667 | 6.142178333 |
| Solyc09g091050.4 | C2 calcium-dependent membrane targeting (AHRD V3.3 *** A0A2U1PUT0_ARTAN) | NA | 0.608869825 | 0.027571356 | 30.419364 | 46.39243567 |
| Solyc06g072300.4 | Argonaute 1 | ELF2C | 0.609940699 | 0.003441854 | 14.25478 | 21.94610767 |
| Solyc02g067620.3 | Metal tolerance protein 8 (AHRD V3.3 *-* A0A2G2Y0P2_CAPAN) | SLC30A5_7 | 0.612218868 | 0.012251303 | 5.111198 | 7.818526 |
| Solyc11g044250.3 | K(+) efflux antiporter 3, chloroplastic (AHRD V3.3 *** A0A1U8F6F8_CAPAN) | NA | 0.61818823 | 0.033937398 | 3.555101667 | 5.486312333 |
| Solyc01g100170.3 | Syntaxin (AHRD V3.3 *** A0A2G3AXP6_CAPCH) | STX16 | 0.618493588 | 0.022556235 | 11.86391533 | 18.36659067 |
| Solyc02g080110.3 | transmembrane protein (AHRD V3.3 *** AT4G21215.2) | NA | 0.618948163 | 0.002379415 | 27.412395 | 42.409191 |
| Solyc10g081360.2 | HSP20-like chaperones superfamily protein (AHRD V3.3 *** A0A2U1L7K6_ARTAN) | NA | 0.619828599 | 0.015118872 | 11.23699767 | 17.38598633 |
| Solyc09g042260.3 | Protein kinase domain (AHRD V3.3 *** A0A200R3J7_9MAGN) | NA | 0.622873099 | 0.017716345 | 5.994299667 | 9.302899667 |
| Solyc08g015630.3 | Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** A0A200PM73_9MAGN) | ITPK4 | 0.623012932 | 0.012306387 | 4.850049667 | 7.554014667 |
| Solyc09g008190.3 | Acylphosphatase (AHRD V3.3 *** A0A2G2YPW3_CAPAN) | ACYP | 0.623344458 | 0.005454959 | 15.52161567 | 24.016351 |
| Solyc11g065830.2 | Dicarboxylate transporter 1, chloroplastic (AHRD V3.3 *** A0A2G2VN77_CAPBA) | NA | 0.623469455 | 0.036479223 | 21.996022 | 34.20244467 |
| Solyc01g107510.3 | DNA repair protein REV1 (AHRD V3.3 *** A0A2G2Y2A0_CAPAN) | REV1 | 0.624803425 | 0.030860357 | 10.110983 | 15.725512 |
| Solyc10g085440.1 | Non-specific serine/threonine protein kinase (AHRD V3.3 *-* G4XMX4_SOLLC) | NA | 0.627257511 | 0.049118514 | 10.886078 | 16.94516233 |
| Solyc01g101090.3 | Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** A0A1I9LLP9_ARATH) | EVI5 | 0.627475626 | 0.029079362 | 17.36133133 | 27.08131667 |
| Solyc03g031750.2 | Vacuolar protein sorting-associated protein 28 homolog (AHRD V3.3 *** A0A2G3CKJ2_CAPCH) | VPS28 | 0.627832688 | 0.010774986 | 61.375281 | 95.78548933 |
| Solyc06g075400.3 | V-type proton ATPase subunit a (AHRD V3.3 *** A0A1U8H960_CAPAN) | ATPEV0A | 0.629012505 | 0.017741203 | 2.701913333 | 4.210864 |
| Solyc01g091750.3 | Arginine/serine-rich-splicing factor (AHRD V3.3 *-* G5DW02_SILLA) | SRSF4_5_6 | 0.629529353 | 0.001997293 | 10.00772533 | 15.56528933 |
| Solyc11g069500.2 | Auxin Response Factor 10A | NA | 0.629984674 | 0.018959876 | 5.01964 | 7.792244 |
| Solyc01g090410.3 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A2U1KLU2_ARTAN) | PPT | 0.632112893 | 0.036859571 | 3.159032 | 4.933982333 |
| Solyc08g061520.3 | Myosin (AHRD V3.3 *-* A0A2U1NL80_ARTAN) | MYO5 | 0.634005938 | 0.013117796 | 5.073941333 | 7.951681333 |
| Solyc07g047610.3 | Transcriptional adapter (AHRD V3.3 *** A0A1U8HAU7_CAPAN) | TADA2A | 0.636816684 | 0.048855017 | 5.215403 | 8.139717667 |
| Solyc05g014260.3 | Two-component response regulator (AHRD V3.3 *** A0A2G3B918_CAPCH) | ARR-B | 0.637481596 | 0.048359434 | 1.569300333 | 2.471628 |
| Solyc04g079300.3 | Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** F4JPS4_ARATH) | NA | 0.637963391 | 0.048844753 | 3.099301 | 4.816176333 |
| Solyc04g072230.4 | Protein kinase superfamily protein (AHRD V3.3 *** A0A2U1PVM4_ARTAN) | ADCK | 0.638095685 | 0.016083135 | 5.855487667 | 9.108884333 |
| Solyc02g062500.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1LXD5_ARTAN) | NA | 0.638609558 | 0.003601613 | 1380.482585 | 2166.108602 |
| Solyc06g008870.2 | Gibberellin receptor (AHRD V3.3 *** E3VJP7_9FABA) | GID1 | 0.641041057 | 0.000787553 | 42.67439667 | 66.99662367 |

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| Solyc03g097120.3 | Heat stress transcription factor A-1 (AHRD V3.3 *** A0A2G3ARP3_CAPCH) | HSFF | 0.641364731 | 0.031010235 | 22.34463167 | 34.94346267 |
| Solyc02g071860.4 | LRR_1 domain-containing protein/Pkinase_Tyr domain-containing protein/Malectin domain-containing protein (AHRD V3.3 *** A0A1Q3CJY9_CEPFO) | NA | 0.642660115 | 0.025648474 | 7.724932667 | 12.06242433 |
| Solyc09g092530.4 | Protein TIC 22-like, chloroplastic (AHRD V3.3 *** A0A1U8G491_CAPAN) | NA | 0.643300431 | 0.004646427 | 12.01447733 | 18.96986133 |
| Solyc12g007190.2 | Protein tesmin/TSO1-like CXC 5 (AHRD V3.3 *-* A0A2G3BNP4_CAPCH) | NA | 0.643808725 | 0.042662291 | 7.768831333 | 12.21985967 |
| Solyc04g081230.3 | TLD-domain containing nucleolar protein (AHRD V3.3 *** A0A2U1P606_ARTAN) | NA | 0.644072486 | 0.010130083 | 11.28004133 | 17.79257367 |
| Solyc02g083960.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1N614_ARTAN) | ALKBH5 | 0.645101119 | 0.019543094 | 4.940579 | 7.836516667 |
| Solyc04g005820.4 | DnaJ-like protein (AHRD V3.3 *** Q9SP09_TOBAC) | DNAJB4 | 0.645506703 | 0.00785656 | 5.789672667 | 9.143266333 |
| Solyc08g078190.2 | Ethylene-responsive transcription factor 5 (AHRD V3.3 *** A0A2G2XL45_CAPBA) | EREBP | 0.647022216 | 0.027798637 | 105.0866317 | 166.6840363 |
| Solyc07g045420.4 | Protein kinase superfamily protein (AHRD V3.3 *** A0A2U1MTH5_ARTAN) | NA | 0.647260983 | 0.030806318 | 7.929741667 | 12.58205633 |
| Solyc07g065700.4 | Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** A0A2U1NTZ9_ARTAN) | NA | 0.647607311 | 0.008026402 | 10.33918667 | 16.231117 |
| Solyc08g080200.4 | SPX domain-containing protein (AHRD V3.3 *** D7MDY2_ARALL) | NA | 0.648171844 | 0.016274724 | 12.31371367 | 19.35296433 |
| Solyc02g080520.4 | Actin cytoskeleton-regulatory complex pan-like protein (AHRD V3.3 *** Q9LPT5_ARATH) | NA | 0.649682768 | 0.018560427 | 4.510896 | 7.080481 |
| Solyc03g063600.4 | Guanylate kinase 1 (AHRD V3.3 *** A0A2G2X5F7_CAPBA) | GMK | 0.654751507 | 0.005104753 | 108.5659967 | 171.3878273 |
| Solyc03g112160.3 | Drought induced 19 protein-like (AHRD V3.3 *** A0A200RD12_9MAGN) | NA | 0.655365626 | 0.009963535 | 16.88846233 | 26.57369567 |
| Solyc03g114830.3 | FRUITFULL-like MADS-box 2 | K09264 | 0.656071689 | 0.001210679 | 47.469189 | 75.437828 |
| Solyc01g010290.4 | Ureide permease (AHRD V3.3 *** A0A2R6PBP7_ACTCH) | NA | 0.656170091 | 0.037794546 | 2.991804 | 4.728927 |
| Solyc10g085910.2 | Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* B6T8A4_MAIZE) | NA | 0.6569625 | 0.047065909 | 13.973243 | 22.055713 |
| Solyc11g010330.3 | RING/U-box superfamily protein (AHRD V3.3 *-* F4JJ02_ARATH) | NA | 0.657491412 | 0.005806732 | 68.57013333 | 109.167455 |
| Solyc04g082200.2 | dehydrin | NA | 0.658126069 | 0.011663708 | 1304.073852 | 2069.1663 |
| Solyc04g074190.3 | Protein phosphatase 2C family protein (AHRD V3.3 *** A0A2U1PV28_ARTAN) | PPM1L | 0.658364906 | 0.009002249 | 4.356366 | 6.895711333 |
| Solyc07g064550.3 | Polyadenylate-binding protein interacting protein (AHRD V3.3 *** Q93V36_ARATH) | NA | 0.659192826 | 0.005595544 | 3.125012333 | 4.980365 |
| Solyc08g076860.3 | PLATZ transcription factor family protein (AHRD V3.3 *** F4IEB6_ARATH) | NA | 0.659205135 | 0.005828192 | 45.21788033 | 71.91419733 |
| Solyc04g010110.3 | Glycosyltransferase (AHRD V3.3 *** V4NB36_EUTSA) | UGT79B1 | 0.660264377 | 0.001326944 | 9.174784333 | 14.59131633 |
| Solyc09g031600.2 | Sorting nexin 2A (AHRD V3.3 *** A0A2G3BLH8_CAPCH) | NA | 0.660623737 | 0.001457346 | 9.498023333 | 15.07557167 |
| Solyc06g082520.3 | B3 domain-containing protein (AHRD V3.3 *** A0A2K3NLM2_TRIPR) | NA | 0.661123613 | 0.040500265 | 2.490199667 | 3.977613667 |
| Solyc04g079420.3 | Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** A0A1P8BE24_ARATH) | NA | 0.663742213 | 0.010870294 | 12.35290767 | 19.845969 |
| Solyc09g064240.3 | PfkB-like carbohydrate kinase family protein (AHRD V3.3 *** A0A2U1QKJ7_ARTAN) | NA | 0.666275593 | 0.006175713 | 5.138627333 | 8.222272667 |
| Solyc05g052620.4 | Coronatine-insensitive 1 | COI-1 | 0.667162203 | 8.84892E-05 | 15.514138 | 24.796575 |

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| Solyc02g092870.2 | Nucleolar-like protein (AHRD V3.3 *** F4J3H8_ARATH) | NA | 0.667860776 | 0.006033302 | 2.783697 | 4.440142667 |
| Solyc03g006130.3 | Protein male discoverer 2 (AHRD V3.3 *** A0A1J6HZQ5_NICAT) | NA | 0.667926505 | 0.003664905 | 18.34833333 | 29.483549 |
| Solyc08g041860.1 | serine/arginine repetitive matrix-like protein (AHRD V3.3 *-* AT4G32020.1) | NA | 0.668476014 | 0.000669645 | 362.909027 | 581.815165 |
| Solyc07g042080.4 | Inter-alpha-trypsin inhibitor heavy chain-like protein (AHRD V3.3 *** Q8L798_ARATH) | NA | 0.670332851 | 0.000138825 | 8.734132 | 13.993247 |
| Solyc11g042470.1 | Tubulin-folding cofactor E (AHRD V3.3 *** A0A2G2W6C5_CAPBA) | TBCE | 0.670494123 | 0.019499432 | 3.50955 | 5.601098 |
| Solyc08g006460.3 | RING/U-box superfamily protein (AHRD V3.3 *** A0A1P8BF19_ARATH) | NA | 0.672929526 | 0.037386768 | 5.543570333 | 8.864491 |
| Solyc02g093150.3 | APETALA2c | AP2 | 0.67326461 | 0.040409992 | 1.907609333 | 3.052764333 |
| Solyc05g051680.4 | Structural maintenance of chromosomes protein 6 (AHRD V3.3 *** A0A2G2WTI5_CAPBA) | SMC6 | 0.674056242 | 0.030806318 | 4.113446 | 6.590082667 |
| Solyc06g065900.4 | Serine-rich protein (AHRD V3.3 *** Q8L8M8_ARATH) | NA | 0.675194578 | 0.017648456 | 17.92608 | 28.67496867 |
| Solyc01g007110.3 | LRAT-like domain (AHRD V3.3 *** A0A200Q9S3_9MAGN) | NA | 0.675686389 | 0.045256767 | 72.078588 | 117.261907 |
| Solyc11g072150.3 | Dr1-associated corepressor (AHRD V3.3 *** A0A2G3BAH8_CAPCH) | DRAP1 | 0.676205436 | 0.017648456 | 4.067427667 | 6.550528333 |
| Solyc04g007890.3 | Hmg-y-related protein a (AHRD V3.3 *-* A0A314LC60_NICAT) | NA | 0.677280472 | 0.000815979 | 121.2480597 | 195.8251143 |
| Solyc07g055290.3 | LES245570 Rab11 GTPase | RAB11A | 0.678705737 | 0.004352068 | 15.11062367 | 24.457372 |
| Solyc01g094860.4 | Transmembrane protein-related protein (AHRD V3.3 *** A0A2U1LWU9_ARTAN) | NA | 0.678953879 | 0.0161939 | 4.607477333 | 7.414113333 |
| Solyc06g066330.3 | Poly [ADP-ribose] polymerase (AHRD V3.3 *** A0A200PXE3_9MAGN) | NA | 0.679270004 | 0.027848765 | 14.83593267 | 24.02787267 |
| Solyc06g064460.4 | 60S ribosomal protein L7a (AHRD V3.3 *** A0A2G3DGL0_CAPCH) | RP-L7AE | 0.680154739 | 0.00066444 | 10.14544733 | 16.35500333 |
| Solyc08g005050.4 | transcription factor MYC2 (AHRD V3.3 *-* R4S7B4_NICAT) | MYC2 | 0.681786734 | 0.008048085 | 53.72001767 | 87.07197067 |
| Solyc03g116570.3 | Thiol-disulfide oxidoreductase DCC family protein (AHRD V3.3 *** A0A2U1Z9Z9_PSEAV) | NA | 0.682009782 | 0.006416238 | 20.85776267 | 33.482141 |
| Solyc11g072220.2 | Ubiquitin-like-specific protease 1D (AHRD V3.3 *-* A0A1J3EWQ3_NOCCA) | NA | 0.683672432 | 0.017882056 | 1.628667667 | 2.631390333 |
| Solyc10g078600.3 | Jacalin-related lectin 3 (AHRD V3.3 *** A0A2G2Y0W6_CAPAN) | NA | 0.684987706 | 0.047434411 | 9.661123 | 15.80428767 |
| Solyc10g081370.3 | Unknown protein | NA | 0.68849737 | 0.001999099 | 36.61111567 | 59.48794933 |
| Solyc11g011120.2 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A2U1NG96_ARTAN) | NA | 0.689268518 | 0.022118879 | 12.55822133 | 20.56747967 |
| Solyc08g006010.3 | WD-40 repeat containing protein (AHRD V3.3 *** A0A0K0XR07_TOBAC) | WDR45 | 0.692763738 | 0.03158044 | 1.814231333 | 2.963772667 |
| Solyc06g073850.1 | hypothetical protein (AHRD V3.3 *** AT2G27180.1) | NA | 0.694445551 | 0.039530623 | 53.75693033 | 88.44093933 |
| Solyc05g051620.3 | RNA polymerase III RPC4 (AHRD V3.3 *** A0A2U1QBZ9_ARTAN) | RPC4 | 0.694792021 | 0.033212421 | 3.876873667 | 6.290912333 |
| Solyc03g119060.3 | divaricata | DOX | 0.700586901 | 0.009039768 | 6.790400667 | 11.179154 |
| Solyc03g059490.1 | Leucine rich repeat receptor protein kinase 2 (AHRD V3.3 *** F8WS89_SOLLC) | NA | 0.700684687 | 0.000670128 | 14.75833133 | 24.23948867 |
| Solyc10g011980.3 | Erythronate-4-phosphate dehydrogenase family protein (AHRD V3.3 *** Q8VYC6_ARATH) | NA | 0.701509509 | 0.002613706 | 11.865352 | 19.56204267 |
| Solyc06g076250.4 | PGR5-like protein (AHRD V3.3 *** A0A2K3NGZ6_TRIPR) | NA | 0.702871198 | 0.002214248 | 7.480321 | 12.24679967 |

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| Solyc04g012160.4 | SNF1-related kinase | SNRK2 | 0.702910834 | 0.013888699 | 66.771624 | 108.2949753 |
| Solyc12g099200.2 | Invertase inhibitor (AHRD V3.3 *** O49908_TOBAC) | NA | 0.702948426 | 0.004410088 | 37.432404 | 61.17639167 |
| Solyc01g111130.4 | bHLH transcription factor 011 | NA | 0.702989495 | 0.021651332 | 2.781289 | 4.528564667 |
| Solyc02g072530.3 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G3A7N9_CAPAN) | NA | 0.7050161 | 0.005454959 | 4.419924333 | 7.256899333 |
| Solyc05g054560.3 | CASP-like protein (AHRD V3.3 *** A0A2G3CIG5_CAPCH) | NA | 0.705789187 | 0.028487624 | 19.67842733 | 32.06556833 |
| Solyc06g068330.1 | Serine-rich protein (AHRD V3.3 *-* Q8L8M8_ARATH) | NA | 0.709414942 | 0.025648474 | 6.371490667 | 10.460925 |
| Solyc03g111320.1 | Exocyst subunit Exo70 family protein (AHRD V3.3 *** A0A1S4CY62_TOBAC) | EXOC7 | 0.710133518 | 0.049078022 | 118.396754 | 196.9029487 |
| Solyc11g005380.2 | Trihelix transcription factor GTL1 (AHRD V3.3 *** A0A2G2VFX7_CAPBA) | NA | 0.710171052 | 0.033212421 | 76.076388 | 126.3116047 |
| Solyc10g085340.1 | Protein DETOXIFICATION (AHRD V3.3 *** A0A328E6G5_9ASTE) | NA | 0.711336953 | 0.048870058 | 1.184404 | 1.953159 |
| Solyc10g006750.4 | Unknown protein | NA | 0.71155543 | 0.039670048 | 7.197819333 | 11.92793533 |
| Solyc03g025940.3 | F-box/LRR-repeat protein (AHRD V3.3 *** A0A1U8G7I8_CAPAN) | NA | 0.712595027 | 0.01082244 | 3.882779667 | 6.403957 |
| Solyc07g064170.3 | pectin methylesterase 1 | pectinesterase | 0.713526787 | 0.034688446 | 644.2823893 | 1068.701782 |
| Solyc08g080500.3 | Rhomboid-like protein (AHRD V3.3 *** A0A1U8G8L0_CAPAN) | NA | 0.715083209 | 0.002029036 | 38.239423 | 63.69412833 |
| Solyc07g066060.3 | Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A2U1QLT6_ARTAN) | THOC3 | 0.715415234 | 0.01653334 | 11.87326633 | 19.54614833 |
| Solyc07g056050.1 | Transmembrane 9 superfamily member (AHRD V3.3 *** A0A2G2Z4P1_CAPAN) | TM9SF2_4 | 0.715681529 | 0.009530342 | 25.61296533 | 42.49882 |
| Solyc02g085600.1 | Scarecrow-like protein 15 (AHRD V3.3 *** A0A2G3AAH7_CAPAN) | NA | 0.716080773 | 0.018534163 | 23.32371133 | 38.81613867 |
| Solyc04g074580.1 | Histone H3 (AHRD V3.3 *** A0A2K1J132_PHYPA) | H3 | 0.716408423 | 0.017750036 | 220.7568767 | 365.4962463 |
| Solyc06g073920.3 | CRABS CLAW-like protein 2a | NA | 0.717608202 | 0.000415316 | 87.345975 | 144.022705 |
| Solyc11g011090.1 | Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** A0A2K3P9P3_TRIPR) | NA | 0.718372065 | 0.002097476 | 3.597226 | 5.938468333 |
| Solyc01g099045.1 | Unknown protein | NA | 0.723491733 | 0.020165481 | 25.76314033 | 42.40042867 |
| Solyc09g091690.1 | F-box protein (AHRD V3.3 *** A0A2K3P6V3_TRIPR) | NA | 0.724473458 | 0.01194481 | 4.603638333 | 7.623718333 |
| Solyc06g071100.4 | plasma membrane H+-ATPase | PMA1 | 0.724698991 | 0.000462107 | 38.41745367 | 63.778005 |
| Solyc01g088660.3 | FCS-Like Zinc finger 3 (AHRD V3.3 *** FLZ3_ARATH) | NA | 0.724772719 | 0.00167474 | 26.16384333 | 43.57548033 |
| Solyc01g007980.4 | Cysteine-rich receptor-like protein kinase 2 (AHRD V3.3 *** A0A2G2YVX5_CAPAN) | NA | 0.725828685 | 0.0115994 | 1.939349667 | 3.243282 |
| Solyc09g075970.3 | Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** F4I8Q8_ARATH) | NA | 0.726891249 | 0.010656369 | 5.795313667 | 9.613013667 |
| Solyc02g068530.4 | UDP-N-acetylglucosamine diphosphorylase 1 (AHRD V3.3 *** A0A1U8FKE1_CAPAN) | UAP1 | 0.727317235 | 0.000205224 | 7.766764 | 12.98548 |
| Solyc05g005720.4 | Potassium transporter (AHRD V3.3 *** A0A2G2VMI2_CAPBA) | KUP | 0.731365222 | 0.003236912 | 22.937491 | 38.21539933 |
| Solyc01g007990.4 | Cysteine-rich receptor-like protein kinase 2 (AHRD V3.3 *** A0A2G2XSC5_CAPBA) | NA | 0.731913215 | 0.021023664 | 4.672231333 | 7.86505 |
| Solyc03g118200.4 | Calcium-dependent phospholipid-binding Copine family protein (AHRD V3.3 *** | NA | 0.735817279 | 0.00199861 | 44.757327 | 75.10438767 |

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|---|---|---|---|---|---|---|
| | A0A2U1NDK1_ARTAN) | | | | | |
| Solyc05g054760.4 | dehydroascorbate reductase 1 | DHAR | 0.736962672 | 0.00187031 | 40.64416367 | 68.51450367 |
| Solyc09g018670.3 | TRAM%2C LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRD V3.3 *** AT4G10360.3) | NA | 0.741641298 | 0.000643131 | 7.301929667 | 12.34646767 |
| Solyc03g096380.3 | proline transporter 2 | NA | 0.742253679 | 0.019742851 | 7.057140667 | 11.91195033 |
| Solyc08g068010.2 | zinc finger FYVE domain protein (AHRD V3.3 *** AT2G25730.3) | ZFYVE26 | 0.742492404 | 0.000312396 | 3.719304333 | 6.250187 |
| Solyc08g076000.4 | Disease resistance protein RGA2 (AHRD V3.3 *** A0A2G2XMC9_CAPBA) | NA | 0.744195411 | 0.040527754 | 0.546150333 | 0.919647667 |
| Solyc02g092710.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1KVM6_ARTAN) | P4HA | 0.745113768 | 0.002465397 | 7.270950333 | 12.31767533 |
| Solyc03g095510.3 | Serine/threonine-protein kinase AtPK1/AtPK6 (AHRD V3.3 *** A0A2G2X4V7_CAPBA) | RPS6KB | 0.751433692 | 0.019936483 | 3.016912333 | 5.081621 |
| Solyc08g082610.4 | DCD (Development and Cell Death) domain protein (AHRD V3.3 *** A0A2U1P2J5_ARTAN) | NA | 0.751523384 | 0.021368715 | 174.1194353 | 297.4118297 |
| Solyc11g017000.2 | DUF668 domain-containing protein/DUF3475 domain-containing protein (AHRD V3.3 *** A0A1Q3CI27_CEPFO) | NA | 0.754002206 | 0.010655939 | 10.97114467 | 18.75192833 |
| Solyc01g110380.3 | Kinesin-like protein (AHRD V3.3 *** A0A2G2XNI5_CAPBA) | CENPE | 0.755753317 | 0.028352404 | 6.073973 | 10.28702933 |
| Solyc02g150141.1 | Cytochrome c oxidase subunit 5C (AHRD V3.3 *** A0A2G3ABW9_CAPAN) | NA | 0.758714271 | 0.009135155 | 12.153089 | 20.542668 |
| Solyc01g095320.4 | Bag family molecular chaperone regulator 6-like protein (AHRD V3.3 *** A0A2K3PRI9_TRIPR) | NA | 0.76008786 | 0.004946063 | 1175.32546 | 1989.187052 |
| Solyc01g094410.3 | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** A0A061G6B5_THECC) | NA | 0.760652705 | 0.035579642 | 68.28639467 | 117.22568 |
| Solyc03g115930.3 | Calcium-binding EF-hand family protein (AHRD V3.3 *-* A0A2U1NCV0_ARTAN) | NA | 0.762066826 | 0.003433157 | 49.97274033 | 85.839546 |
| Solyc10g011740.3 | Ubiquitin-conjugating enzyme (AHRD V3.3 *** H6VUS9_9FABA) | UBE2D | 0.762872101 | 0.024934723 | 107.1663793 | 184.2833507 |
| Solyc03g083290.4 | 40S ribosomal protein S12 (AHRD V3.3 *** A0A2G2W8S0_CAPBA) | RP-S12E | 0.765793237 | 0.02947277 | 5.029654 | 8.591818 |
| Solyc11g065120.3 | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHRD V3.3 *** F4K149_ARATH) | NA | 0.7682326 | 0.00109272 | 2.023047333 | 3.471369667 |
| Solyc01g099040.4 | GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO) | NA | 0.769143292 | 0.025840432 | 81.217944 | 137.8034693 |
| Solyc05g013510.4 | Phosphate transporter (AHRD V3.3 *** Q6J2Q8_SOLTU) | SLC20A | 0.769949458 | 0.037843605 | 17.25238867 | 29.6286 |
| Solyc10g085460.3 | NBS-LRR resistance protein (AHRD V3.3 *** A0A2K3NVA3_TRIPR) | NA | 0.770692788 | 0.024414474 | 2.438923 | 4.198164 |
| Solyc10g084760.3 | E3 ubiquitin-protein ligase ubr3-like protein (AHRD V3.3 *** A0A2K3NLG7_TRIPR) | NA | 0.770922527 | 0.002322303 | 16.41276333 | 27.98266733 |
| Solyc05g013440.3 | Amine oxidase (AHRD V3.3 *** A0A2G2VMP6_CAPBA) | AOC3 | 0.773369755 | 0.000112689 | 21.54696967 | 36.91783533 |
| Solyc07g063630.3 | Vesicle-associated protein 4-1 (AHRD V3.3 *** A0A2G2Z5C6_CAPAN) | NA | 0.776105738 | 0.004526221 | 33.893987 | 58.02766533 |
| Solyc02g021600.1 | F-box/kelch-repeat protein (AHRD V3.3 *** A0A2G2VW95_CAPBA) | NA | 0.781475898 | 0.005563916 | 3.599293 | 6.218466333 |
| Solyc03g007280.4 | DnaJ domain (AHRD V3.3 *-* A0A200R430_9MAGN) | NA | 0.781940298 | 0.007809773 | 3.533427667 | 6.118375667 |
| Solyc04g016550.4 | Folylpolyglutamate synthase (AHRD V3.3 *** A0A1U8GL32_CAPAN) | FPGS | 0.786113293 | 0.042523259 | 1.211242 | 2.114062667 |

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| Solyc09g011740.4 | Phosphatidylinositol:ceramide inositolphosphotransferase (AHRD V3.3 *** A0A1U8EEU4_CAPAN) | SAMD8 | 0.787553165 | 0.038666023 | 29.30799533 | 51.373872 |
| Solyc01g090950.4 | Transcription factor GRAS (AHRD V3.3 *-* A0A2U1PW81_ARTAN) | NA | 0.789997519 | 0.028725043 | 2.618739333 | 4.576552 |
| Solyc07g007390.3 | Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein (AHRD V3.3 *** A0A1R7T3E0_ARATH) | NA | 0.790655931 | 0.004074599 | 21.724169 | 37.6802 |
| Solyc04g080790.3 | BEL1-like homeodomain protein 7 (AHRD V3.3 *** A0A2G3AXA7_CAPCH) | NA | 0.791390996 | 0.011663708 | 0.967674 | 1.680325667 |
| Solyc02g067120.4 | hypothetical protein (DUF1997) (AHRD V3.3 *** AT5G39530.1) | NA | 0.791452645 | 0.003941652 | 13.32475667 | 23.10107167 |
| Solyc11g006410.2 | EEIG1/EHBP1 N-terminal domain (AHRD V3.3 *** A0A200Q9Q9_9MAGN) | NA | 0.791746679 | 0.002370388 | 3.998460333 | 6.962338 |
| Solyc08g081455.1 | Unknown protein | NA | 0.791880062 | 0.005979929 | 12.58526667 | 21.84562233 |
| Solyc09g055700.4 | protein FLX-like 1 (AHRD V3.3 *** A0A2I4GXJ8_9ROSI) | NA | 0.792163473 | 1.66863E-05 | 11.326459 | 19.767303 |
| Solyc08g079510.3 | IRK-interacting protein (AHRD V3.3 *** A0A2I4GUZ8_9ROSI) | NA | 0.793030382 | 0.021278617 | 6.129180667 | 10.769527 |
| Solyc11g009010.2 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* Q058J1_ARATH) | NA | 0.793774502 | 0.002724643 | 16.149887 | 28.03828067 |
| Solyc08g061480.3 | Chalcone-flavanone isomerase family protein (AHRD V3.3 *** A0A2U1NFT5_ARTAN) | NA | 0.793922712 | 0.005633814 | 9.548268333 | 16.61256567 |
| Solyc02g089320.3 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** F4J5H1_ARATH) | ABHD17 | 0.794113287 | 0.014857191 | 4.151260667 | 7.292032333 |
| Solyc06g059870.1 | Unknown protein | NA | 0.795134309 | 0.029499029 | 37.775437 | 66.724421 |
| Solyc02g091500.1 | Calcium-dependent protein kinase (AHRD V3.3 *-* CDPK_DAUCA) | CML | 0.798510597 | 0.009973013 | 147.892067 | 261.326787 |
| Solyc05g008380.4 | envelope glycoprotein B (AHRD V3.3 *** AT1G80540.3) | NA | 0.798585997 | 0.029101716 | 32.48990067 | 56.274719 |
| Solyc08g014290.1 | Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** A0A2U1MM52_ARTAN) | NA | 0.800549369 | 4.30217E-05 | 11.89276033 | 20.79876267 |
| Solyc04g064930.3 | Thioredoxin superfamily protein (AHRD V3.3 *** AT1G21350.3) | NA | 0.801383644 | 0.01016417 | 4.515178333 | 7.867209 |
| Solyc05g011960.4 | DnaJ domain-containing protein (AHRD V3.3 *-* A0A1Q3CHH1_CEPFO) | NA | 0.804546014 | 0.007755267 | 6.258313667 | 11.01583633 |
| Solyc10g081100.3 | 50S ribosomal protein 5, chloroplastic (AHRD V3.3 *** A0A2G2VVL1_CAPBA) | PSRP5 | 0.806599174 | 0.000744532 | 23.494804 | 41.14832033 |
| Solyc07g007690.4 | Chloride channel protein (AHRD V3.3 *** A0A328D084_9ASTE) | CLCN7 | 0.808284282 | 0.036392411 | 0.895172 | 1.572942 |
| Solyc08g068040.3 | zinc finger FYVE domain protein (AHRD V3.3 *-* AT2G25730.3) | ZFYVE26 | 0.808744675 | 0.014936193 | 2.759292 | 4.855928333 |
| Solyc12g006805.1 | SOUL heme-binding family protein (AHRD V3.3 *** Q8VZ90_ARATH) | NA | 0.813391042 | 0.011685379 | 2.684174333 | 4.719379667 |
| Solyc02g064640.4 | ADP-ribosylation factor-like protein 8A (AHRD V3.3 *** A0A2G3BN09_CAPCH) | ARL8 | 0.818307907 | 0.015085586 | 5.657382667 | 10.12654 |
| Solyc07g064020.4 | 21.7 kDa class VI heat shock protein (AHRD V3.3 *** A0A2G2WFJ0_CAPBA) | NA | 0.820816391 | 0.014933038 | 3.975738 | 7.076935667 |
| Solyc09g031680.3 | Mitochondrial uncoupling protein (AHRD V3.3 *** O24391_SOLTU) | UCP2_3 | 0.822660093 | 0.005563916 | 5.956122333 | 10.56086267 |
| Solyc03g123710.3 | Unknown protein | NA | 0.823719434 | 0.004075831 | 30.364462 | 53.75351467 |
| Solyc04g077520.3 | RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* F4JFN7_ARATH) | MSI | 0.828330705 | 0.006508931 | 3.965112667 | 7.108544333 |
| Solyc06g075150.3 | Auxin Response Factor 10B | NA | 0.828415122 | 0.01194056 | 1.167830333 | 2.083096333 |

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| Solyc06g050220.4 | Alpha-soluble NSF attachment protein (AHRD V3.3 *-* A0A1U8GWI2_CAPAN) | NA | 0.831017853 | 0.028900456 | 3.788603667 | 6.789227667 |
| Solyc11g072720.2 | BTB/POZ domain-containing protein (AHRD V3.3 *** A0A2G2VNB3_CAPBA) | NA | 0.831745966 | 0.042538405 | 0.828871667 | 1.480017667 |
| Solyc06g066290.3 | cystic fibrosis transmembrane conductance regulator (AHRD V3.3 *** AT2G35585.1) | NA | 0.832073251 | 0.012135413 | 3.579688 | 6.411152333 |
| Solyc10g009040.4 | defensin-like protein (AHRD V3.3 *-* AT4G21720.3) | NA | 0.838565247 | 0.005481307 | 3.427341667 | 6.192943333 |
| Solyc09g010080.3 | invertase 5 | INV | 0.844424941 | 0.000374227 | 16.362094 | 29.67707567 |
| Solyc03g006250.2 | GDSL esterase/lipase (AHRD V3.3 *** A0A1U8GGV5_CAPAN) | NA | 0.848095559 | 0.000862197 | 2.845653333 | 5.171179 |
| Solyc04g007130.1 | hypothetical protein (AHRD V3.3 *** AT1G13360.1) | NA | 0.849600886 | 0.000116682 | 39.22306167 | 70.874102 |
| Solyc05g055480.3 | NAC domain-containing protein (AHRD V3.3 *** A0A2U1NSV2_ARTAN) | NA | 0.851571483 | 0.023962881 | 2.614966333 | 4.799132667 |
| Solyc11g005630.1 | G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3 (AHRD V3.3 *** A0A2I4HSV3_9ROSI) | NA | 0.854343821 | 0.01402103 | 35.42552633 | 64.98644133 |
| Solyc04g040210.4 | Unknown protein | NA | 0.85541292 | 0.034004846 | 54.98922733 | 101.2035523 |
| Solyc12g013900.3 | Early nodulin-like protein 1 (AHRD V3.3 *-* A0A2G2X2X1_CAPBA) | NA | 0.855546125 | 0.003936292 | 4.943025333 | 9.079013333 |
| Solyc09g057870.4 | protein FAR1-RELATED SEQUENCE 7 (AHRD V3.3 *** A0A2I4EFQ2_9ROSI) | NA | 0.856788385 | 0.007218916 | 2.003068333 | 3.645559667 |
| Solyc10g080370.1 | Unknown protein | NA | 0.859011409 | 0.023727307 | 679.699748 | 1256.446859 |
| Solyc05g009630.4 | Disease resistance protein (AHRD V3.3 *-* A0A2U1N8H9_ARTAN),Pfam:PF18052 | NA | 0.859105618 | 0.014053198 | 3.766907667 | 6.904445333 |
| Solyc01g106000.4 | Nicotinamidase 1 (AHRD V3.3 *** A0A1U8DWC4_CAPAN) | NA | 0.860456637 | 0.001683774 | 22.61358467 | 41.476124 |
| Solyc11g072100.2 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1LUR0_ARTAN) | F6H | 0.86190805 | 0.01258848 | 8.629822 | 15.88603033 |
| Solyc11g062100.1 | E1-E2_ATPase domain-containing protein/HMA domain-containing protein/Hydrolase domain-containing protein (AHRD V3.3 *** A0A1Q3B5J2_CEPFO) | COPA | 0.866560666 | 4.0275E-05 | 6.914734333 | 12.69042367 |
| Solyc03g113430.3 | Protein NRT1/ PTR FAMILY 2.9 (AHRD V3.3 *** A0A2G2WRK6_CAPBA) | NA | 0.867566182 | 0.048936366 | 3.360318 | 6.197062 |
| Solyc02g062490.4 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1LXD5_ARTAN) | NA | 0.871465676 | 0.044166482 | 2.305056 | 4.202399333 |
| Solyc05g023750.3 | Adp-ribosylation factor gtpase-activating protein agd3 (AHRD V3.3 *** A0A314LCP5_NICAT) | ACAP | 0.87385242 | 7.68072E-06 | 13.79157633 | 25.433781 |
| Solyc07g008180.4 | CRABS CLAW-like protein 5a | NA | 0.878260997 | 0.0001485 | 21.04338767 | 38.946734 |
| Solyc01g098560.3 | Sugar facilitator protein 8 | ERD6 | 0.878779594 | 0.033937398 | 3.340561333 | 6.235849667 |
| Solyc03g115560.3 | Flavin-containing monooxygenase (AHRD V3.3 *** A0A2G2WR93_CAPBA) | NA | 0.87927491 | 0.013994038 | 2.440507333 | 4.490286 |
| Solyc08g082750.3 | Plant regulator RWP-RK family protein (AHRD V3.3 *** G7IAL8_MEDTR) | NA | 0.88359728 | 0.000898487 | 5.513081 | 10.26484733 |
| Solyc11g065240.2 | Saccharopine dehydrogenase (AHRD V3.3 *** A0A2K3NVD5_TRIPR) | NA | 0.883800126 | 0.000254818 | 6.011283667 | 11.094751 |
| Solyc09g008200.4 | heavy metal-associated isoprenylated plant protein 3-like (AHRD V3.3 *-* A0A1S4B4L4_TOBAC) | NA | 0.886097594 | 0.011388996 | 64.47306067 | 118.6303 |
| Solyc01g107390.4 | Auxin-responsive GH3 product (AHRD V3.3 *** Q05680_SOYBN) | GH3 | 0.886196735 | 0.00382056 | 24.86120667 | 45.79581067 |

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| Solyc02g079090.4 | Bifunctional riboflavin kinase/FMN phosphatase (AHRD V3.3 *-* A0A2G3D5Y9_CAPCH) | NA | 0.890492598 | 0.001511514 | 2.10481 | 3.921977667 |
| Solyc04g048900.3 | Calreticulin (AHRD V3.3 *** A0A2G3ASL1_CAPCH) | CALR | 0.890741573 | 0.033919666 | 8.640554333 | 16.36422733 |
| Solyc07g053050.1 | Calcium-binding protein PBP1 (AHRD V3.3 *** A0A1U8HB91_CAPAN) | KIC | 0.893265171 | 0.002306383 | 69.679188 | 131.1771087 |
| Solyc02g022920.1 | ethylene-responsive nuclear protein | NA | 0.897157761 | 0.017762483 | 0.954084667 | 1.786367 |
| Solyc11g008720.3 | Beta-glucosidase (AHRD V3.3 *** A0A2G2VEH4_CAPBA) | beta-glucosidase | 0.89766002 | 0.049118514 | 33.69917333 | 62.194832 |
| Solyc08g076120.3 | MIP18 family protein (AHRD V3.3 *** A0A2U1PDT8_ARTAN) | NA | 0.89836404 | 0.014134629 | 7.974571333 | 14.88221233 |
| Solyc09g055570.3 | GPCR kinase (AHRD V3.3 *** A0A2P5AIX2_TREOI) | NA | 0.900744141 | 0.000205021 | 9.945078667 | 18.544059 |
| Solyc03g095990.1 | transmembrane protein (AHRD V3.3 *-* AT3G56010.1) | NA | 0.901081632 | 0.027797058 | 40.738266 | 76.16313067 |
| Solyc11g009000.2 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** Q4PSG2_ARATH) | NA | 0.902559417 | 3.8033E-06 | 12.35892867 | 23.232465 |
| Solyc07g020790.4 | plastidic glucose translocator 3 | NA | 0.904589988 | 0.021625797 | 5.541340667 | 10.38091067 |
| Solyc12g038430.3 | Transposase, Ptta/En/Spm, plant (AHRD V3.3 *-* A0A1R3I9M9_9ROSI) | NA | 0.911096518 | 0.000702161 | 2.926651333 | 5.515345 |
| Solyc03g115840.4 | DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *** A0A2U1LKC9_ARTAN) | NA | 0.911429303 | 0.006416238 | 1.968019333 | 3.766727333 |
| Solyc09g073030.4 | Unknown protein | NA | 0.912496094 | 0.03486988 | 5.535760667 | 10.652378 |
| Solyc07g049135.1 | Fruit-specific protein (AHRD V3.3 *** FSPM_SOLLC) | NA | 0.912747141 | 0.003220354 | 23246.95964 | 43789.07292 |
| Solyc01g080460.3 | Pyruvate, phosphate dikinase (AHRD V3.3 *** A0A0M8KRU1_NICAT) | PPDK | 0.915614942 | 0.002715463 | 186.919276 | 353.3831687 |
| Solyc03g117500.1 | VQ motif-containing protein (AHRD V3.3 *** A0A2U1PE46_ARTAN) | NA | 0.916582798 | 0.036756537 | 3.859747667 | 7.355528333 |
| Solyc11g006505.1 | Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *** AT5G04830.2) | NA | 0.916877661 | 0.008520371 | 10.41700367 | 19.621427 |
| Solyc02g086520.3 | Proline-rich receptor-like kinase, putative (DUF1421) (AHRD V3.3 *-* F4J3J5_ARATH) | NA | 0.922600467 | 7.20789E-06 | 6.164082333 | 11.803343 |
| Solyc02g072120.3 | ER lumen protein-retaining receptor (AHRD V3.3 *** A0A1U8FK40_CAPAN) | KDELR | 0.923302836 | 0.003837379 | 3.598803333 | 6.842476667 |
| Solyc02g092310.4 | Pentatricopeptide repeat-containing protein, chloroplastic (AHRD V3.3 *** A0A2G2XHA6_CAPBA) | NA | 0.926075803 | 0.000592317 | 1.737899667 | 3.321007 |
| Solyc04g051820.4 | sorbin/SH3 domain protein (AHRD V3.3 *** AT5G09960.3) | NA | 0.928790576 | 0.007326335 | 48.028801 | 92.95140433 |
| Solyc01g008700.4 | MutS2 (AHRD V3.3 *** AT2G26840.1) | NA | 0.930804269 | 0.01265603 | 19.976986 | 37.86945767 |
| Solyc01g107180.3 | Phototropic-responsive NPH3 family protein (AHRD V3.3 *** A0A2U1N5P4_ARTAN) | NA | 0.931872765 | 5.70785E-05 | 1.766078333 | 3.391808 |
| Solyc04g051150.3 | Sterol 3-beta-glucosyltransferase (AHRD V3.3 *** A0A2K3NV48_TRIPR) | sterol 3beta-glucosyltransferase | 0.935119389 | 0.034806174 | 0.699220667 | 1.336201667 |
| Solyc07g049550.3 | 1-aminocyclopropane-1-carboxylate oxidase 2 (AHRD V3.3 *** Q7Y257_BETPN) | aminocyclopropanecarboxylate oxidase | 0.937102157 | 0.017493267 | 24.713887 | 48.300416 |
| Solyc06g054580.4 | RING/U-box superfamily protein (AHRD V3.3 *** A0A2U1M9Z7_ARTAN) | NA | 0.937285771 | 4.27373E-05 | 2.650536667 | 5.119689333 |
| Solyc06g010170.3 | Lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** A0A1P8AMP7_ARATH) | NA | 0.938352156 | 0.004194686 | 0.780251333 | 1.511484 |
| Solyc03g118750.4 | phosphoethanolamine N-methyltransferase | NMT | 0.940822468 | 6.02369E-05 | 2.544985333 | 4.929797333 |

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|---|---|---|---|---|---|---|
| Solyc03g098330.2 | Coiled coil protein (AHRD V3.3 *** A0A1P8B4G0_ARATH) | NA | 0.943878757 | 0.022904451 | 2.243622 | 4.312501667 |
| Solyc09g056160.4 | hypothetical protein (AHRD V3.3 *** AT5G48470.1) | NA | 0.945522209 | 1.48761E-06 | 25.660082 | 49.58206933 |
| Solyc04g078840.3 | AREB | ABF | 0.948543276 | 6.27624E-06 | 6.328354 | 12.28322233 |
| Solyc02g083700.4 | Alpha-mannosidase (AHRD V3.3 *** A0A1U8FVM7_CAPAN) | MAN2C1 | 0.948995678 | 0.000434511 | 6.086758 | 11.830332 |
| Solyc01g081450.3 | glycine-rich protein A3 (AHRD V3.3 --* XP_004229538.1) | NA | 0.953610153 | 6.96788E-05 | 123.48189 | 242.482793 |
| Solyc12g013650.2 | DUF1218 domain-containing protein (AHRD V3.3 *** A0A1Q3DB07_CEPFO) | NA | 0.954031685 | 0.04552458 | 3.664672667 | 7.129963667 |
| Solyc12g096310.2 | plant/protein (Protein of unknown function%2C DUF599) (AHRD V3.3 *** AT5G10580.4) | NA | 0.956934993 | 3.68117E-05 | 28.13677 | 54.847927 |
| Solyc02g031740.3 | Phloem protein 2-like (AHRD V3.3 *** A0A200QPN3_9MAGN) | NA | 0.95917288 | 0.00026701 | 6.32083 | 12.452093 |
| Solyc05g011970.3 | Cytochrome (AHRD V3.3 *** A0A1U8EZV2_CAPAN) | NA | 0.962918782 | 8.74648E-05 | 8.466560333 | 16.63277667 |
| Solyc04g009050.4 | agglutinin-like protein (AHRD V3.3 *-* AT3G54500.7) | NA | 0.964397376 | 0.004329654 | 4.234823333 | 8.288524333 |
| Solyc06g071780.4 | Drought induced 19 protein-like (AHRD V3.3 *** A0A200RD12_9MAGN) | NA | 0.964765501 | 0.000483804 | 11.881991 | 23.42016833 |
| Solyc04g074490.3 | F-box protein (AHRD V3.3 *** A0A2G3CNQ6_CAPCH) | NA | 0.966951415 | 0.000156058 | 20.30887267 | 40.09304567 |
| Solyc05g006920.4 | Protein NRT1/ PTR FAMILY 2.13 (AHRD V3.3 *** A0A1U8EVJ4_CAPAN) | NA | 0.96838911 | 0.005315931 | 8.130760667 | 16.23740433 |
| Solyc07g062700.3 | Calcium-binding EF-hand family protein (AHRD V3.3 *** A0A2U1MZJ3_ARTAN) | NA | 0.968982663 | 0.039388113 | 122.0176037 | 243.1717833 |
| Solyc03g113280.3 | Integral membrane HPP family protein (AHRD V3.3 *** A0A2U1NK12_ARTAN) | NA | 0.971246913 | 0.007567707 | 3.278490667 | 6.484332667 |
| Solyc05g006680.4 | Galactosyltransferase family protein (AHRD V3.3 *** A0A2U1KC25_ARTAN) | GALT2S | 0.971307393 | 5.79531E-05 | 1.804663 | 3.570245 |
| Solyc08g082400.1 | Chlororespiratory reduction31 (AHRD V3.3 *** A0A0F7GYA7_9ROSI) | NDHS | 0.977359165 | 0.002659551 | 12.56420467 | 24.70772067 |
| Solyc03g026300.4 | Per1-like (AHRD V3.3 *** A0A200PW77_9MAGN) | PGAP3 | 0.97757979 | 0.0002612 | 2.015924333 | 3.994123667 |
| Solyc03g008010.3 | PPPDE putative thiol peptidase family protein (AHRD V3.3 *** A0A2U1P9D8_ARTAN) | NA | 0.977833146 | 0.005660623 | 15.687097 | 31.40655033 |
| Solyc06g060830.3 | Homeobox-leucine zipper protein HAT2 (AHRD V3.3 *** A0A2G2WJU4_CAPBA) | HD-ZIP | 0.980621759 | 0.00093276 | 1.726139667 | 3.442577667 |
| Solyc03g026220.3 | BAG family molecular chaperone regulator 1 (AHRD V3.3 *** A0A2G2ZYV9_CAPAN) | NA | 0.98132069 | 0.001675671 | 12.89790833 | 25.80196967 |
| Solyc08g006950.4 | AT-hook motif nuclear-localized protein 8-like (AHRD V3.3 *** A0A2I4DIF4_9ROSI) | NA | 0.982523883 | 0.030265732 | 1.044436 | 2.088855333 |
| Solyc07g045300.4 | transmembrane protein (AHRD V3.3 *** AT2G04360.1) | NA | 0.987259737 | 0.001157639 | 2.427131333 | 4.827605 |
| Solyc06g060310.3 | Chlorophyllide a oxygenase, chloroplastic (AHRD V3.3 *** A0A2G3C7C2_CAPCH) | CAO | 0.988275288 | 0.035358376 | 2.285370333 | 4.590689333 |
| Solyc02g069030.3 | Phloem protein 2-like protein (AHRD V3.3 *** A0A2U1PTN1_ARTAN) | NA | 0.988466195 | 0.048961177 | 1.169532667 | 2.310963333 |
| Solyc06g062690.4 | Nucleosome assembly protein family (AHRD V3.3 *** A9TVZ4_PHYPA) | NAP1L1 | 0.989517534 | 0.002980238 | 9.33063 | 18.675636 |
| Solyc06g076700.1 | UPF0503 protein, chloroplastic (AHRD V3.3 *** A0A1J3D8K5_NOCCA) | NA | 0.990641674 | 0.01194481 | 2.744596333 | 5.432278667 |
| Solyc05g012580.1 | Unknown protein | NA | 0.991521295 | 0.005255523 | 167.7190857 | 337.5696153 |
| Solyc11g068515.1 | Unknown protein | NA | 0.991766613 | 0.006112487 | 3.945673667 | 7.971711333 |

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| Solyc05g041530.3 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A2U1LLS3_ARTAN) | NA | 1.000518533 | 0.006693008 | 1.964631 | 3.964372667 |
| Solyc12g044240.3 | Dynein light chain (AHRD V3.3 *** A0A2G3D067_CAPCH) | DYNLL | 1.003778707 | 0.00943797 | 4.062172 | 8.174056 |
| Solyc04g076530.3 | GATA transcription factor 28 (AHRD V3.3 *** A0A2G3CP85_CAPCH) | NA | 1.003843979 | 1.02139E-06 | 14.46226333 | 29.30218 |
| Solyc01g095150.3 | late embryogenesis-like protein | NA | 1.005194285 | 0.004018346 | 193.5357613 | 395.4363503 |
| Solyc06g082210.1 | Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6 (AHRD V3.3 *** A0A1J3GXN6_NOCCA) | NA | 1.008638814 | 2.81506E-05 | 11.41979067 | 23.00808133 |
| Solyc02g082400.4 | Transcription factor jumonji (JmjC) domain-containing protein (AHRD V3.3 *** C0SV12_ARATH) | KDM3 | 1.009102121 | 5.16428E-09 | 5.157555333 | 10.45891233 |
| Solyc02g082633.1 | DNA mismatch repair protein MLH3 (AHRD V3.3 *-* A0A2G2XFY3_CAPBA) | NA | 1.00940854 | 0.037611613 | 3.146699667 | 6.359873667 |
| Solyc08g067100.2 | Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A2U1P524_ARTAN) | NA | 1.010166603 | 0.013730163 | 3.026375 | 6.208982667 |
| Solyc03g112300.3 | Octicosapeptide/phox/Bem1p domain kinase superfamily protein (AHRD V3.3 *-* A0A2K3MP92_TRIPR) | NA | 1.01051595 | 4.1122E-05 | 13.99635633 | 28.33131033 |
| Solyc06g069360.3 | PHD and RING finger domain-containing protein (AHRD V3.3 *-* A0A2K3N8F5_TRIPR) | NA | 1.013412453 | 0.000256258 | 1.272176333 | 2.589526333 |
| Solyc05g005480.2 | Quinone oxidoreductase-like protein (AHRD V3.3 *** Q8LEB8_ARATH) | EO | 1.018440923 | 0.00059044 | 38.215482 | 77.56702933 |
| Solyc12g010420.1 | hypothetical protein (AHRD V3.3 --* AT5G11070.1) | NA | 1.024415536 | 0.011781552 | 44.80413467 | 92.73030567 |
| Solyc05g012770.3 | WRKY transcription factor 4 | NA | 1.026686156 | 8.59556E-05 | 7.435279333 | 15.214493 |
| Solyc08g083060.3 | Metal-nicotianamine transporter YSL1 (AHRD V3.3 *** A0A2G3AD61_CAPAN) | NA | 1.027299873 | 0.001141243 | 4.216700333 | 8.677887667 |
| Solyc11g008250.2 | P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A2U1LNZ5_ARTAN) | NA | 1.027398931 | 0.014581569 | 2.388605333 | 4.869170333 |
| Solyc09g065020.4 | F-box protein (AHRD V3.3 *** A0A2I0WY04_9ASPA) | NA | 1.032610744 | 0.000483284 | 4.966660667 | 10.137845 |
| Solyc11g010660.2 | Protein SGT1-like protein (AHRD V3.3 *** A0A2G3B092_CAPCH) | NA | 1.032673009 | 0.011621183 | 9.491746333 | 19.53184833 |
| Solyc10g078190.2 | cytosine-5 DNA methyltransferaseL1 | NA | 1.033693383 | 6.65874E-06 | 8.562177 | 17.57582433 |
| Solyc02g086900.4 | HD domain-containing metal-dependent phosphohydrolase family protein (AHRD V3.3 *** A0A2U1PYT8_ARTAN) | SAMHD1 | 1.039639223 | 0.011906718 | 4.066997 | 8.514404667 |
| Solyc11g007510.2 | transmembrane protein (AHRD V3.3 --* AT2G37300.6) | NA | 1.04299414 | 0.000538813 | 1.558263 | 3.252111333 |
| Solyc02g078810.4 | Bromodomain protein (AHRD V3.3 *** A0A2K3P7T0_TRIPR) | NA | 1.05141014 | 0.000166785 | 1.777907667 | 3.70262 |
| Solyc02g065240.3 | Methyl esterase 1 (AHRD V3.3 *** A0A2U1LMY0_ARTAN) | NA | 1.053914578 | 0.035883044 | 291.6488547 | 605.944875 |
| Solyc02g036350.3 | 1-aminocyclopropane-1-carboxylate oxidase EF501822 | aminocyclopropanecarboxylate oxidase | 1.057137192 | 0.013341081 | 128.4668707 | 266.3999227 |
| Solyc04g074270.3 | Outer arm dynein light chain 1 (AHRD V3.3 *** A0A2K3NQ00_TRIPR) | NA | 1.059632028 | 0.001114279 | 17.333453 | 36.607058 |
| Solyc01g098740.4 | Protein kinase superfamily protein (AHRD V3.3 *** F4HYK7_ARATH) | NA | 1.060765141 | 0.001899289 | 5.598971 | 11.66208833 |
| Solyc11g013470.1 | Auxin response factor (AHRD V3.3 *-* E5LMG0_SOLLC) | NA | 1.062114108 | 0.003718131 | 2.987994333 | 6.238445667 |
| Solyc02g088560.4 | Cyclic nucleotide-gated ion channel protein, putative (AHRD V3.3 *** G7L453_MEDTR) | CNGC | 1.063048845 | 0.000106194 | 9.593058667 | 20.08940633 |

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|---|---|---|---|---|---|---|
| Solyc03g112980.1 | Unknown protein | NA | 1.067868768 | 0.028391254 | 5.629201667 | 11.99299833 |
| Solyc05g006640.4 | Phospholipid-transporting ATPase (AHRD V3.3 *** A0A1U8EVI0_CAPAN) | DRS2 | 1.068798701 | 0.000290874 | 7.716286333 | 16.38085267 |
| Solyc08g005760.1 | Alcohol acyl transferase (AHRD V3.3 *** Q6QLX4_SOLLC) | NA | 1.069227545 | 0.045609329 | 1.918209 | 3.998815333 |
| Solyc07g066020.2 | Amino acid permease (AHRD V3.3 *** S8CYC9_9LAMI) | AAP | 1.072605481 | 0.000140398 | 1.016704 | 2.156841333 |
| Solyc12g008350.3 | dehydration responsive element binding protein 2 | EREBP | 1.073780343 | 0.006130461 | 2.372768667 | 5.072110333 |
| Solyc04g010030.1 | PITH domain-containing protein (AHRD V3.3 *-* A0A1U8E514_CAPAN) | NA | 1.074298628 | 0.003091034 | 0.616497 | 1.303427 |
| Solyc12g013620.2 | jasmonic acid 2 | NA | 1.075991177 | 0.00528796 | 16.65218567 | 34.82338033 |
| Solyc04g054740.3 | myo-inositol-1-phosphate synthase | INO1 | 1.076219063 | 0.018312496 | 1.176718 | 2.507713667 |
| Solyc02g085580.4 | Protein indeterminate-domain 1 (AHRD V3.3 *** A0A2G3D7R8_CAPCH) | NA | 1.082789536 | 0.00043989 | 1.423769333 | 3.0381 |
| Solyc01g108250.3 | DEM2 | NA | 1.084262647 | 5.25029E-07 | 86.633588 | 185.8214113 |
| Solyc11g006720.2 | Transcription factor DIVARICATA (AHRD V3.3 *** A0A2G3AV26_CAPCH) | NA | 1.085575082 | 2.09271E-09 | 21.02581333 | 45.086014 |
| Solyc01g010060.2 | Unknown protein | NA | 1.086126792 | 3.57178E-05 | 53.591479 | 114.906621 |
| Solyc03g095310.3 | Cytochrome P450 (AHRD V3.3 *** A0A2U1PRC1_ARTAN) | CYP714A1 | 1.093065412 | 0.03444643 | 1.273014333 | 2.754613 |
| Solyc11g069040.3 | glyoxalase 1 | GLO1 | 1.096653117 | 8.4165E-06 | 9.372546333 | 20.30729733 |
| Solyc07g047850.3 | Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** A0A1U8HAX7_CAPAN) | LHCB2 | 1.097317866 | 0.002604384 | 3.748712667 | 8.100196667 |
| Solyc09g089940.1 | DUF2828 domain-containing protein (AHRD V3.3 *** A0A1Q3B0Q4_CEPFO) | NA | 1.101313902 | 3.82046E-07 | 42.87133033 | 93.1141 |
| Solyc10g084060.2 | cysteine-rich/transmembrane domain A-like protein (AHRD V3.3 -** AT2G32210.1) | NA | 1.102191342 | 0.002900634 | 2.481286 | 5.408883333 |
| Solyc07g061950.4 | C2 domain-containing protein (AHRD V3.3 *** A0A2G2WER0_CAPBA) | NA | 1.104260793 | 0.001578764 | 8.991026 | 19.68051067 |
| Solyc05g013640.1 | Unknown protein | NA | 1.112078897 | 0.00302436 | 75.156563 | 165.7809423 |
| Solyc10g084070.1 | Unknown protein | NA | 1.114090516 | 0.000434019 | 27.908959 | 61.13848233 |
| Solyc03g118710.3 | Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** A0A2U1LMA8_ARTAN) | NA | 1.121019209 | 8.43284E-05 | 2.647477333 | 5.792689333 |
| Solyc01g005080.3 | 65-kDa microtubule-associated protein 6 (AHRD V3.3 *** A0A2G2XSF2_CAPBA),Pfam:PF03999 | PRC1 | 1.121651033 | 0.001354916 | 1.321481333 | 2.905963 |
| Solyc09g061320.4 | thiamine-repressible mitochondrial transport protein THI74 (AHRD V3.3 *** A0A2I4GA08_9ROSI) | SLC35F5 | 1.123113736 | 0.010426539 | 7.148712333 | 15.88479567 |
| Solyc06g060380.3 | Sister chromatid cohesion protein PDS5-like protein A (AHRD V3.3 *** A0A1J3GEG2_NOCCA) | PDS5 | 1.125843959 | 0.002079926 | 1.534643667 | 3.386462 |
| Solyc08g006160.4 | Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** A0A2U1N400_ARTAN) | NA | 1.126326407 | 2.57466E-06 | 38.800283 | 85.45677433 |
| Solyc05g009070.4 | Protein phosphatase 2C family protein (AHRD V3.3 *** A0A2U1KGE8_ARTAN) | NA | 1.13162266 | 0.010613649 | 8.761340667 | 19.66813933 |
| Solyc09g063090.4 | methyl-coenzyme M reductase II subunit gamma%2C putative (DUF3741) (AHRD V3.3 *-* AT5G43880.4) | NA | 1.134827011 | 3.9132E-07 | 5.514264 | 12.11132933 |
| Solyc09g074380.4 | DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* F4IUS3_ARATH) | NA | 1.13709246 | 2.3087E-07 | 2.629630667 | 5.812388 |

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| Solyc11g013480.3 | Auxin Response Factor 17 | NA | 1.137339142 | 0.0068124 | 3.800295 | 8.392625333 |
| Solyc01g094690.4 | plasma membrane intrinsic protein 1.2 | PIP | 1.138061705 | 2.98845E-06 | 16.22666433 | 35.76841167 |
| Solyc06g060100.3 | Mannose-6-phosphate isomerase (AHRD V3.3 *** A0A1U8GQ16_CAPAN) | MANA | 1.140525395 | 0.000117207 | 2.068436333 | 4.580468667 |
| Solyc12g005120.2 | inositol-1%2C4%2C5-trisphosphate 5-phosphatase (AHRD V3.3 *-* AT5G54870.2) | NA | 1.140592731 | 0.008550209 | 2.179806 | 4.810623333 |
| Solyc10g081420.2 | Protein kinase (AHRD V3.3 *** Q2HVC0_MEDTR) | NA | 1.141189701 | 0.03941703 | 2.495008 | 5.652073667 |
| Solyc11g007610.2 | ATP-dependent RNA helicase (AHRD V3.3 *** B6TU64_MAIZE) | NA | 1.14249896 | 0.000509295 | 1.996677333 | 4.474579333 |
| Solyc01g096620.4 | Cilia-and flagella-associated protein 20 (AHRD V3.3 *-* A0A2G2YYL7_CAPAN) | NA | 1.143093238 | 0.019812119 | 5.087739 | 11.23891433 |
| Solyc04g150162.1 | Vacuolar iron transporter-like protein 4 (AHRD V3.3 *** A0A2G3CN36_CAPCH) | VIT | 1.143187169 | 0.00029482 | 9.138065 | 20.24576133 |
| Solyc03g098630.4 | DUF789 domain-containing protein (AHRD V3.3 *-* A0A1Q3BTC9_CEPFO) | NA | 1.147784788 | 0.000362192 | 1.785605667 | 3.957612333 |
| Solyc05g009060.2 | Unknown protein | NA | 1.150798042 | 0.023714296 | 3.015118333 | 6.853495 |
| Solyc09g009220.4 | histone-lysine N-methyltransferase SETD1B-like protein (AHRD V3.3 *** AT5G03670.1) | NA | 1.150804262 | 0.008269123 | 1.341415667 | 2.974578667 |
| Solyc10g084690.2 | ADP-ribosylation factor GTPase-activating protein 1 (AHRD V3.3 *** A0A1U8EA26_CAPAN) | ARFGAP1 | 1.151852591 | 0.001078439 | 0.682441667 | 1.545167667 |
| Solyc06g071750.3 | Octicosapeptide/Phox/Bem1p (AHRD V3.3 *-* B6SZC5_MAIZE) | NA | 1.152299528 | 0.029035015 | 22.07402167 | 48.51260733 |
| Solyc11g012680.3 | Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* B3H4A8_ARATH) | NA | 1.155060154 | 0.016093724 | 1.418751 | 3.224014 |
| Solyc08g042140.3 | translation initiation factor 3 subunit I (AHRD V3.3 *** AT1G54680.4) | NA | 1.155935566 | 3.12823E-05 | 2.240453667 | 5.017858333 |
| Solyc11g009060.2 | ATP synthase subunit B (AHRD V3.3 *** AT5G10320.1) | NA | 1.159410518 | 0.001457998 | 1.306829667 | 2.925536667 |
| Solyc01g094370.3 | remorin 2 | NA | 1.162556778 | 0.000203833 | 11.02238067 | 24.905088 |
| Solyc04g076680.2 | MADS box transcription factor AGAMOUS (AHRD V3.3 *-* A0A1Q1NK16_PAELC) | K09264 | 1.165092004 | 1.55348E-05 | 4.949440667 | 11.156323 |
| Solyc12g007300.1 | B3 domain plant protein (AHRD V3.3 *-* G7IYP2_MEDTR) | NA | 1.165201451 | 0.000113324 | 4.567988667 | 10.27675333 |
| Solyc01g068490.4 | RING-type E3 ubiquitin transferase (AHRD V3.3 *** A0A200RD53_9MAGN) | VAC8 | 1.168743651 | 0.040226683 | 1.798292 | 4.099802667 |
| Solyc07g045460.3 | SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** A0A2G3BYB4_CAPCH) | PRKAB | 1.170899219 | 0.006200288 | 1.281948333 | 2.903439667 |
| Solyc09g010640.2 | FYD (AHRD V3.3 *** AT3G12570.4) | NA | 1.173591008 | 1.44271E-06 | 20.86268833 | 47.67422 |
| Solyc09g020190.3 | Non-specific phospholipase C1 (AHRD V3.3 *** A0A2G2YK91_CAPAN) | PLC | 1.174453102 | 1.38564E-08 | 14.61576 | 33.24367333 |
| Solyc09g064200.4 | Myosin (AHRD V3.3 *** W5ZTD6_MAIZE) | MYO5 | 1.176792807 | 1.80249E-05 | 17.988651 | 41.265331 |
| Solyc09g059970.3 | Small ubiquitin-related modifier (AHRD V3.3 *** A0A218VRF2_PUNGR) | NA | 1.177121044 | 2.76754E-07 | 15.14241567 | 34.59022767 |
| Solyc03g115370.3 | Diacylglycerol kinase (AHRD V3.3 *** A0A1U8G5K6_CAPAN) | DGKA | 1.181187939 | 9.87905E-08 | 18.91030367 | 43.11075867 |
| Solyc10g008220.4 | Disease resistance protein (AHRD V3.3 *** A0A2U1N8H9_ARTAN) | NA | 1.182238673 | 1.88263E-05 | 5.528730667 | 12.56887733 |
| Solyc02g087970.1 | Mini zinc finger protein (AHRD V3.3 *** A0ZXL1_SOLLC) | NA | 1.18427718 | 1.06177E-06 | 140.768379 | 323.9763997 |
| Solyc08g075440.4 | conserved oligomeric Golgi complex subunit 6 (AHRD V3.3 *** A0A2I4E5B9_9ROSI) | COG6 | 1.190275224 | 4.7271E-08 | 3.777370333 | 8.705768 |

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| Solyc01g110110.3 | Cysteine protease (AHRD V3.3 *** Q9AUC5_IPOBA) | CTSF | 1.192702377 | 0.017309071 | 1.278683667 | 2.956504 |
| Solyc02g071580.4 | Subtilisin-like protease SBT5.3 (AHRD V3.3 *** A0A2G2XF91_CAPBA) | NA | 1.193762902 | 0.002694538 | 1.049918333 | 2.391447667 |
| Solyc12g049420.2 | 25.3 kDa vesicle transport protein (AHRD V3.3 *** A0A2G3AXE7_CAPCH) | SEC22 | 1.195317044 | 0.009310237 | 8.451713667 | 19.43922867 |
| Solyc11g069350.2 | Zinc finger, RING-CH-type, Zinc finger, RING/FYVE/PHD-type (AHRD V3.3 *** A0A2U1QK69_ARTAN) | NA | 1.197044987 | 0.019264161 | 5.901940667 | 13.46511867 |
| Solyc08g078060.3 | Transmembrane protein (AHRD V3.3 *** Q1PDG7_ARATH) | NA | 1.197714984 | 0.000605154 | 16.15931333 | 37.64200267 |
| Solyc03g114750.3 | 18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 --* NP_178475.2) | NA | 1.201941258 | 0.000193804 | 4.383271 | 10.08126233 |
| Solyc05g008060.4 | SlPIN4 | PIN | 1.202539149 | 0.006563225 | 1.756539667 | 4.126930333 |
| Solyc01g100230.3 | DnaJ-like protein subfamily B member 6 (AHRD V3.3 *** A0A2G2V7W8_CAPBA) | NA | 1.211748004 | 2.03199E-08 | 20.71534033 | 48.08793633 |
| Solyc04g051280.4 | nucleolin (AHRD V3.3 *-* AT1G65090.3) | NA | 1.21244144 | 0.048654386 | 2.296295333 | 5.443073 |
| Solyc04g008260.3 | Purple acid phosphatase (AHRD V3.3 *** Q6J5M7_SOLTU) | ACP5 | 1.216845197 | 0.009563973 | 1.475527667 | 3.476672333 |
| Solyc12g010950.2 | 2-alkenal reductase (NADP(+)-dependent) (AHRD V3.3 *** A0A1U8EE67_CAPAN) | DBR | 1.224644805 | 0.048226811 | 34.616403 | 82.820637 |
| Solyc06g071280.4 | Enhanced disease susceptibility 1 protein (AHRD V3.3 *** Q2TQV0_SOLTU) | EDS1 | 1.229961851 | 0.038004491 | 12.05808267 | 28.71056933 |
| Solyc03g006640.3 | F-box family protein (AHRD V3.3 *** A0A2U1N101_ARTAN) | NA | 1.230240958 | 0.001233079 | 4.683676667 | 11.13005767 |
| Solyc07g005330.3 | Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A2U1LWN7_ARTAN) | NA | 1.230736883 | 0.003941652 | 20.12534833 | 48.35464933 |
| Solyc09g061710.3 | Alba DNA/RNA-binding protein (AHRD V3.3 *-* A0A1I9LSC0_ARATH) | NA | 1.232961428 | 4.77062E-10 | 9.569663667 | 22.62998133 |
| Solyc07g053140.3 | Zinc finger protein/CONSTANS-like protein (AHRD V3.3 *-* A0A2K3M573_TRIPR) | NA | 1.233864781 | 0.002193544 | 29.61711967 | 70.69016533 |
| Solyc11g044310.2 | Proline iminopeptidase (AHRD V3.3 *** A0A1U8GCK3_CAPAN) | PIP | 1.240137425 | 6.9519E-11 | 6.812405667 | 16.240493 |
| Solyc06g053140.3 | Rhodanese-like domain-containing protein 14, chloroplastic (AHRD V3.3 *** A0A2G2WIJ1_CAPBA) | NA | 1.245473621 | 8.82991E-06 | 5.675236667 | 13.572799 |
| Solyc02g081480.4 | Receptor-like protein kinase (AHRD V3.3 *** A0A2K3NJB3_TRIPR) | NA | 1.246750272 | 1.47826E-05 | 2.248037667 | 5.419676667 |
| Solyc02g082630.2 | Phosphoinositide phosphatase family protein (AHRD V3.3 *-* A0A2U1LC37_ARTAN) | NA | 1.247654272 | 0.002498141 | 1.403064667 | 3.337341667 |
| Solyc09g031580.3 | Zinc finger, RING-type (AHRD V3.3 *** A0A1R3IP44_COCAP) | NA | 1.253115763 | 4.51421E-10 | 3.258131333 | 7.823325333 |
| Solyc10g084000.3 | heavy metal-associated isoprenylated plant protein 3-like (AHRD V3.3 *** A0A1U8EC89_CAPAN) | NA | 1.258110301 | 0.027571356 | 5.347076333 | 13.120542 |
| Solyc05g024430.3 | transmembrane protein (AHRD V3.3 *-* AT4G13500.1) | NA | 1.259176362 | 0.001283735 | 2.638954667 | 6.339719667 |
| Solyc11g007770.2 | Glycosyltransferase family protein 64 protein C5 (AHRD V3.3 *** A0A2G2VEI7_CAPBA) | NA | 1.261689749 | 1.01877E-05 | 2.986195667 | 7.183294 |
| Solyc11g010670.1 | Unknown protein | NA | 1.266381014 | 0.01450563 | 64.437936 | 157.67291 |
| Solyc12g005910.2 | B-cell receptor-associated 31-like (AHRD V3.3 *** A0A200QH03_9MAGN) | BCAP31 | 1.266773309 | 0.000393007 | 9.490121 | 23.25585033 |
| Solyc01g097650.3 | Serinc-domain containing serine and sphingolipid biosynthesis protein (AHRD V3.3 *** A0A2U1MZP6_ARTAN) | SERINC1_3 | 1.270335431 | 0.001448631 | 0.749436333 | 1.843053 |
| Solyc01g068500.4 | ERD (Early-responsive to dehydration stress) family protein (AHRD V3.3 *** A0A2K3NJK3_TRIPR) | TMEM63 | 1.272128805 | 0.005690381 | 1.128623333 | 2.730249667 |

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|---|---|---|---|---|---|---|
| Solyc02g062140.2 | Armadillo repeat only 1 (AHRD V3.3 *** Q9SW41_ARATH) | NA | 1.273436101 | 3.6654E-05 | 9.561504667 | 23.41940167 |
| Solyc02g082440.2 | Unknown protein | NA | 1.277129521 | 0.000311077 | 0.496251667 | 1.211845333 |
| Solyc08g066390.3 | SAWADEE HOMEODOMAIN protein (AHRD V3.3 *** A0A178W211_ARATH) | NA | 1.277747452 | 0.003903727 | 3.299001667 | 8.035586333 |
| Solyc03g043740.4 | Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** A0A2U1M3E1_ARTAN) | NA | 1.278665719 | 0.003999501 | 4.003358333 | 9.650998333 |
| Solyc02g065280.3 | Methylesterase 1 (AHRD V3.3 *** A0A2G3D300_CAPCH) | NA | 1.280478638 | 0.007984224 | 20.868858 | 50.555411 |
| Solyc02g077270.4 | Calcium-binding EF-hand family protein (AHRD V3.3 *-* A0A2U1MZJ3_ARTAN) | NA | 1.282605509 | 0.010463521 | 0.561874333 | 1.357458333 |
| Solyc02g093600.3 | Class I heat shock protein (AHRD V3.3 *** A0A2K3K1J3_TRIPR) | HSP20 | 1.28544463 | 0.011527611 | 9.840018 | 23.93031267 |
| Solyc02g071770.3 | oil body-associated protein 2A-like (AHRD V3.3 *** A0A2I4FEE8_9ROSI) | NA | 1.286481376 | 0.005367019 | 4.507508667 | 11.203763 |
| Solyc07g006630.4 | Zinc finger protein CONSTANS-like 5-like (AHRD V3.3 *** A0A2K3N2C5_TRIPR) | NA | 1.286774329 | 0.048298916 | 3.011494 | 7.466192 |
| Solyc09g065200.4 | cyclinU3_1 | NA | 1.28768787 | 1.59019E-05 | 1.952925667 | 4.799309333 |
| Solyc07g045160.3 | ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** A0A2G2WC06_CAPBA) | PFKA | 1.295874946 | 3.2266E-05 | 7.279707333 | 17.85754033 |
| Solyc09g055940.3 | Bile acid:sodium symporter (AHRD V3.3 *** A0A200PU00_9MAGN) | TC.BASS | 1.306980634 | 8.19268E-13 | 8.446907667 | 20.97756267 |
| Solyc05g017900.3 | EamA domain-containing protein (AHRD V3.3 *-* A0A2U1MSW3_ARTAN) | NA | 1.30896404 | 0.028554814 | 1.013172333 | 2.513332667 |
| Solyc01g010490.4 | Cytochrome P450 (AHRD V3.3 *** A0A2U1NH79_ARTAN) | NA | 1.318846913 | 0.000242999 | 11.484509 | 28.74837233 |
| Solyc03g124110.2 | Dehydration-responsive element-binding transcription factor (AHRD V3.3 *** A0A1S6M2D0_9CARY) | NA | 1.322872582 | 0.003976355 | 25.25985533 | 64.244264 |
| Solyc06g051190.3 | RNA-dependent RNA polymerase (AHRD V3.3 *** A0A328DJK0_9ASTE) | RDR | 1.325925097 | 0.000692242 | 0.299620667 | 0.761318 |
| Solyc06g068510.1 | MAP kinase kinase kinase 38 | NA | 1.327041459 | 0.013812728 | 0.728984 | 1.838919 |
| Solyc01g106250.4 | B3 domain-containing protein (AHRD V3.3 *-* A0A1Q3CKL9_CEPFO) | NA | 1.33607531 | 3.5997E-05 | 1.101225667 | 2.819628 |
| Solyc01g098570.2 | FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* F4HX10_ARATH) | NA | 1.338682598 | 9.50041E-05 | 8.341415333 | 21.20151667 |
| Solyc10g049270.2 | Serine carboxypeptidase (AHRD V3.3 *** A0A2U1P833_ARTAN) | SCPL-I | 1.342787141 | 0.022101234 | 0.696149333 | 1.755615 |
| Solyc11g072310.2 | gibberellin 20-oxidase-3 | GA20OX | 1.345513084 | 3.9535E-06 | 29.163014 | 73.872036 |
| Solyc06g068520.3 | Hydroxyproline-rich systemin (AHRD V3.3 *** HSY1_SOLLC) | NA | 1.35339955 | 0.046372593 | 8.389442333 | 21.968761 |
| Solyc01g100310.2 | DUF1645 family protein (AHRD V3.3 *-* G7I9G3_MEDTR) | NA | 1.355527657 | 1.33178E-07 | 6.441536333 | 16.46434733 |
| Solyc01g091630.3 | cutin deficient 2 | HD-ZIP | 1.35765827 | 0.022330938 | 2.601970667 | 6.653974333 |
| Solyc12g011370.3 | Cationic amino acid transporter (AHRD V3.3 *** A0A2K3LDF0_TRIPR) | NA | 1.358143092 | 0.044520007 | 1.017244667 | 2.618363333 |
| Solyc01g008440.3 | Calcium-dependent protein kinase (AHRD V3.3 *** B2KTB2_WHEAT) | CPK | 1.358807026 | 0.022227926 | 3.269253 | 8.369710667 |
| Solyc03g080190.3 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A2U1QGX7_ARTAN) | DMR6 | 1.35989059 | 2.33978E-05 | 2.395053667 | 6.215812333 |
| Solyc09g056350.4 | Lipase class 3 family protein (AHRD V3.3 *** S8D401_9LAMI) | NA | 1.363956729 | 6.68114E-12 | 5.048150333 | 13.08640933 |

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| Solyc07g054670.4 | External alternative NAD(P)H-ubiquinone oxidoreductase B1, mitochondrial (AHRD V3.3 *** A0A2G2Z3L2_CAPAN) | NDH1 | 1.365634789 | 3.0457E-05 | 10.505559 | 27.22405967 |
| Solyc02g087975.1 | Unknown protein | NA | 1.378034211 | 1.14168E-06 | 4.083118667 | 10.75015 |
| Solyc01g100040.3 | Protein phosphatase 2C family protein (AHRD V3.3 *** A0A2U1N538_ARTAN) | NA | 1.380171024 | 0.014675733 | 1.910005667 | 5.050352333 |
| Solyc03g082420.3 | Small heat shock protein, chloroplastic (AHRD V3.3 *** HS21C_SOLLC) | HSP20 | 1.380274004 | 0.002759341 | 99.882047 | 258.2266387 |
| Solyc09g031610.4 | DAMAGED DNA BINDING PROTEIN1 | DDB2 | 1.384875197 | 7.24517E-07 | 2.726638667 | 7.113909 |
| Solyc09g063070.3 | Tetraspanin/Peripherin (AHRD V3.3 *** A0A200PVL6_9MAGN) | NA | 1.388091526 | 0.007218916 | 1.114915 | 2.991687 |
| Solyc09g082870.3 | Calcium-transporting ATPase (AHRD V3.3 *** A0A2G2W115_CAPBA) | ATP2C | 1.399668438 | 0.026181742 | 4.753401667 | 12.882358 |
| Solyc10g052490.2 | Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU) | PCBER1 | 1.400265319 | 0.002831451 | 7.511396 | 19.855366 |
| Solyc09g055890.4 | Lipoxygenase (AHRD V3.3 *** A0A1S3YEP0_TOBAC) | LOX2S | 1.401385686 | 2.97845E-05 | 0.796381 | 2.136899 |
| Solyc09g005200.3 | transmembrane protein (AHRD V3.3 *-* AT5G01015.1) | NA | 1.4028267 | 0.001553646 | 2.899543333 | 7.727536667 |
| Solyc01g095510.3 | Mitochondrial carrier protein MTM1 (AHRD V3.3 *** A0A2G3BTD4_CAPCH) | SLC25A39_40 | 1.404518477 | 0.005315931 | 1.621190333 | 4.345067667 |
| Solyc07g053010.3 | Disease resistance protein (AHRD V3.3 *** A0A200QY03_9MAGN) | NA | 1.405107897 | 0.000930362 | 1.349505333 | 3.577914 |
| Solyc08g083130.4 | Homeobox-leucine zipper protein HOX6 (AHRD V3.3 *** A0A2G3DAJ5_CAPCH) | HD-ZIP | 1.406910106 | 0.001428554 | 12.52945933 | 32.82738767 |
| Solyc05g008400.4 | Repressor of RNA polymerase III transcription (AHRD V3.3 *** A0A1U8F9V8_CAPAN) | NA | 1.415675218 | 0.00045803 | 1.808619667 | 4.821432 |
| Solyc09g018060.4 | MAP kinase kinase kinase  69 | NA | 1.416901751 | 9.93489E-06 | 2.311120667 | 6.252399 |
| Solyc01g109420.3 | Quinone reductase family protein (AHRD V3.3 *** A0A1P8B767_ARATH) | WRBA | 1.431782379 | 7.0229E-08 | 4.989758333 | 13.50735667 |
| Solyc02g069020.3 | Phloem protein 2-like protein (AHRD V3.3 *** A0A2U1PTN1_ARTAN) | NA | 1.432232377 | 2.54149E-06 | 4.004053667 | 10.99400133 |
| Solyc06g036310.3 | Heavy metal-associated isoprenylated plant protein (AHRD V3.3 *** A0A2R6RSL8_ACTCH) | NA | 1.446060854 | 0.013637353 | 4.177786667 | 11.575228 |
| Solyc06g011575.1 | Unknown protein | NA | 1.455876371 | 0.000405222 | 7.097215667 | 19.792215 |
| Solyc02g062340.3 | Fructose-bisphosphate aldolase (AHRD V3.3 *** Q9SXX4_NICPA) | ALDO | 1.464330606 | 0.008975504 | 0.965659333 | 2.710332667 |
| Solyc11g072500.2 | Dof zinc finger protein (AHRD V3.3 *** A0A2K3LIE4_TRIPR) | NA | 1.484768825 | 9.30143E-05 | 1.16336 | 3.281964 |
| Solyc08g066705.1 | Gag-pol polyprotein (AHRD V3.3 *** E6Y5Q4_SOLLC) | NA | 1.4980857 | 8.91288E-07 | 2.798965 | 7.962968667 |
| Solyc01g014560.4 | G-type lectin S-receptor-like serine/threonine-protein kinase (AHRD V3.3 *** A0A2K3PIJ6_TRIPR) | NA | 1.513285181 | 2.19056E-07 | 2.580202667 | 7.382219667 |
| Solyc10g080100.3 | Villin (AHRD V3.3 *** A0A2P5EN25_TREOI) | NA | 1.517744205 | 0.025648474 | 0.900617667 | 2.581321 |
| Solyc10g018120.2 | Neuronal PAS domain protein (AHRD V3.3 *** Q6DR18_ARATH) | NA | 1.519425706 | 0.015066589 | 2.043850667 | 5.863100667 |
| Solyc05g051850.3 | putative myo-inositol-1-phosphatase | INO1 | 1.520125605 | 9.41021E-05 | 4.808015 | 14.02114467 |
| Solyc10g081170.2 | Calmodulin 2 | CALM | 1.520309026 | 2.31682E-09 | 468.158183 | 1359.295125 |
| Solyc01g098490.3 | Sugar facilitator protein 1 | ERD6 | 1.520310112 | 0.026224835 | 2.221740667 | 6.454505667 |

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| Solyc10g005200.3 | galactan beta-1,4-galactosyltransferase GALS3 (AHRD V3.3 *** A0A2I4EYQ4_9ROSI) | GALS | 1.520431618 | 8.33087E-05 | 0.584117667 | 1.713278667 |
| Solyc09g056360.3 | Cytochrome b561 and DOMON domain-containing protein (AHRD V3.3 *** A0A1U8E5P6_CAPAN) | NA | 1.526900301 | 2.91574E-06 | 5.089383 | 14.943134 |
| Solyc04g081910.4 | Calcium-dependent protein kinase (AHRD V3.3 *** Q8RW36_SOLLC) | CPK | 1.527711452 | 4.23244E-07 | 7.950364 | 23.22472133 |
| Solyc11g011300.2 | Rhamnogalacturonate lyase (AHRD V3.3 *** A0A200QXQ6_9MAGN) | RGL4 | 1.528647553 | 0.000865751 | 0.507172667 | 1.492855 |
| Solyc03g007230.4 | Protein phosphatase 2C (AHRD V3.3 *** A0A2U1KYU0_ARTAN) | PP2C | 1.533999661 | 0.042523259 | 2.161223 | 6.138973667 |
| Solyc02g088630.4 | Hexosyltransferase (AHRD V3.3 *** A0A1U8FQ34_CAPAN) | GAUT12S | 1.539300083 | 0.04764847 | 6.471503 | 19.235786 |
| Solyc02g091250.1 | Mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** Q9ZU37_ARATH) | NA | 1.543569536 | 0.009973667 | 16.71300267 | 50.001233 |
| Solyc07g065320.4 | ABC transporter C family member 3 (AHRD V3.3 *** A0A2G2WFH5_CAPBA) | NA | 1.546187614 | 0.004029323 | 0.410306667 | 1.235491333 |
| Solyc12g008430.3 | Malic enzyme (AHRD V3.3 *** A0A2G3BMK9_CAPCH) | MAEB | 1.551226862 | 7.67577E-06 | 3.267355333 | 9.585785333 |
| Solyc04g079460.1 | Serpin-ZX (AHRD V3.3 *** A0A2G3CQ68_CAPCH) | SERPINB | 1.554458828 | 0.038130377 | 2.171127667 | 6.543814333 |
| Solyc11g012360.2 | Tonoplast dicarboxylate transporter (AHRD V3.3 *** A0A2G3AZI6_CAPCH) | SLC13A2_3_5 | 1.555907726 | 0.003447039 | 1.541312667 | 4.640798 |
| Solyc01g112120.4 | Flavin-containing monooxygenase (AHRD V3.3 *** A0A2G2XYN9_CAPAN) | FMO | 1.556542391 | 0.002525551 | 12.74175 | 36.80251767 |
| Solyc10g007690.3 | Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** A0A0F7H033_EROTE) | LHCA3 | 1.563199269 | 4.76279E-09 | 1.514855667 | 4.513352333 |
| Solyc09g092380.3 | S-adenosyl-l-homocysteine hydrolase | AHCY | 1.564325887 | 5.32159E-09 | 945.7087607 | 2791.413493 |
| Solyc09g059670.4 | Alpha/beta hydrolase family protein (AHRD V3.3 *** Q8RX69_ARATH) | NA | 1.567606339 | 8.18985E-06 | 0.534124333 | 1.619288333 |
| Solyc11g020960.2 | Proteinase inhibitor type-2 (AHRD V3.3 *** A0A2G3AT14_CAPCH) | NA | 1.599475719 | 0.010130083 | 1.272446 | 3.870154 |
| Solyc08g007850.1 | Unknown protein | NA | 1.607168183 | 2.8955E-05 | 96.050044 | 292.5111543 |
| Solyc08g016720.1 | 9-cis-epoxycarotenoid dioxygenase2 | NCED | 1.622553653 | 1.71671E-05 | 0.865728333 | 2.699494667 |
| Solyc04g007070.3 | Disease resistance protein (AHRD V3.3 *** A0A2U1N8H9_ARTAN) | NA | 1.624765312 | 0.026007282 | 1.046319 | 3.299187667 |
| Solyc03g071590.3 | chloroplast malate dehydrogenase | malate dehydrogenase (NADP+) | 1.647757209 | 2.13962E-07 | 2.219003333 | 7.013276333 |
| Solyc05g005940.3 | Protein NRT1/ PTR FAMILY 1.2 (AHRD V3.3 *** A0A1J3DU78_NOCCA) | SLC15A3_4 | 1.648004065 | 0.001458266 | 0.278486 | 0.883300333 |
| Solyc09g008370.1 | Major facilitator superfamily (AHRD V3.3 *** A0A2U1PF99_ARTAN) | NA | 1.654998558 | 0.000444722 | 2.544584 | 7.993141333 |
| Solyc12g099430.2 | Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A2U1MWY4_ARTAN) | NA | 1.655050551 | 1.06508E-07 | 4.584426333 | 14.68212533 |
| Solyc09g091830.4 | plastid transcriptionally active 5 (AHRD V3.3 *** AT4G13670.1) | PTAC5 | 1.655183959 | 5.38759E-09 | 2.739577333 | 8.656024 |
| Solyc07g049150.2 | Dicer-like 3 (AHRD V3.3 *-* B3SRQ0_PHYPA) | NA | 1.668067847 | 0.000221348 | 15.09060733 | 48.89933867 |
| Solyc11g069570.2 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** A0A2G2YHS4_CAPAN) | LOG | 1.672186323 | 0.018231529 | 1.614707 | 5.247545333 |
| Solyc09g065110.4 | non-structural protein (AHRD V3.3 *** AT1G03180.5) | NA | 1.67529646 | 3.3907E-06 | 0.749582333 | 2.426534 |
| Solyc08g082440.3 | UDP-glucose 4-epimerase (AHRD V3.3 *** Q6XZA0_SOLTU) | GALE | 1.675388259 | 2.09566E-05 | 4.013610333 | 12.773686 |

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| Solyc02g085170.4 | Sugar facilitator protein 10 | ERD6 | 1.680852292 | 0.014435075 | 0.481824333 | 1.547917333 |
| Solyc01g111430.2 | Pentatricopeptide repeat (AHRD V3.3 *** A0A200RA79_9MAGN) | NA | 1.692638393 | 9.30839E-06 | 3.872531333 | 12.76204133 |
| Solyc10g005030.4 | Two-component response regulator-like APRR5 (AHRD V3.3 *** A0A1U8EDA4_CAPAN) | PRR5 | 1.703284301 | 0.004068961 | 1.25785 | 4.21404 |
| Solyc04g073980.3 | Pumilio 7 (AHRD V3.3 *-* A0A1P8AT22_ARATH) | NA | 1.708113537 | 0.011343954 | 0.836407 | 2.793352333 |
| Solyc02g078010.4 | transmembrane protein (AHRD V3.3 *** AT1G28250.1) | NA | 1.738567009 | 4.51234E-05 | 3.135512667 | 10.655657 |
| Solyc07g045140.4 | transmembrane protein (AHRD V3.3 *** AT4G12680.1) | NA | 1.749791445 | 5.16131E-05 | 7.248284 | 24.27328 |
| Solyc01g007100.3 | Digalactosyldiacylglycerol synthase 1, chloroplastic (AHRD V3.3 *** A0A1U8EIN3_CAPAN) | DGD | 1.758928146 | 0.002181557 | 1.295132 | 4.389711 |
| Solyc02g083850.3 | Calcium-dependent kinase (AHRD V3.3 *** Q5D875_MEDTR) | CPK | 1.759985308 | 0.003726148 | 0.722868 | 2.504662 |
| Solyc04g071150.3 | Cytochrome P450 (AHRD V3.3 *** A0A2U1NTV8_ARTAN) | NA | 1.770935013 | 3.15034E-05 | 24.32483467 | 83.75300067 |
| Solyc07g017220.3 | DUF581 domain-containing protein (AHRD V3.3 *** A0A1Q3AVJ7_CEPFO) | NA | 1.778280546 | 5.0384E-06 | 1.698382667 | 5.838809667 |
| Solyc08g076970.3 | Acetylornithine deacetylase (AHRD V3.3 *** A0A2G2XLB1_CAPBA) | ARGE | 1.799026674 | 5.9965E-15 | 31.12026 | 108.1704483 |
| Solyc06g068960.1 | Calcium-binding allergen Ole e 8 (AHRD V3.3 *** A0A2G2WLM3_CAPBA) | CML | 1.800762892 | 0.007809773 | 1.56866 | 5.617576 |
| Solyc04g081290.3 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** A0A2G2X1Q5_CAPBA) | LOG | 1.821396268 | 0.005563916 | 1.732587 | 6.227678667 |
| Solyc04g076340.3 | hypothetical protein (AHRD V3.3 *-* AT4G38060.4) | NA | 1.838979997 | 0.001687989 | 0.977088333 | 3.470432667 |
| Solyc12g097000.2 | Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *-* A0A2U1MRL7_ARTAN) | NA | 1.84193521 | 0.000308752 | 4.936516333 | 18.018683 |
| Solyc04g015520.3 | Remorin (AHRD V3.3 *** A0A200Q6K8_9MAGN) | NA | 1.842212433 | 0.000125509 | 2.408736 | 8.631145 |
| Solyc10g076550.1 | Wall-associated receptor kinase 1 (AHRD V3.3 *-* A0A2G2Y6I2_CAPAN) | NA | 1.842798446 | 0.001735441 | 0.668723667 | 2.441712667 |
| Solyc04g079450.4 | Serpin-ZX (AHRD V3.3 *** A0A2G2ZRU3_CAPAN) | SERPINB | 1.855338049 | 0.005307488 | 1.648673333 | 6.117998 |
| Solyc01g106700.3 | MADS-box transcription factor 23 (AHRD V3.3 *** A0A2G2Y5S9_CAPAN) | NA | 1.865218445 | 0.040500265 | 2.948821333 | 10.91439967 |
| Solyc02g081190.4 | 1-aminocyclopropane-1-carboxylate oxidase 4 | aminocyclopropanecarboxylate oxidase | 1.865619673 | 0.00012452 | 10.430069 | 39.14799167 |
| Solyc09g010970.4 | Carbonic anhydrase (AHRD V3.3 *** A0A2G3BK77_CAPCH) | CYNT | 1.879931797 | 0.001069012 | 2.717172667 | 10.04599667 |
| Solyc03g005760.1 | Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** A0A2G2W7Q4_CAPBA) | LHCB1 | 1.887234047 | 0.003960482 | 6.667594 | 25.46312333 |
| Solyc02g081030.4 | ERD (Early-responsive to dehydration stress) family protein (AHRD V3.3 *-* A0A2U1NFB6_ARTAN) | TMEM63 | 1.8894851 | 8.78696E-14 | 9.278308333 | 34.78257367 |
| Solyc06g076040.3 | RING-type E3 ubiquitin transferase (AHRD V3.3 *** A0A2G2WNK7_CAPBA) | NA | 1.903424783 | 9.88341E-05 | 10.66039167 | 40.70031533 |
| Solyc02g081970.4 | Vacuolar-sorting receptor 1 (AHRD V3.3 *** A0A1U8FV38_CAPAN) | NA | 1.916733849 | 0.006811815 | 5.732779667 | 21.697716 |
| Solyc06g009130.3 | Magnesium/proton exchanger family member (AHRD V3.3 *** K4C3U3_SOLLC) | MHX | 1.933081681 | 0.001553221 | 1.243216333 | 4.753560667 |
| Solyc01g099840.3 | Dormancy/auxin associated protein (AHRD V3.3 *** A0A2K3MXX9_TRIPR) | NA | 1.944984946 | 0.000188988 | 20.314464 | 78.32843033 |
| Solyc12g098580.1 | Glycosyltransferase (AHRD V3.3 *** A0A2Z4BSF1_9APIA) | NA | 1.952625162 | 0.001600179 | 0.549173667 | 2.197500667 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Solyc06g007440.4 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G3C4Q5_CAPCH) | NA | 1.987963494 | 0.029827297 | 0.984245333 | 4.023251333 |
| Solyc12g062200.1 | Unknown protein | NA | 2.004847704 | 0.0001485 | 3.333056667 | 13.50067067 |
| Solyc07g065190.4 | Heavy metal-associated isoprenylated plant protein (AHRD V3.3 *-* A0A2R6RV38_ACTCH) | NA | 2.020661625 | 0.000156058 | 1.766342667 | 7.183254333 |
| Solyc12g006590.3 | Zinc finger protein (AHRD V3.3 *** A0A200PQI4_9MAGN) | NA | 2.05800135 | 0.000179157 | 1.697745667 | 7.163203333 |
| Solyc01g079150.4 | HCO3-transporter family (AHRD V3.3 *** A0A2U1KUW6_ARTAN) | BOR | 2.075569699 | 2.66593E-14 | 0.579973333 | 2.492035667 |
| Solyc09g064610.3 | Disease resistance protein RGA2 (AHRD V3.3 *** A0A1U8GK21_CAPAN) | NA | 2.083791026 | 1.32666E-14 | 0.773072 | 3.302090333 |
| Solyc02g082910.4 | Acyl-CoA synthetase (AHRD V3.3 *** A0A1Y0KWS9_9PSED) | NA | 2.093924102 | 0.003046211 | 0.484302667 | 2.151386333 |
| Solyc10g084560.3 | Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC) | NA | 2.121796373 | 0.000328365 | 1.140885667 | 5.017989667 |
| Solyc09g057650.3 | 40S ribosomal protein S8 (AHRD V3.3 *** A0A1J7GEB5_LUPAN) | RP-S8E | 2.137402615 | 1.95074E-32 | 29.76826633 | 132.3594337 |
| Solyc02g088090.1 | Calmodulin-like protein 45 (AHRD V3.3 *** A0A2P0QD45_CAMSI) | CALM | 2.154357067 | 0.00031742 | 40.92471167 | 182.574219 |
| Solyc04g150102.1 | Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN) | NA | 2.170130769 | 0.000302756 | 65.29974633 | 288.774124 |
| Solyc10g078440.2 | Sigma factor binding protein 1, chloroplastic (AHRD V3.3 *** A0A2G3BI49_CAPCH) | NA | 2.172329617 | 0.00067447 | 18.20668067 | 82.303248 |
| Solyc04g079470.3 | Serpin-ZX (AHRD V3.3 *** A0A2G2ZRV1_CAPAN) | SERPINB | 2.205769159 | 0.00128893 | 2.807640333 | 13.278697 |
| Solyc06g036120.3 | Unknown protein | NA | 2.210105319 | 0.001979836 | 0.932708 | 4.336770333 |
| Solyc06g084770.2 | cytochrome P450 CYP72A219 (AHRD V3.3 --* XP_004244272.1) | NA | 2.24988781 | 1.26594E-08 | 2.952679667 | 14.03889033 |
| Solyc05g011890.1 | Sulfotransferase (AHRD V3.3 *** A0A2G3B6Y2_CAPCH) | NA | 2.251877914 | 0.013759446 | 25.027981 | 121.1354117 |
| Solyc01g099140.4 | Vacuole membrane protein KMS1 (AHRD V3.3 *** A0A2G2Y0A8_CAPAN) | VMP1 | 2.266485134 | 4.11366E-13 | 0.410584 | 2.006202667 |
| Solyc01g100920.3 | WAT1-related protein (AHRD V3.3 *** K4B1C3_SOLLC) | NA | 2.278103137 | 3.61454E-09 | 0.409101 | 2.017651667 |
| Solyc01g111270.3 | Armadillo repeat only 1 (AHRD V3.3 *** Q9SW41_ARATH) | NA | 2.291301228 | 0.002103781 | 0.353027667 | 1.781739 |
| Solyc10g006740.4 | Calcium-binding protein PBP1 (AHRD V3.3 *** A0A2G2XZK3_CAPAN) | KIC | 2.316161579 | 9.10342E-11 | 2.601852667 | 13.12719167 |
| Solyc03g123830.4 | D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** A0A1U8G334_CAPAN) | SERA | 2.345899381 | 0.002737417 | 2.343594333 | 12.08381333 |
| Solyc08g081520.1 | Plant/F1M20-13 protein (AHRD V3.3 *** A0A072TUL8_MEDTR) | NA | 2.365314464 | 0.00034474 | 0.511638667 | 2.702539 |
| Solyc09g031750.4 | Phosphate transporter (AHRD V3.3 *** A0A2H4H6T0_MALDO) | SLC17A | 2.408117117 | 1.8082E-25 | 1.666207333 | 8.862398667 |
| Solyc03g034140.4 | NAD(P)H dehydrogenase (Quinone) (AHRD V3.3 *** A0A2G2XZH4_CAPAN) | WRBA | 2.45300261 | 6.31063E-10 | 3.647466667 | 20.25137067 |
| Solyc06g009830.3 | Fumarate hydratase class II (AHRD V3.3 *-* A0A318TWL7_9RHOB) | FUMC | 2.490256046 | 2.74362E-12 | 0.988952 | 5.673404333 |
| Solyc02g092490.3 | Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** A0A1P8B3D5_ARATH) | NA | 2.565477274 | 1.61275E-05 | 1.612270333 | 9.752190667 |
| Solyc09g018170.4 | MAP kinase kinase kinase 70 | WNK | 2.611747201 | 9.41942E-06 | 0.210759667 | 1.303023667 |
| Solyc06g035700.1 | Ethylene-responsive transcription factor (AHRD V3.3 *** A0A2G2WIL9_CAPBA) | NA | 2.662633095 | 7.91831E-06 | 1.035064 | 6.754406 |
| Solyc09g031920.1 | Late embryogenesis abundant protein, LEA-14 (AHRD V3.3 *** A0A2U1NFB4_ARTAN) | NA | 2.673266556 | 1.80112E-17 | 15.94392333 | 103.452408 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Solyc09g061930.4 | Ovary receptor kinase 7 (AHRD V3.3 *** S4WHD2_SOLCH) | NA | 2.863660538 | 1.27104E-21 | 0.810257667 | 5.988775667 |
| Solyc09g064720.3 | endo-1,31,4-beta-D-glucanase-like (AHRD V3.3 *** A0A2I4F2X5_9ROSI) | NA | 2.865866949 | 1.57841E-24 | 15.94848233 | 115.7015127 |
| Solyc02g092820.4 | IAA-amido synthetase 3-4 | GH3 | 2.9423603 | 0.005329273 | 0.179765 | 1.413703 |
| Solyc09g015470.4 | Protein TIC 56, chloroplastic (AHRD V3.3 *** A0A1U8F621_CAPAN) | NA | 2.956598635 | 1.97077E-18 | 0.233791333 | 1.851672 |
| Solyc08g076880.3 | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (AHRD V3.3 *-* A0A2G2XLC0_CAPBA) | NA | 2.965522455 | 4.65555E-12 | 5.509447 | 42.95117033 |
| Solyc05g015370.3 | DNA-binding HORMA (AHRD V3.3 *-* A0A200QG98_9MAGN) | HORMAD | 2.978420417 | 0.000359922 | 1.296739333 | 10.38111 |
| Solyc12g056850.2 | Chaperone protein DnaJ (AHRD V3.3 *** A0A1J3GRV8_NOCCA) | NA | 2.98177237 | 0.00027533 | 0.735064 | 5.783708333 |
| Solyc01g008710.5.1 | mannan endo-1,4-beta-mannosidase | MAN | 2.984505707 | 2.2164E-29 | 60.65093733 | 482.160909 |
| Solyc05g015380.2 | DNA-binding HORMA (AHRD V3.3 *-* A0A200R484_9MAGN) | NA | 3.02392396 | 9.68689E-05 | 1.774631667 | 14.61229833 |
| Solyc04g007780.3 | Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN) | NA | 3.07842858 | 4.60859E-11 | 0.901675 | 7.645723667 |
| Solyc06g035940.3 | Homeobox-leucine zipper protein ROC5 (AHRD V3.3 *** A0A2G2X6G6_CAPBA) | HD-ZIP | 3.113332821 | 4.37382E-26 | 1.883360333 | 16.474609 |
| Solyc05g015360.2 | HORMA domain-containing protein (AHRD V3.3 *-* A0A2K3NRQ7_TRIPR) | NA | 3.1818215 | 2.7677E-08 | 1.340309 | 12.38337633 |
| Solyc01g099660.4 | Heat shock protein 70 family (AHRD V3.3 *** A0A200QCN5_9MAGN) | HSPA5 | 3.238730693 | 0.000444044 | 1.234400667 | 11.71843433 |
| Solyc01g095140.4 | Desiccation protectant protein Lea14-like protein (AHRD V3.3 *** A0A2G3BT76_CAPCH) | NA | 3.288284657 | 2.26478E-08 | 6.310107667 | 62.663518 |
| Solyc09g008170.3 | Small auxin up-regulated RNA69 | SAUR | 3.439768949 | 1.68104E-07 | 9.302483667 | 99.670011 |
| Solyc09g064530.3 | auxin-regulated IAA12 | IAA | 3.506157937 | 7.85268E-16 | 0.593806 | 6.829434 |
| Solyc08g081620.4 | LEU13054 endo-1,4-beta-glucanase precursor | NA | 3.519030078 | 8.09372E-15 | 3.534052 | 39.976384 |
| Solyc09g063140.4 | protein LOW PSII ACCUMULATION 1, chloroplastic (AHRD V3.3 *** A0A2I4GK27_9ROSI) | NA | 3.55947578 | 2.64984E-14 | 0.519621667 | 6.156164333 |
| Solyc06g071580.3 | ATPase, histidine kinase, DNA gyrase B-, and HSP90-like domain containing protein, expressed (AHRD V3.3 *** Q33AG5_ORYSJ) | NA | 3.666495528 | 1.8082E-25 | 1.137635667 | 14.62260333 |
| Solyc06g059720.3 | Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A2I4GZ93_9ROSI) | FAB2 | 4.245106555 | 4.24226E-12 | 2.520262667 | 47.49880333 |
| Solyc09g059650.4 | Unknown protein | NA | 4.472668753 | 5.116E-13 | 1.045371667 | 23.43142167 |
| Solyc09g056180.3 | Glutathione S-transferase (AHRD V3.3 *-* A0A200PZB1_9MAGN) | NA | 11.21449977 | 1.94395E-42 | 0 | 7.6019 |
| Solyc09g060215.1 | Unknown protein | NA | 11.39485013 | 3.03662E-56 | 0 | 12.04204567 |
| Solyc09g056200.3 | Unknown protein | NA | 11.53693239 | 6.79542E-62 | 0 | 12.13350833 |
| Solyc09g015490.3 | Phosphoenolpyruvate carboxylase (AHRD V3.3 *-* Q6Q2Z9_SOYBN) | NA | 11.73642082 | 6.13013E-68 | 0 | 3.324280667 |
| Solyc09g055545.1 | Unknown protein | NA | 11.79214123 | 5.55356E-60 | 0 | 3.156361 |
| Solyc01g081250.3 | Glutathione S-transferase (AHRD V3.3 *** A0A200PVK3_9MAGN) | GST | 11.95470301 | 2.01593E-34 | 0.167494333 | 702.4864707 |
| Solyc09g042780.2 | Unknown protein | NA | 12.01426124 | 1.85376E-64 | 0 | 4.049452333 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| Solyc09g018830.2 | MLO-like protein (AHRD V3.3 *** M1BT43_SOLTU) | MLO | 12.37264069 | 1.26168E-55 | 0 | 4.761563667 |
| Solyc09g018960.4 | Chaperone DnaJ-domain superfamily protein (AHRD V3.3 *-* A0A1P8B6Z5_ARATH) | NA | 12.52477967 | 1.5428E-249 | 0.002028333 | 18.002265 |
| Solyc09g064730.3 | Heavy metal-associated isoprenylated plant protein (AHRD V3.3 *-* A0A2R6P541_ACTCH) | NA | 12.78299209 | 1.37194E-24 | 0 | 14.11778233 |
| Solyc09g016950.3 | Unknown protein | NA | 13.13272978 | 7.11101E-86 | 0 | 4.347948667 |
| Solyc08g077460.3 | SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** Q8LCK5_ARATH) | BOI | 13.6267581 | 1.9559E-238 | 0.003376667 | 71.742686 |

**Table S4. List of GO terms with top significance retrieved from the RNAseq analysis of the AM fruits.**

|  | GO.ID | Term | Annotated | Significant | Expected | classic |
|---|---|---|---|---|---|---|
| O.E. Molecular function | GO:0036094 | small molecule binding | 3924 | 259 | 165.82 | 1.1E-14 |
|  | GO:0043168 | anion binding | 3089 | 215 | 130.53 | 2.3E-14 |
|  | GO:0016491 | oxidoreductase activity | 2396 | 176 | 101.25 | 9.6E-14 |
|  | GO:0003824 | catalytic activity | 13097 | 651 | 553.44 | 2.4E-11 |
|  | GO:0016829 | lyase activity | 701 | 68 | 29.62 | 1.6E-10 |
|  | GO:0043177 | organic acid binding | 154 | 27 | 6.51 | 3.1E-10 |
|  | GO:0043167 | ion binding | 6727 | 371 | 284.26 | 5.6E-10 |
|  | GO:0050661 | NADP binding | 157 | 26 | 6.63 | 2.3E-09 |
|  | GO:0016853 | isomerase activity | 346 | 41 | 14.62 | 2.8E-09 |
|  | GO:0016840 | carbon-nitrogen lyase activity | 42 | 13 | 1.77 | 0.00000001 |
| U.E. Molecular function | GO:0005509 | calcium ion binding | 343 | 23 | 7.55 | 0.0000025 |
|  | GO:0005515 | protein binding | 13199 | 333 | 290.52 | 0.000049 |
|  | GO:0000976 | transcription cis-regulatory region bind... | 764 | 33 | 16.82 | 0.0002 |
|  | GO:0001067 | transcription regulatory region nucleic ... | 769 | 33 | 16.93 | 0.00022 |
|  | GO:0043565 | sequence-specific DNA binding | 1767 | 60 | 38.89 | 0.00053 |
|  | GO:0031418 | L-ascorbic acid binding | 34 | 5 | 0.75 | 0.00083 |
|  | GO:1990837 | sequence-specific double-stranded DNA bi... | 840 | 33 | 18.49 | 0.00103 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  | GO:0043394 | proteoglycan binding | 10 | 3 | 0.22 | 0.00113 |
|  | GO:0042393 | histone binding | 275 | 15 | 6.05 | 0.00122 |
|  | GO:0030246 | carbohydrate binding | 247 | 14 | 5.44 | 0.00122 |

|  | GO.ID | Term | Annotated | Significant | Expected | classic |
|---|---|---|---|---|---|---|
| O.E. Cellular component | GO:0009570 | chloroplast stroma | 1202 | 133 | 52.01 | 6.8E-24 |
|  | GO:0009532 | plastid stroma | 1240 | 133 | 53.65 | 1.2E-22 |
|  | GO:0009507 | chloroplast | 4138 | 299 | 179.04 | 2E-21 |
|  | GO:0009536 | plastid | 4620 | 317 | 199.89 | 2.5E-19 |
|  | GO:0005829 | cytosol | 5948 | 374 | 257.35 | 7.1E-17 |
|  | GO:0071162 | CMG complex | 7 | 7 | 0.3 | 2.8E-10 |
|  | GO:0005737 | cytoplasm | 17679 | 834 | 764.91 | 0.000000039 |
|  | GO:0009941 | chloroplast envelope | 1151 | 89 | 49.8 | 0.000000075 |
|  | GO:0042555 | MCM complex | 11 | 7 | 0.48 | 0.000000079 |
|  | GO:0009526 | plastid envelope | 1648 | 116 | 71.3 | 0.00000012 |
| U.E. Cellular component | GO:0012506 | vesicle membrane | 849 | 38 | 19.41 | 0.00007 |
|  | GO:0030659 | cytoplasmic vesicle membrane | 808 | 36 | 18.47 | 0.00012 |
|  | GO:0016514 | SWI/SNF complex | 26 | 5 | 0.59 | 0.00027 |
|  | GO:0098936 | intrinsic component of postsynaptic memb… | 17 | 4 | 0.39 | 0.00051 |
|  | GO:0099055 | integral component of postsynaptic membr… | 8 | 3 | 0.18 | 0.00061 |
|  | GO:0099503 | secretory vesicle | 475 | 23 | 10.86 | 0.00066 |
|  | GO:0000785 | chromatin | 488 | 23 | 11.16 | 0.00094 |
|  | GO:0099240 | intrinsic component of synaptic membrane | 21 | 4 | 0.48 | 0.00119 |
|  | GO:0001669 | acrosomal vesicle | 36 | 5 | 0.82 | 0.00129 |
|  | GO:0005886 | plasma membrane | 6238 | 173 | 142.6 | 0.0018 |

|  | GO.ID | Term | Annotated | Significant | Expected | classic |
|---|---|---|---|---|---|---|
| O.E. Biological processes | GO:0044281 | small molecule metabolic process | 4042 | 313 | 170.25 | 7.1E-30 |
|  | GO:0019752 | carboxylic acid metabolic process | 2386 | 216 | 100.5 | 2E-28 |
|  | GO:0043436 | oxoacid metabolic process | 2857 | 236 | 120.34 | 1.8E-25 |
|  | GO:0006082 | organic acid metabolic process | 3051 | 245 | 128.51 | 8.9E-25 |
|  | GO:0044283 | small molecule biosynthetic process | 1783 | 158 | 75.1 | 1.3E-19 |
|  | GO:0006520 | cellular amino acid metabolic process | 805 | 93 | 33.91 | 7.8E-19 |
|  | GO:0055086 | nucleobase-containing small molecule met… | 761 | 86 | 32.05 | 6.7E-17 |
|  | GO:0006753 | nucleoside phosphate metabolic process | 626 | 76 | 26.37 | 9.3E-17 |
|  | GO:0032787 | monocarboxylic acid metabolic process | 1560 | 137 | 65.71 | 1.1E-16 |
|  | GO:0009117 | nucleotide metabolic process | 621 | 75 | 26.16 | 2E-16 |
| U.E. Biological processes | GO:0050896 | response to stimulus | 15114 | 391 | 338.67 | 0.00000068 |
|  | GO:0065007 | biological regulation | 13786 | 363 | 308.91 | 0.00000068 |
|  | GO:0006873 | cellular ion homeostasis | 574 | 32 | 12.86 | 0.0000026 |
|  | GO:0030003 | cellular cation homeostasis | 530 | 30 | 11.88 | 0.0000039 |
|  | GO:0055082 | cellular chemical homeostasis | 721 | 36 | 16.16 | 0.0000074 |
|  | GO:0010035 | response to inorganic substance | 3727 | 120 | 83.51 | 0.000017 |
|  | GO:0006875 | cellular metal ion homeostasis | 409 | 24 | 9.16 | 0.00002 |
|  | GO:0050789 | regulation of biological process | 12747 | 332 | 285.63 | 0.000025 |
|  | GO:0055080 | cation homeostasis | 837 | 37 | 18.76 | 0.000075 |
|  | GO:0006911 | phagocytosis, engulfment | 36 | 6 | 0.81 | 0.00014 |

**Table S5. Top 25 genes overexpressed in the AM fruits contributing to the chloroplast and plastid-related GO terms of the cellular component.**

| gene | description | logFC | FDR |
|---|---|---:|---:|
| Solyc09g059020.4 | Quinone-oxidoreductase QR1, chloroplastic (AHRD V3.3 *** QR1_TRIVS) | -9.275 | 7.00E-197 |
| Solyc03g044330.1 | Acetolactate synthase (AHRD V3.3 *** C0L093_TOBAC) | -9.673 | 1.89E-92 |
| Solyc09g059060.1 | Quinone-oxidoreductase QR1, chloroplastic (AHRD V3.3 *-* QR1_TRIVS),Pfam:PF13602 | -12.768 | 4.29E-73 |
| Solyc05g050980.3 | 3-phosphoshikimate 1-carboxyvinyltransferase (AHRD V3.3 *** A0A0M8KSM3_NICAT) | -4.822 | 2.05E-70 |
| Solyc11g066890.1 | Arogenate dehydratase (AHRD V3.3 *** A0A2G3BBC7_CAPCH) | -3.002 | 4.00E-49 |
| Solyc09g059070.3 | Quinone-oxidoreductase chloroplastic-like (AHRD V3.3 *-* A0A2K3P901_TRIPR) | -11.991 | 3.95E-48 |
| Solyc06g075010.4 | 60 kDa chaperonin (AHRD V3.3 *** B2IXD2_NOSP7) | -5.960 | 9.48E-47 |
| Solyc10g084400.2 | Glutathione S-transferase (AHRD V3.3 *** Q76KW1_PEA) | -2.941 | 9.92E-43 |
| Solyc08g067310.1 | Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A2G2W7U9_CAPBA) | -4.071 | 2.74E-38 |
| Solyc04g011390.1 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | -4.686 | 2.17E-37 |
| Solyc01g008920.4 | NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A2U1L7S8_ARTAN) | -2.977 | 1.35E-30 |
| Solyc06g074790.2 | Histone H2B (AHRD V3.3 *** A0A2G3CAQ8_CAPCH) | -3.575 | 5.87E-26 |
| Solyc10g007100.3 | Protein DETOXIFICATION (AHRD V3.3 *** A0A218WWW8_PUNGR) | -3.341 | 1.20E-25 |
| Solyc03g114500.4 | Enolase (AHRD V3.3 *** A0A2G2WR88_CAPBA) | -5.816 | 2.97E-25 |
| Solyc03g025840.3 | Cytochrome b561/ferric reductase transmembrane protein family (AHRD V3.3 *** A0A178UZ09_ARATH) | -2.894 | 1.15E-23 |
| Solyc06g083440.3 | Cytochrome b5 (AHRD V3.3 *** A0A2G3CCB6_CAPCH) | -2.895 | 2.07E-22 |
| Solyc06g073190.3 | fructokinase 2 | -1.687 | 9.22E-22 |
| Solyc10g083360.2 | Calmodulin-binding family protein, putative, expressed (AHRD V3.3 *** Q2QXN6_ORYSJ) | -1.778 | 1.06E-20 |
| Solyc06g005160.4 | cytosolic ascorbate peroxidase 1 | -1.731 | 5.71E-19 |
| Solyc06g005430.1 | Histone H4 (AHRD V3.3 *-* F2E7L1_HORVV) | -1.903 | 8.15E-19 |
| Solyc10g005300.3 | Serine/threonine-protein kinase PBS1 (AHRD V3.3 *** A0A2G2VSF8_CAPBA) | -3.347 | 1.55E-18 |
| Solyc05g053100.3 | Dihydrolipoyl dehydrogenase-like protein (AHRD V3.3 *** A0A2K3PDU3_TRIPR) | -2.126 | 6.86E-18 |
| Solyc09g065180.3 | binding protein precursor AF106660 | -2.061 | 3.65E-17 |
| Solyc11g056680.1 | Leucine-rich repeat receptor-like protein (AHRD V3.3 *** H6V788_MALDO) | -2.784 | 6.79E-17 |
| Solyc04g049350.4 | chorismate synthase 1 precursor | -1.543 | 1.34E-16 |

**Table S6. List of primers used in this work.**

| Name | Sequence | Use |
|---|---|---|
| M13MAY01ALS1aOF | GCGCCGTCTCACTCGAATGGCGGCTGCTGCCTCACC | Cloning |
| M13MAY02ALS1aOR | GCGCCGTCTCATGACACTTGACCTGTAATAGCAACAATCGG | Cloning |
| M13MAY03ALS1bOF | GCGCCGTCTCAGTCAAGGAGGATGATTGGTAC | Cloning |
| M13MAY04ALS1bOR | GCGCCGTCTCAGCCTCAGCTCCTCACTTGATTG | Cloning |
| M13MAY05ALS2OF | GCGCCGTCTCAAGGCGATTTGTGGAGCTTACAGG | Cloning |
| M13MAY06ALS2OR | GCGCCGTCTCACCTCCCAACAGCCGCACCTAT | Cloning |
| M13MAY07ALS3OF | GCGCCGTCTCAGAGGCCGGGTGAGATTGTGG | Cloning/Genotyping |
| M13MAY08ALS3OR | GCGCCGTCTCACTCGAAGCTCAATAGGAACATCTCCCGTCGCC | Cloning |
| M13OCT01_PE8F1 | GCGCCGTCTCACTCGGGAGTCCCTAATGATATTGTTCATG | Cloning |
| M13OCT02_PE8R1 | GCGCCGTCTCACTCGCATTCTTCTTTTGCACTGTGAATGATTAG | Cloning |
| M12MAY03TermE8F1 | GCGCCGTCTCGCTCGGCTTGAATAAGAATAATAATG | Cloning |
| M12MAY04TermE8R1 | GCGCCGTCTCGCTCGAGCGCGTAAATTAGATAAGGAAAAC | Cloning |
| M12ENE24TmtbR1 | GCGCCGTCTCGCTCGAGCGTCGCAAAAACTATATGCTCTC | Genotyping |
| MV18OCT58 qPCR SlAct7 F | CCTCAGCACATTCCAGCAG | RT-qPCR actin |
| MV18OCT59 qPCR SlAct7 R | CCACCAAACTTCTCCATCCC | RT-qPCR actin |
| MV18OCT60 qPCR 3UTRMtb F | cagccatagaaggctaacacc | RT-qPCR cALS |
| MV18OCT61 qPCR SlmutALS R | acactcctgggccatacttg | RT-qPCR cALS |
| MV18OCT62 qPCR SlMyb12 F | tgaagaagcaacaacaatgga | RT-qPCR cMYB |
| MV18OCT63 qPCR 3UTRE8 R | ctcaaacatttgcttcaaattca | RT-qPCR cMYB |
| MV19APR01 qPCR SlMyb12end F2 | catagtaccattgtatcttggcttt | RT-qPCR eMYB |
| MV18OCT65 qPCR SlMyb12end R | tcccacattccaaatataaaacg | RT-qPCR eMYB |
| MV18OCT66 qPCR SlALSend F | gcgatgggagatgttcctatt | RT-qPCR eALS |
| MV18OCT67 qPCR SlALSend R | acaacagccacaacaagcaa | RT-qPCR eALS |

## Methods S1. Absolute quantification of valine, leucine and isoleucine

For amino acid quantification, 100 mg of tomato fruit samples were homogenized with liquid nitrogen and extracted in 1400 µl 100% methanol supplemented with 60 µL internal standard (0.2 mg/mL ribitol). After extraction for 15 min at 70 °C and centrifugation for 10 min at 14,000 rpms, 500 µl of the supernatant were transferred to a new vial. Then 250 µl of $CHCl_3$ and 500 µl of water were added. The mixture was vortexed for 15 s and centrifuged for 15 min at 14,000 rpms. 110 µl aliquots of the aqueous phase were speed-dried for 3 hours. For derivatisation, dry residues were resuspended in 40 µl of 20 mg/ml methoxyamine hydrochloride in pyridine and incubated for 90 min at 37 °C. Then, 70 µL MSTFA (N-methyl-N-[trimethylsilyl]trifluoroacetamide) and 6 µl of a retention time standard mixture (3.7% [w/v] mix of fatty acid methyl esters ranging from 8 to 24C) were added and the samples were incubated for 30 min at 37 °C.

Sample volumes of 2 µl were injected in 1:10 split mode in a 6890 N gas chromatograph (Agilent Technologies Inc. Santa Clara, CA) coupled to a Pegasus4D TOF mass spectrometer (LECO, St. Joseph, MI). Gas chromatography was performed on a BPX35 column (30 m × 0.32 mm × 0.25 µm) (SGE Analytical Science Pty Ltd., Australia) with helium as carrier gas, constant flow 2 mL $min^{-1}$. The liner was set at 250 °C. Oven program was 85 °C for 2 min, 8 °C $min^{-1}$ ramp until 360 °C. Mass spectra were collected at 6.25 spectra $s^{-1}$ in the m/z range 35–900 and ionization energy of 70 eV. Chromatograms and mass spectra were evaluated using the CHROMATOF program (LECO, St. Joseph, MI). For metabolite identification and absolute quantification a standard curve was made with authentic standards.

## Methods S2. Determination of volatile compounds

Volatile compounds were captured by means of headspace solid phase microextraction (HS-SPME) and separated and detected by means of gas chromatography coupled to mass spectrometry (GC/MS). Samples were processed as described in Rambla et al. (2017) with minor modifications. Roughly, 500 mg of frozen tomato powder were introduced in a 15 mL glass vial, the cap closed and incubated at 37 °C for 10 min in a water bath. 500 mL of an EDTA 100 mM, pH 7.5 solution and 1.1 g of CaCl2.2H2O were added, gently mixed and sonicated for 5 min. One mL of the resulting paste was transferred to a 10 mL screw cap headspace vial with silicon/PTFE septum and analyzed within 10 hours. Volatile compounds were extracted from the headspace by first preincubating the vials at 50 °C for 10 min under 500 rpm agitation. A 65 µm PDMS/DVB SPME fiber (SUPELCO) was then introduced in the vial and exposed to the headspace for 20 min, with identical conditions of agitation and temperature. The volatile compounds adsorbed in the fiber were desorbed in the injection port of the gas chromatograph at 250 °C for 1 min in splitless mode. The fiber was then cleaned at 250 °C for an additional 5 min in an SPME Fiber Conditioning Module (CTC Analytics) to prevent cross-contamination between samples. Incubation, extraction, injection and fiber cleaning were performed by means of a CombiPAL autosampler (CTC Analytics). Chromatography was performed on a 6890N gas chromatograph (Agilent) with a DB-5ms (60 m, 0.25 mm, 1.00 µm) capillary column (J&W) with a constant helium flow of 1.2 mL min-1. Oven ramp conditions were: 40 °C for 2 min, 5 °C min-1 ramp until 250 °C and a final hold at 250 °C for 5 min. GC interface and MS source temperatures were 260 °C and 230 °C respectively. Detection was performed in a 5975B mass spectrometer (Agilent) in the 35–300 m/z range at 6.2 scans/s, with 70 eV electron impact ionization. Data were recorded and processed with the Enhanced ChemStation E.02.02 software. Unequivocal identification of volatile compounds was performed by comparison of both mass spectra and retention time with those of pure standards (Sigma). For quantitation, one specific ion was selected for each compound and the corresponding peak from the extracted ion chromatogram was integrated. An admixture reference sample was prepared for each season by mixing thoroughly equal amounts of each sample. A 500 mg aliquot of the admixture was analyzed every six samples and processed as any other sample as part of the injection series. This admixture was used as a reference to normalize for temporal variation and fiber aging.

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### Methods S3. Flavonol absolute quantification

50 mg of frozen tomato grinded tissue were resuspended in 500 µl of 75% acetonitrile with 1 ppm genistein. The homogenate was vortexed, sonicated for 10 min and centrifuged for 5 min at 14,000 rpms. 200 µl of the supernatant were mixed with an equal volume of HCl 2N and incubated at 80 °C for 2 hours. Samples were filtered with a 0.2 µM filter and 1 µl was injected. Three replicates of each genotype were extracted and analysed. Flavonol quantification was performed using a Orbitrap Exploris 120 mass spectrometer coupled with a Vanquish UHPLC System (Thermo Fisher Scientific, Waltham, MA, USA). LC was carried out by reverse-phase ultraperformance liquid chromatography using a Acquity PREMIER BEH C18 UPLC column (1.7 µM particle size, dimensions 2.1 x 150 mm) (Waters Corp., Mildford, MA, USA). The mobile phase consisted 0.1% formic acid in water (phase A), and 0.1% formic acid in acetonitrile (phase B). The solvent gradient program was conditioned as follows: 0.5% solvent B over the first 2 min, 0.5–30% solvent B over 25 min, 30–100% solvent B over 13 min, 2 min at 100% B, return to the initial 0.5% solvent B over 1 min, and conditioning at 0.5% B for 2 minutes. The flow rate was 0.4 mL min$^{-1}$ and the injection volume was 1 µl. The column temperature was set at 40 °C. Ionisation was performed with heated electrospray ionization (H-ESI) in positive and negative mode. Samples were acquired in full scan mode (resolution set at 120000 measured at FWHM). For absolute quantification a standard curve was performed with authentic standards using genistein as internal standard. Data processing was performed with TraceFinder software (Thermo Scientific, Waltham, MA, USA).