**Supplemental Information**

## Title: Transcriptional response to petiole heat girdling in cassava

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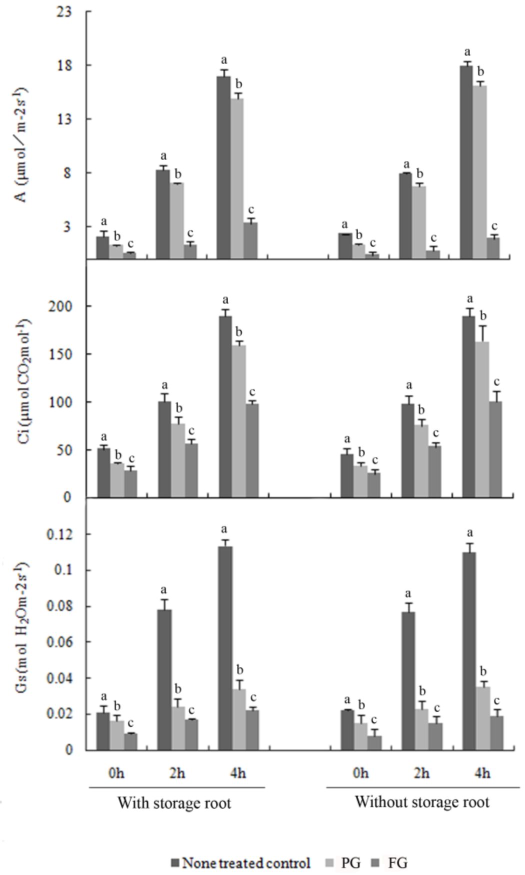
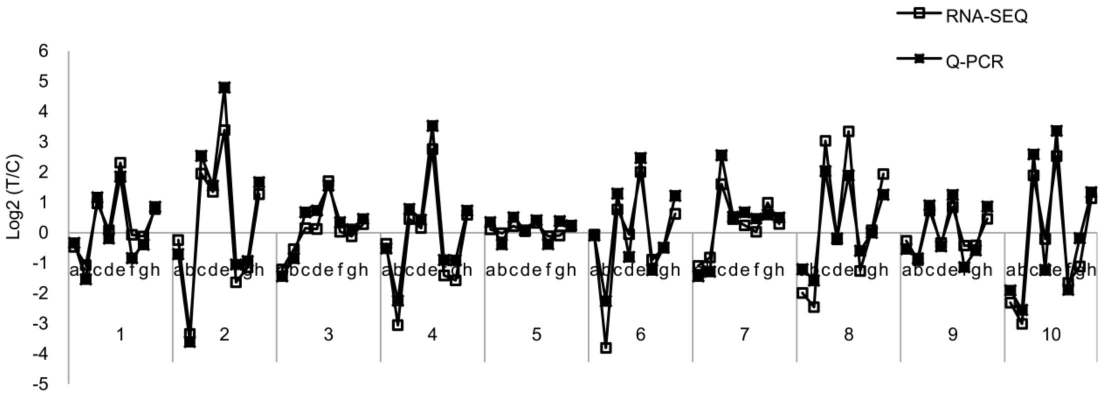
**Supplemental Figure 1| Cassava plant with developing storage root in pot.**



**Supplemental Figure 2| Photosynthetic parameters of control, PG and FG Leaves of cassava plants. Measurements were made at an average ambient relative humidity of 46.6 ± 3.4% and an irradiance of 2000 μmol $m^{-2}$ $s^{-1}$. A: net photosynthesis rates (Pn); Gs: stomata conductance, Ci: intercellular $CO_2$ concentration.**



**Supplemental Figure 3| Verification of microarray results by real-time quantitative RT-PCR. Log$_2$ (treat/control) values for genes (a–k) in the six experimental conditions. Genes: (a) cassava4.1_017330m.g ; (b) cassava4.1_008668m.g; (c) cassava4.1_001840m.g ; (d) cassava4.1_000732m.g ; (e) cassava4.1_005409m.g; (f) cassava4.1_002278m.g ; (g) cassava4.1_004345m.g ; (h) cassava4.1_006138m.g . Experimental conditions (1) 0-h PG leaves, (2) 0-h FG leaves, (3) 2-h PG leaves, (4) 2-h FG leaves, (5) 4-h PG leaves, (6) 4-h FG leaves; conditions 7–10 (left to right) lack storage roots: (7) 0-h PG leaves, (8) 0-h FG leaves, (9) 2-h PG leaves, (10) 2-h FG leaves. Primers are listed in Supplemental Table S1.**

**Supplemental Table S1. Glucose and fructose measurements for control, PG and FG leaves. All leaves were harvested and processed concurrently**

| | | Glucose (mg/g FW) | | | Fructose (mg/g FW) | | |
|---|---|---|---|---|---|---|---|
| | | Control | PG | FG | Control | PG | FG |
| 120day | 0h | 1.80±0.40 | 0.49±0.45 | 1.48±0.16 | 0.51±0.02 | 0.12±0.04 | 0.20±0.01 |
| | 2h | 1.15±0.25 | 0.92±0.06 | 0.35±0.08 | 0.36±0.02 | 0.12±0.01 | 0.02±0.01 |
| | 4h | 0.67±0.14 | 0.43±0.07 | 0.58±0.20 | 0.21±0.01 | 0.09±0.02 | 0.04±0.01 |
| 45 day | 0h | 3.78±0.42 | 2.08±0.16 | 3.00±0.24 | 0.21±0.04 | 0.08±0.02 | 0.41±0.03 |
| | 2h | 3.91±0.38 | 3.47±0.21 | 2.00±0.29 | 0.29±0.04 | 0.19±0.01 | 0.09±0.04 |
| | 4h | 3.73±0.37 | 2.66±0.25 | 3.86±0.34 | 0.19±0.01 | 0.11±0.01 | 0.31±0.03 |

**Supplemental Table S2. Primer sequences used for Real-time PCR .**

| Maize ID | Class | Forward (5'-3') | Reverse (5'-3') |
|---|---|---|---|
| cassava4.1_017330m.g | rubisco | CTCATACCTTCCACCACTCTCA | TGGCAGCTTCCACATTGTC |
| cassava4.1_008668m.g | FBPase | GGAGTGTTTGCCTTCACC | CCACTTCCGTTTGTGAGG |
| cassava4.1_001840m.g | Susy | CATGGCTCCCTCGGAGAT | GTTTGCCAACCTTTGCTACC |
| cassava4.1_000732m.g | SPS | AGTGGGGCGGGTGCTATTGA | CTTCGCTCGCGGGTGTTG |
| cassava4.1_005409m.g | AGPase | CAGAGCCAAGGCAAAGGTCA | CCAGAGGTCATTAGCATGAGA |
| cassava4.1_002278m.g | starch synthase | GTGGAGAATTATTACTGGATGTG | TCCTTGAGCAGCCTTGAC |
| cassava4.1_004345m.g | beta amylase | CATCAGCCAAGGCCATCC | AGGTAACCGTCCCGAAAT |
| cassava4.1_006138m.g | hexokinase | GTAACTTTCGGTCCTCACA | GTAACTTTCGGTCCTCACA |

## Supplemental Table S3. GO term enrichment of DE genes.

| GO.ID | GO_class | Term | Annotated | Significant | Expected | Fisher_pvalue | Group |
|---|---|---|---|---|---|---|---|
| GO:1901607 | BP | alpha-amino acid biosynthetic process | 63 | 20 | 10.48 | 0.00226 | 0FG_0CK |
| GO:1901607 | BP | alpha-amino acid biosynthetic process | 63 | 19 | 9.34 | 0.00142 | 120d_0FG_120d_0CK |
| GO:1901605 | BP | alpha-amino acid metabolic process | 96 | 30 | 15.97 | 0.00028 | 0FG_0CK |
| GO:1901605 | BP | alpha-amino acid metabolic process | 96 | 24 | 11.71 | 0.0004 | 120d_4FG_120d_4CK |
| GO:1901605 | BP | alpha-amino acid metabolic process | 96 | 27 | 14.23 | 0.00055 | 120d_0FG_120d_0CK |
| GO:1901605 | BP | alpha-amino acid metabolic process | 96 | 22 | 11.08 | 0.00114 | 120d_2FG_120d_2CK |
| GO:0042886 | BP | amide transport | 66 | 16 | 3.26 | 8.50E-08 | 120d_0PG_120d_0CK |
| GO:0042886 | BP | amide transport | 66 | 11 | 2.09 | 6.20E-06 | 120d_2PG_120d_2CK |
| GO:0043038 | BP | amino acid activation | 60 | 18 | 9.98 | 0.00712 | 0FG_0CK |
| GO:0043038 | BP | amino acid activation | 60 | 17 | 8.48 | 0.00308 | 2FG_2CK |
| GO:0009073 | BP | aromatic amino acid family biosynthetic ... | 18 | 9 | 2.54 | 0.00032 | 2FG_2CK |
| GO:0009073 | BP | aromatic amino acid family biosynthetic ... | 18 | 8 | 2.2 | 0.00068 | 120d_4FG_120d_4CK |
| GO:0009073 | BP | aromatic amino acid family biosynthetic ... | 18 | 9 | 2.08 | 6.50E-05 | 120d_2FG_120d_2CK |
| GO:0009072 | BP | aromatic amino acid family metabolic pro... | 24 | 10 | 3.39 | 0.00091 | 2FG_2CK |
| GO:0009072 | BP | aromatic amino acid family metabolic pro... | 24 | 10 | 2.93 | 0.00027 | 120d_4FG_120d_4CK |
| GO:0009072 | BP | aromatic amino acid family metabolic pro... | 24 | 10 | 3.56 | 0.00133 | 120d_0FG_120d_0CK |
| GO:0009072 | BP | aromatic amino acid family metabolic pro... | 24 | 10 | 2.77 | 0.00017 | 120d_2FG_120d_2CK |
| GO:0046034 | BP | ATP metabolic process | 51 | 14 | 6.22 | 0.00247 | 120d_4FG_120d_4CK |
| GO:0015986 | BP | ATP synthesis coupled proton transport | 23 | 10 | 2.81 | 0.00018 | 120d_4FG_120d_4CK |
| GO:0009058 | BP | biosynthetic process | 2697 | 518 | 448.52 | 2.50E-05 | 0FG_0CK |
| GO:0009058 | BP | biosynthetic process | 2697 | 430 | 381.01 | 0.00112 | 2FG_2CK |
| GO:0009058 | BP | biosynthetic process | 2697 | 395 | 328.96 | 6.30E-06 | 120d_4FG_120d_4CK |
| GO:0016052 | BP | carbohydrate catabolic process | 89 | 28 | 14.8 | 0.0004 | 0FG_0CK |
| GO:0016052 | BP | carbohydrate catabolic process | 89 | 29 | 12.57 | 7.20E-06 | 2FG_2CK |
| GO:0016052 | BP | carbohydrate catabolic process | 89 | 29 | 10.86 | 3.50E-07 | 120d_4FG_120d_4CK |
| GO:0016052 | BP | carbohydrate catabolic process | 89 | 29 | 13.19 | 1.80E-05 | 120d_0FG_120d_0CK |
| GO:0016052 | BP | carbohydrate catabolic process | 89 | 8 | 2.82 | 0.00711 | 120d_2PG_120d_2CK |
| GO:0016052 | BP | carbohydrate catabolic process | 89 | 30 | 10.27 | 2.70E-08 | 120d_2FG_120d_2CK |
| GO:0005975 | BP | carbohydrate metabolic process | 778 | 40 | 25.21 | 0.00239 | 0PG_0CK |
| GO:0005975 | BP | carbohydrate metabolic process | 778 | 139 | 109.91 | 0.00148 | 2FG_2CK |
| GO:0015977 | BP | carbon fixation | 10 | 6 | 1.66 | 0.0024 | 0FG_0CK |
| GO:0046394 | BP | carboxylic acid biosynthetic process | 194 | 49 | 32.26 | 0.00132 | 0FG_0CK |
| GO:0046394 | BP | carboxylic acid biosynthetic process | 194 | 41 | 27.41 | 0.0047 | 2FG_2CK |
| GO:0046394 | BP | carboxylic acid biosynthetic process | 194 | 44 | 23.66 | 2.80E-05 | 120d_4FG_120d_4CK |
| GO:0046394 | BP | carboxylic acid biosynthetic process | 194 | 55 | 28.75 | 7.60E-07 | 120d_0FG_120d_0CK |
| GO:0046394 | BP | carboxylic acid biosynthetic process | 194 | 44 | 22.39 | 7.00E-06 | 120d_2FG_120d_2CK |
| GO:0019752 | BP | carboxylic acid metabolic process | 361 | 94 | 60.04 | 2.70E-06 | 0FG_0CK |
| GO:0019752 | BP | carboxylic acid metabolic process | 361 | 82 | 51 | 5.40E-06 | 2FG_2CK |
| GO:0019752 | BP | carboxylic acid metabolic process | 361 | 78 | 44.03 | 2.20E-07 | 120d_4FG_120d_4CK |
| GO:0019752 | BP | carboxylic acid metabolic process | 361 | 90 | 53.5 | 2.10E-07 | 120d_0FG_120d_0CK |
| GO:0019752 | BP | carboxylic acid metabolic process | 361 | 71 | 41.67 | 3.70E-06 | 120d_2FG_120d_2CK |

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|---|---|---|---|---|---|---|---|
| GO:0009056 | BP | catabolic process | 355 | 75 | 52.61 | 0.00073 | 120d_0FG_120d_0CK |
| GO:0008652 | BP | cellular amino acid biosynthetic process | 111 | 36 | 18.46 | 3.00E-05 | 0FG_0CK |
| GO:0008652 | BP | cellular amino acid biosynthetic process | 111 | 30 | 15.68 | 0.00025 | 2FG_2CK |
| GO:0008652 | BP | cellular amino acid biosynthetic process | 111 | 28 | 13.54 | 0.00012 | 120d_4FG_120d_4CK |
| GO:0008652 | BP | cellular amino acid biosynthetic process | 111 | 32 | 16.45 | 0.00011 | 120d_0FG_120d_0CK |
| GO:0008652 | BP | cellular amino acid biosynthetic process | 111 | 24 | 12.81 | 0.00165 | 120d_2FG_120d_2CK |
| GO:0006520 | BP | cellular amino acid metabolic process | 233 | 69 | 38.75 | 4.50E-07 | 0FG_0CK |
| GO:0006520 | BP | cellular amino acid metabolic process | 233 | 60 | 32.92 | 1.60E-06 | 2FG_2CK |
| GO:0006520 | BP | cellular amino acid metabolic process | 233 | 47 | 28.42 | 0.00031 | 120d_4FG_120d_4CK |
| GO:0006520 | BP | cellular amino acid metabolic process | 233 | 57 | 34.53 | 6.20E-05 | 120d_0FG_120d_0CK |
| GO:0006520 | BP | cellular amino acid metabolic process | 233 | 40 | 26.89 | 0.00637 | 120d_2FG_120d_2CK |
| GO:0044249 | BP | cellular biosynthetic process | 2498 | 460 | 415.42 | 0.00376 | 0FG_0CK |
| GO:0044249 | BP | cellular biosynthetic process | 2498 | 353 | 304.69 | 0.00052 | 120d_4FG_120d_4CK |
| GO:0044262 | BP | cellular carbohydrate metabolic process | 152 | 13 | 4.93 | 0.00132 | 0PG_0CK |
| GO:0044262 | BP | cellular carbohydrate metabolic process | 152 | 11 | 4.81 | 0.00894 | 120d_2PG_120d_2CK |
| GO:0044255 | BP | cellular lipid metabolic process | 210 | 39 | 24.24 | 0.00172 | 120d_2FG_120d_2CK |
| GO:0044264 | BP | cellular polysaccharide metabolic proces... | 91 | 8 | 2.95 | 0.00923 | 0PG_0CK |
| GO:0043623 | BP | cellular protein complex assembly | 40 | 6 | 1.3 | 0.00168 | 0PG_0CK |
| GO:0006732 | BP | coenzyme metabolic process | 74 | 7 | 2.34 | 0.0088 | 120d_2PG_120d_2CK |
| GO:0051188 | BP | cofactor biosynthetic process | 62 | 19 | 9.19 | 0.00115 | 120d_0FG_120d_0CK |
| GO:0051186 | BP | cofactor metabolic process | 92 | 29 | 15.3 | 0.0003 | 0FG_0CK |
| GO:0051186 | BP | cofactor metabolic process | 92 | 5 | 1.27 | 0.0089 | 2PG_2CK |
| GO:0051186 | BP | cofactor metabolic process | 92 | 25 | 13 | 0.00074 | 2FG_2CK |
| GO:0051186 | BP | cofactor metabolic process | 92 | 32 | 13.63 | 1.40E-06 | 120d_0FG_120d_0CK |
| GO:0051186 | BP | cofactor metabolic process | 92 | 8 | 2.91 | 0.00863 | 120d_2PG_120d_2CK |
| GO:0005984 | BP | disaccharide metabolic process | 37 | 13 | 6.15 | 0.00493 | 0FG_0CK |
| GO:0005984 | BP | disaccharide metabolic process | 37 | 12 | 5.23 | 0.00367 | 2FG_2CK |
| GO:0005984 | BP | disaccharide metabolic process | 37 | 6 | 1.83 | 0.00884 | 120d_0PG_120d_0CK |
| GO:0015985 | BP | energy coupled proton transport, down el... | 23 | 10 | 2.81 | 0.00018 | 120d_4FG_120d_4CK |
| GO:0006633 | BP | fatty acid biosynthetic process | 76 | 22 | 11.26 | 0.00114 | 120d_0FG_120d_0CK |
| GO:0006633 | BP | fatty acid biosynthetic process | 76 | 20 | 8.77 | 0.00029 | 120d_2FG_120d_2CK |
| GO:0006631 | BP | fatty acid metabolic process | 91 | 8 | 2.95 | 0.00923 | 0PG_0CK |
| GO:0006631 | BP | fatty acid metabolic process | 91 | 27 | 13.49 | 0.00021 | 120d_0FG_120d_0CK |
| GO:0006631 | BP | fatty acid metabolic process | 91 | 25 | 10.5 | 2.40E-05 | 120d_2FG_120d_2CK |
| GO:0006091 | BP | generation of precursor metabolites and ... | 99 | 35 | 16.46 | 4.60E-06 | 0FG_0CK |
| GO:0006091 | BP | generation of precursor metabolites and ... | 99 | 36 | 13.99 | 2.50E-08 | 2FG_2CK |
| GO:0006091 | BP | generation of precursor metabolites and ... | 99 | 32 | 12.08 | 1.10E-07 | 120d_4FG_120d_4CK |
| GO:0006091 | BP | generation of precursor metabolites and ... | 99 | 29 | 14.67 | 0.00016 | 120d_0FG_120d_0CK |
| GO:0006091 | BP | generation of precursor metabolites and ... | 99 | 35 | 11.43 | 4.30E-10 | 120d_2FG_120d_2CK |
| GO:0006007 | BP | glucose catabolic process | 76 | 25 | 12.64 | 0.00037 | 0FG_0CK |
| GO:0006007 | BP | glucose catabolic process | 76 | 26 | 10.74 | 7.90E-06 | 2FG_2CK |
| GO:0006007 | BP | glucose catabolic process | 76 | 27 | 9.27 | 1.20E-07 | 120d_4FG_120d_4CK |
| GO:0006007 | BP | glucose catabolic process | 76 | 23 | 11.26 | 0.00045 | 120d_0FG_120d_0CK |
| GO:0006007 | BP | glucose catabolic process | 76 | 25 | 8.77 | 6.50E-07 | 120d_2FG_120d_2CK |

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|---|---|---|---|---|---|---|---|
| GO:0006006 | BP | glucose metabolic process | 86 | 30 | 14.3 | 2.90E-05 | 0FG_0CK |
| GO:0006006 | BP | glucose metabolic process | 86 | 29 | 12.15 | 3.30E-06 | 2FG_2CK |
| GO:0006006 | BP | glucose metabolic process | 86 | 30 | 10.49 | 3.90E-08 | 120d_4FG_120d_4CK |
| GO:0006006 | BP | glucose metabolic process | 86 | 25 | 12.74 | 0.00051 | 120d_0FG_120d_0CK |
| GO:0006006 | BP | glucose metabolic process | 86 | 27 | 9.93 | 6.70E-07 | 120d_2FG_120d_2CK |
| GO:0009084 | BP | glutamine family amino acid biosynthetic... | 12 | 6 | 1.7 | 0.00339 | 2FG_2CK |
| GO:0009084 | BP | glutamine family amino acid biosynthetic... | 12 | 6 | 1.46 | 0.00156 | 120d_4FG_120d_4CK |
| GO:0009064 | BP | glutamine family amino acid metabolic pr... | 21 | 8 | 2.97 | 0.00572 | 2FG_2CK |
| GO:0009064 | BP | glutamine family amino acid metabolic pr... | 21 | 8 | 2.56 | 0.00225 | 120d_4FG_120d_4CK |
| GO:0006096 | BP | glycolysis | 58 | 19 | 9.65 | 0.00192 | 0FG_0CK |
| GO:0006096 | BP | glycolysis | 58 | 19 | 8.19 | 0.00025 | 2FG_2CK |
| GO:0006096 | BP | glycolysis | 58 | 20 | 7.07 | 8.70E-06 | 120d_4FG_120d_4CK |
| GO:0006096 | BP | glycolysis | 58 | 19 | 6.69 | 1.50E-05 | 120d_2FG_120d_2CK |
| GO:0019320 | BP | hexose catabolic process | 76 | 25 | 12.64 | 0.00037 | 0FG_0CK |
| GO:0019320 | BP | hexose catabolic process | 76 | 26 | 10.74 | 7.90E-06 | 2FG_2CK |
| GO:0019320 | BP | hexose catabolic process | 76 | 27 | 9.27 | 1.20E-07 | 120d_4FG_120d_4CK |
| GO:0019320 | BP | hexose catabolic process | 76 | 23 | 11.26 | 0.00045 | 120d_0FG_120d_0CK |
| GO:0019320 | BP | hexose catabolic process | 76 | 25 | 8.77 | 6.50E-07 | 120d_2FG_120d_2CK |
| GO:0019318 | BP | hexose metabolic process | 105 | 34 | 17.46 | 5.20E-05 | 0FG_0CK |
| GO:0019318 | BP | hexose metabolic process | 105 | 35 | 14.83 | 4.60E-07 | 2FG_2CK |
| GO:0019318 | BP | hexose metabolic process | 105 | 32 | 12.81 | 4.90E-07 | 120d_4FG_120d_4CK |
| GO:0019318 | BP | hexose metabolic process | 105 | 29 | 15.56 | 0.00048 | 120d_0FG_120d_0CK |
| GO:0019318 | BP | hexose metabolic process | 105 | 28 | 12.12 | 1.50E-05 | 120d_2FG_120d_2CK |
| GO:1902600 | BP | hydrogen ion transmembrane transport | 60 | 16 | 7.32 | 0.00174 | 120d_4FG_120d_4CK |
| GO:0006818 | BP | hydrogen transport | 71 | 18 | 8.66 | 0.00173 | 120d_4FG_120d_4CK |
| GO:0008299 | BP | isoprenoid biosynthetic process | 33 | 12 | 4.66 | 0.00121 | 2FG_2CK |
| GO:0008299 | BP | isoprenoid biosynthetic process | 33 | 10 | 3.81 | 0.00309 | 120d_2FG_120d_2CK |
| GO:0006720 | BP | isoprenoid metabolic process | 33 | 12 | 4.66 | 0.00121 | 2FG_2CK |
| GO:0006720 | BP | isoprenoid metabolic process | 33 | 10 | 3.81 | 0.00309 | 120d_2FG_120d_2CK |
| GO:0008610 | BP | lipid biosynthetic process | 170 | 42 | 25.19 | 0.00044 | 120d_0FG_120d_0CK |
| GO:0008610 | BP | lipid biosynthetic process | 170 | 37 | 19.62 | 9.30E-05 | 120d_2FG_120d_2CK |
| GO:0006563 | BP | L-serine metabolic process | 17 | 11 | 2.83 | 1.20E-05 | 0FG_0CK |
| GO:0006563 | BP | L-serine metabolic process | 17 | 7 | 2.4 | 0.00589 | 2FG_2CK |
| GO:0006563 | BP | L-serine metabolic process | 17 | 5 | 0.84 | 0.00108 | 120d_0PG_120d_0CK |
| GO:0006563 | BP | L-serine metabolic process | 17 | 8 | 1.96 | 0.00029 | 120d_2FG_120d_2CK |
| GO:0008152 | BP | metabolic process | 8536 | 1481 | 1419.56 | 7.10E-05 | 0FG_0CK |
| GO:0008152 | BP | metabolic process | 8536 | 1268 | 1205.89 | 1.80E-05 | 2FG_2CK |
| GO:0008152 | BP | metabolic process | 8536 | 1102 | 1041.17 | 7.90E-06 | 120d_4FG_120d_4CK |
| GO:0008152 | BP | metabolic process | 8536 | 1330 | 1264.94 | 1.10E-05 | 120d_0FG_120d_0CK |
| GO:0008152 | BP | metabolic process | 8536 | 1046 | 985.22 | 4.80E-06 | 120d_2FG_120d_2CK |
| GO:0072330 | BP | monocarboxylic acid biosynthetic process | 83 | 23 | 12.3 | 0.0017 | 120d_0FG_120d_0CK |
| GO:0072330 | BP | monocarboxylic acid biosynthetic process | 83 | 20 | 9.58 | 0.00097 | 120d_2FG_120d_2CK |
| GO:0032787 | BP | monocarboxylic acid metabolic process | 102 | 28 | 15.12 | 0.00067 | 120d_0FG_120d_0CK |
| GO:0032787 | BP | monocarboxylic acid metabolic process | 102 | 25 | 11.77 | 0.00018 | 120d_2FG_120d_2CK |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GO:0046365 | BP | monosaccharide catabolic process | 76 | 25 | 12.64 | 0.00037 | 0FG_0CK |
| GO:0046365 | BP | monosaccharide catabolic process | 76 | 26 | 10.74 | 7.90E-06 | 2FG_2CK |
| GO:0046365 | BP | monosaccharide catabolic process | 76 | 27 | 9.27 | 1.20E-07 | 120d_4FG_120d_4CK |
| GO:0046365 | BP | monosaccharide catabolic process | 76 | 23 | 11.26 | 0.00045 | 120d_0FG_120d_0CK |
| GO:0046365 | BP | monosaccharide catabolic process | 76 | 25 | 8.77 | 6.50E-07 | 120d_2FG_120d_2CK |
| GO:0005996 | BP | monosaccharide metabolic process | 106 | 34 | 17.63 | 6.40E-05 | 0FG_0CK |
| GO:0005996 | BP | monosaccharide metabolic process | 106 | 36 | 14.97 | 1.90E-07 | 2FG_2CK |
| GO:0005996 | BP | monosaccharide metabolic process | 106 | 32 | 12.93 | 6.20E-07 | 120d_4FG_120d_4CK |
| GO:0005996 | BP | monosaccharide metabolic process | 106 | 29 | 15.71 | 0.00057 | 120d_0FG_120d_0CK |
| GO:0005996 | BP | monosaccharide metabolic process | 106 | 28 | 12.23 | 1.80E-05 | 120d_2FG_120d_2CK |
| GO:0043086 | BP | negative regulation of catalytic activit... | 66 | 7 | 2.14 | 0.00533 | 0PG_0CK |
| GO:0044092 | BP | negative regulation of molecular functio... | 66 | 7 | 2.14 | 0.00533 | 0PG_0CK |
| GO:0046496 | BP | nicotinamide nucleotide metabolic proces... | 21 | 8 | 2.97 | 0.00572 | 2FG_2CK |
| GO:0071705 | BP | nitrogen compound transport | 103 | 16 | 5.08 | 4.10E-05 | 120d_0PG_120d_0CK |
| GO:0071705 | BP | nitrogen compound transport | 103 | 11 | 3.26 | 0.00041 | 120d_2PG_120d_2CK |
| GO:0033865 | BP | nucleoside bisphosphate metabolic proces... | 17 | 9 | 2.83 | 0.00065 | 0FG_0CK |
| GO:0006753 | BP | nucleoside phosphate metabolic process | 193 | 14 | 6.25 | 0.00407 | 0PG_0CK |
| GO:0009117 | BP | nucleotide metabolic process | 187 | 14 | 6.06 | 0.00306 | 0PG_0CK |
| GO:0006857 | BP | oligopeptide transport | 66 | 16 | 3.26 | 8.50E-08 | 120d_0PG_120d_0CK |
| GO:0006857 | BP | oligopeptide transport | 66 | 11 | 2.09 | 6.20E-06 | 120d_2PG_120d_2CK |
| GO:0006857 | BP | oligopeptide transport | 66 | 15 | 7.62 | 0.00718 | 120d_2FG_120d_2CK |
| GO:0016053 | BP | organic acid biosynthetic process | 194 | 49 | 32.26 | 0.00132 | 0FG_0CK |
| GO:0016053 | BP | organic acid biosynthetic process | 194 | 41 | 27.41 | 0.0047 | 2FG_2CK |
| GO:0016053 | BP | organic acid biosynthetic process | 194 | 44 | 23.66 | 2.80E-05 | 120d_4FG_120d_4CK |
| GO:0016053 | BP | organic acid biosynthetic process | 194 | 55 | 28.75 | 7.60E-07 | 120d_0FG_120d_0CK |
| GO:0016053 | BP | organic acid biosynthetic process | 194 | 44 | 22.39 | 7.00E-06 | 120d_2FG_120d_2CK |
| GO:0006082 | BP | organic acid metabolic process | 362 | 94 | 60.2 | 3.10E-06 | 0FG_0CK |
| GO:0006082 | BP | organic acid metabolic process | 362 | 83 | 51.14 | 3.20E-06 | 2FG_2CK |
| GO:0006082 | BP | organic acid metabolic process | 362 | 78 | 44.15 | 2.50E-07 | 120d_4FG_120d_4CK |
| GO:0006082 | BP | organic acid metabolic process | 362 | 91 | 53.64 | 1.20E-07 | 120d_0FG_120d_0CK |
| GO:0006082 | BP | organic acid metabolic process | 362 | 72 | 41.78 | 2.10E-06 | 120d_2FG_120d_2CK |
| GO:1901576 | BP | organic substance biosynthetic process | 2535 | 468 | 421.58 | 0.00281 | 0FG_0CK |
| GO:1901576 | BP | organic substance biosynthetic process | 2535 | 360 | 309.2 | 0.0003 | 120d_4FG_120d_4CK |
| GO:1901575 | BP | organic substance catabolic process | 326 | 73 | 48.31 | 0.00014 | 120d_0FG_120d_0CK |
| GO:1901575 | BP | organic substance catabolic process | 326 | 53 | 37.63 | 0.006 | 120d_2FG_120d_2CK |
| GO:1901566 | BP | organonitrogen compound biosynthetic pro... | 279 | 74 | 46.4 | 1.60E-05 | 0FG_0CK |
| GO:1901566 | BP | organonitrogen compound biosynthetic pro... | 279 | 65 | 39.41 | 2.20E-05 | 2FG_2CK |
| GO:1901566 | BP | organonitrogen compound biosynthetic pro... | 279 | 56 | 34.03 | 9.90E-05 | 120d_4FG_120d_4CK |
| GO:1901566 | BP | organonitrogen compound biosynthetic pro... | 279 | 67 | 41.34 | 2.80E-05 | 120d_0FG_120d_0CK |
| GO:1901564 | BP | organonitrogen compound metabolic | 576 | 138 | 95.79 | 2.30E-06 | 0FG_0CK |

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|---|---|---|---|---|---|---|---|
| | | proces... | | | | | |
| GO:1901564 | BP | organonitrogen compound metabolic proces... | 576 | 124 | 81.37 | 4.80E-07 | 2FG_2CK |
| GO:1901564 | BP | organonitrogen compound metabolic proces... | 576 | 98 | 70.26 | 0.00032 | 120d_4FG_120d_4CK |
| GO:1901564 | BP | organonitrogen compound metabolic proces... | 576 | 126 | 85.36 | 2.10E-06 | 120d_0FG_120d_0CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 274 | 223.68 | 6.90E-05 | 0FG_0CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 37 | 18.61 | 2.60E-05 | 2PG_2CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 244 | 190.01 | 7.00E-06 | 2FG_2CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 235 | 164.05 | 1.00E-09 | 120d_4FG_120d_4CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 101 | 66.36 | 7.10E-06 | 120d_0PG_120d_0CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 261 | 199.31 | 5.90E-07 | 120d_0FG_120d_0CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 68 | 42.61 | 5.10E-05 | 120d_2PG_120d_2CK |
| GO:0055114 | BP | oxidation-reduction process | 1345 | 231 | 155.24 | 3.50E-11 | 120d_2FG_120d_2CK |
| GO:0043436 | BP | oxoacid metabolic process | 361 | 94 | 60.04 | 2.70E-06 | 0FG_0CK |
| GO:0043436 | BP | oxoacid metabolic process | 361 | 82 | 51 | 5.40E-06 | 2FG_2CK |
| GO:0043436 | BP | oxoacid metabolic process | 361 | 78 | 44.03 | 2.20E-07 | 120d_4FG_120d_4CK |
| GO:0043436 | BP | oxoacid metabolic process | 361 | 90 | 53.5 | 2.10E-07 | 120d_0FG_120d_0CK |
| GO:0043436 | BP | oxoacid metabolic process | 361 | 71 | 41.67 | 3.70E-06 | 120d_2FG_120d_2CK |
| GO:0015833 | BP | peptide transport | 66 | 16 | 3.26 | 8.50E-08 | 120d_0PG_120d_0CK |
| GO:0015833 | BP | peptide transport | 66 | 11 | 2.09 | 6.20E-06 | 120d_2PG_120d_2CK |
| GO:0015833 | BP | peptide transport | 66 | 15 | 7.62 | 0.00718 | 120d_2FG_120d_2CK |
| GO:0015979 | BP | photosynthesis | 72 | 48 | 11.97 | 2.90E-21 | 0FG_0CK |
| GO:0015979 | BP | photosynthesis | 72 | 6 | 1 | 0.00047 | 2PG_2CK |
| GO:0015979 | BP | photosynthesis | 72 | 51 | 10.17 | 8.20E-28 | 2FG_2CK |
| GO:0015979 | BP | photosynthesis | 72 | 47 | 8.78 | 3.90E-26 | 120d_4FG_120d_4CK |
| GO:0015979 | BP | photosynthesis | 72 | 51 | 10.67 | 8.20E-27 | 120d_0FG_120d_0CK |
| GO:0015979 | BP | photosynthesis | 72 | 48 | 8.31 | 2.20E-28 | 120d_2FG_120d_2CK |
| GO:0009765 | BP | photosynthesis, light harvesting | 12 | 9 | 2 | 1.30E-05 | 0FG_0CK |
| GO:0009765 | BP | photosynthesis, light harvesting | 12 | 9 | 1.7 | 3.20E-06 | 2FG_2CK |
| GO:0009765 | BP | photosynthesis, light harvesting | 12 | 9 | 1.46 | 9.10E-07 | 120d_4FG_120d_4CK |
| GO:0009765 | BP | photosynthesis, light harvesting | 12 | 10 | 1.78 | 2.50E-07 | 120d_0FG_120d_0CK |
| GO:0009765 | BP | photosynthesis, light harvesting | 12 | 10 | 1.39 | 2.20E-08 | 120d_2FG_120d_2CK |
| GO:0019684 | BP | photosynthesis, light reaction | 20 | 12 | 3.33 | 1.50E-05 | 0FG_0CK |
| GO:0019684 | BP | photosynthesis, light reaction | 20 | 13 | 2.83 | 2.50E-07 | 2FG_2CK |
| GO:0019684 | BP | photosynthesis, light reaction | 20 | 11 | 2.44 | 5.00E-06 | 120d_4FG_120d_4CK |
| GO:0019684 | BP | photosynthesis, light reaction | 20 | 12 | 2.96 | 4.30E-06 | 120d_0FG_120d_0CK |
| GO:0019684 | BP | photosynthesis, light reaction | 20 | 12 | 2.31 | 2.80E-07 | 120d_2FG_120d_2CK |
| GO:0046148 | BP | pigment biosynthetic process | 14 | 7 | 2.33 | 0.00403 | 0FG_0CK |
| GO:0046148 | BP | pigment biosynthetic process | 14 | 7 | 1.98 | 0.00153 | 2FG_2CK |
| GO:0046148 | BP | pigment biosynthetic process | 14 | 9 | 1.71 | 6.60E-06 | 120d_4FG_120d_4CK |
| GO:0046148 | BP | pigment biosynthetic process | 14 | 10 | 2.07 | 2.80E-06 | 120d_0FG_120d_0CK |
| GO:0046148 | BP | pigment biosynthetic process | 14 | 7 | 1.62 | 0.00044 | 120d_2FG_120d_2CK |

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|---|---|---|---|---|---|---|---|
| GO:0042440 | BP | pigment metabolic process | 19 | 9 | 3.16 | 0.00179 | 0FG_0CK |
| GO:0042440 | BP | pigment metabolic process | 19 | 9 | 2.68 | 0.00053 | 2FG_2CK |
| GO:0042440 | BP | pigment metabolic process | 19 | 10 | 2.32 | 2.30E-05 | 120d_4FG_120d_4CK |
| GO:0042440 | BP | pigment metabolic process | 19 | 12 | 2.82 | 2.00E-06 | 120d_0FG_120d_0CK |
| GO:0042440 | BP | pigment metabolic process | 19 | 9 | 2.19 | 0.00011 | 120d_2FG_120d_2CK |
| GO:0006779 | BP | porphyrin-containing compound biosynthet... | 11 | 6 | 1.34 | 0.00087 | 120d_4FG_120d_4CK |
| GO:0006779 | BP | porphyrin-containing compound biosynthet... | 11 | 8 | 1.63 | 2.50E-05 | 120d_0FG_120d_0CK |
| GO:0006779 | BP | porphyrin-containing compound biosynthet... | 11 | 5 | 1.27 | 0.00516 | 120d_2FG_120d_2CK |
| GO:0006778 | BP | porphyrin-containing compound metabolic ... | 16 | 7 | 1.95 | 0.00166 | 120d_4FG_120d_4CK |
| GO:0006778 | BP | porphyrin-containing compound metabolic ... | 16 | 10 | 2.37 | 1.70E-05 | 120d_0FG_120d_0CK |
| GO:0006778 | BP | porphyrin-containing compound metabolic ... | 16 | 7 | 1.85 | 0.00119 | 120d_2FG_120d_2CK |
| GO:0006457 | BP | protein folding | 131 | 12 | 4.25 | 0.00111 | 0PG_0CK |
| GO:0051258 | BP | protein polymerization | 33 | 6 | 1.07 | 0.00059 | 0PG_0CK |
| GO:0015992 | BP | proton transport | 71 | 18 | 8.66 | 0.00173 | 120d_4FG_120d_4CK |
| GO:0034032 | BP | purine nucleoside bisphosphate metabolic... | 17 | 9 | 2.83 | 0.00065 | 0FG_0CK |
| GO:0019362 | BP | pyridine nucleotide metabolic process | 21 | 8 | 2.97 | 0.00572 | 2FG_2CK |
| GO:0019362 | BP | pyridine nucleotide metabolic process | 21 | 9 | 3.11 | 0.00183 | 120d_0FG_120d_0CK |
| GO:0072524 | BP | pyridine-containing compound metabolic p... | 27 | 10 | 3.81 | 0.00262 | 2FG_2CK |
| GO:0072524 | BP | pyridine-containing compound metabolic p... | 27 | 11 | 4 | 0.00096 | 120d_0FG_120d_0CK |
| GO:0033875 | BP | ribonucleoside bisphosphate metabolic pr... | 17 | 9 | 2.83 | 0.00065 | 0FG_0CK |
| GO:0009070 | BP | serine family amino acid biosynthetic pr... | 10 | 6 | 1.66 | 0.0024 | 0FG_0CK |
| GO:0009070 | BP | serine family amino acid biosynthetic pr... | 10 | 6 | 1.48 | 0.00129 | 120d_0FG_120d_0CK |
| GO:0009069 | BP | serine family amino acid metabolic proce... | 26 | 14 | 4.32 | 1.60E-05 | 0FG_0CK |
| GO:0009069 | BP | serine family amino acid metabolic proce... | 26 | 6 | 1.28 | 0.00139 | 120d_0PG_120d_0CK |
| GO:0009069 | BP | serine family amino acid metabolic proce... | 26 | 10 | 3 | 0.00038 | 120d_2FG_120d_2CK |
| GO:0044711 | BP | single-organism biosynthetic process | 514 | 106 | 72.61 | 2.40E-05 | 2FG_2CK |
| GO:0044711 | BP | single-organism biosynthetic process | 514 | 92 | 62.69 | 7.80E-05 | 120d_4FG_120d_4CK |
| GO:0044711 | BP | single-organism biosynthetic process | 514 | 114 | 76.17 | 3.30E-06 | 120d_0FG_120d_0CK |
| GO:0044711 | BP | single-organism biosynthetic process | 514 | 92 | 59.33 | 9.10E-06 | 120d_2FG_120d_2CK |
| GO:0044724 | BP | single-organism carbohydrate catabolic p... | 79 | 25 | 13.14 | 0.00072 | 0FG_0CK |
| GO:0044724 | BP | single-organism carbohydrate catabolic p... | 79 | 26 | 11.16 | 1.70E-05 | 2FG_2CK |
| GO:0044724 | BP | single-organism carbohydrate catabolic p... | 79 | 29 | 9.64 | 1.80E-08 | 120d_4FG_120d_4CK |
| GO:0044724 | BP | single-organism carbohydrate catabolic p... | 79 | 25 | 11.71 | 0.00012 | 120d_0FG_120d_0CK |
| GO:0044724 | BP | single-organism carbohydrate catabolic p... | 79 | 8 | 2.5 | 0.00344 | 120d_2PG_120d_2CK |
| GO:0044724 | BP | single-organism carbohydrate catabolic p... | 79 | 27 | 9.12 | 9.50E-08 | 120d_2FG_120d_2CK |
| GO:0044723 | BP | single-organism carbohydrate metabolic p... | 290 | 73 | 40.97 | 3.20E-07 | 2FG_2CK |

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|---|---|---|---|---|---|---|---|
| GO:0044723 | BP | single-organism carbohydrate metabolic p... | 290 | 53 | 33.47 | 0.00043 | 120d_2FG_120d_2CK |
| GO:0044712 | BP | single-organism catabolic process | 168 | 39 | 20.49 | 4.60E-05 | 120d_4FG_120d_4CK |
| GO:0044712 | BP | single-organism catabolic process | 168 | 43 | 24.9 | 0.00017 | 120d_0FG_120d_0CK |
| GO:0044712 | BP | single-organism catabolic process | 168 | 12 | 5.32 | 0.00715 | 120d_2PG_120d_2CK |
| GO:0044712 | BP | single-organism catabolic process | 168 | 34 | 19.39 | 0.00072 | 120d_2FG_120d_2CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 508 | 435.71 | 1.00E-05 | 0FG_0CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 467 | 370.13 | 6.70E-10 | 2FG_2CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 414 | 319.57 | 1.80E-10 | 120d_4FG_120d_4CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 165 | 129.26 | 0.00019 | 120d_0PG_120d_0CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 486 | 388.25 | 9.60E-10 | 120d_0FG_120d_0CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 108 | 82.99 | 0.00113 | 120d_2PG_120d_2CK |
| GO:0044710 | BP | single-organism metabolic process | 2620 | 406 | 302.4 | 1.10E-12 | 120d_2FG_120d_2CK |
| GO:0044699 | BP | single-organism process | 4479 | 694 | 632.75 | 0.00037 | 2FG_2CK |
| GO:0044699 | BP | single-organism process | 4479 | 597 | 546.32 | 0.0015 | 120d_4FG_120d_4CK |
| GO:0044699 | BP | single-organism process | 4479 | 259 | 220.97 | 0.00041 | 120d_0PG_120d_0CK |
| GO:0044699 | BP | single-organism process | 4479 | 739 | 663.74 | 2.40E-05 | 120d_0FG_120d_0CK |
| GO:0044699 | BP | single-organism process | 4479 | 169 | 141.88 | 0.00168 | 120d_2PG_120d_2CK |
| GO:0044699 | BP | single-organism process | 4479 | 581 | 516.96 | 6.10E-05 | 120d_2FG_120d_2CK |
| GO:0044283 | BP | small molecule biosynthetic process | 220 | 53 | 36.59 | 0.00264 | 0FG_0CK |
| GO:0044283 | BP | small molecule biosynthetic process | 220 | 45 | 26.83 | 0.0003 | 120d_4FG_120d_4CK |
| GO:0044283 | BP | small molecule biosynthetic process | 220 | 59 | 32.6 | 2.30E-06 | 120d_0FG_120d_0CK |
| GO:0044283 | BP | small molecule biosynthetic process | 220 | 47 | 25.39 | 1.80E-05 | 120d_2FG_120d_2CK |
| GO:0044282 | BP | small molecule catabolic process | 19 | 5 | 0.6 | 0.00025 | 120d_2PG_120d_2CK |
| GO:0044281 | BP | small molecule metabolic process | 665 | 155 | 110.59 | 3.00E-06 | 0FG_0CK |
| GO:0044281 | BP | small molecule metabolic process | 665 | 138 | 93.95 | 9.60E-07 | 2FG_2CK |
| GO:0044281 | BP | small molecule metabolic process | 665 | 130 | 81.11 | 1.40E-08 | 120d_4FG_120d_4CK |
| GO:0044281 | BP | small molecule metabolic process | 665 | 147 | 98.55 | 1.40E-07 | 120d_0FG_120d_0CK |
| GO:0044281 | BP | small molecule metabolic process | 665 | 111 | 76.75 | 2.80E-05 | 120d_2FG_120d_2CK |
| GO:0006814 | BP | sodium ion transport | 10 | 3 | 0.32 | 0.00342 | 0PG_0CK |
| GO:0006694 | BP | steroid biosynthetic process | 13 | 4 | 0.41 | 0.00056 | 120d_2PG_120d_2CK |
| GO:0008202 | BP | steroid metabolic process | 14 | 4 | 0.44 | 0.00077 | 120d_2PG_120d_2CK |
| GO:0005985 | BP | sucrose metabolic process | 12 | 3 | 0.39 | 0.00597 | 0PG_0CK |
| GO:0005985 | BP | sucrose metabolic process | 12 | 7 | 2 | 0.00127 | 0FG_0CK |
| GO:0005985 | BP | sucrose metabolic process | 12 | 6 | 1.7 | 0.00339 | 2FG_2CK |
| GO:0033014 | BP | tetrapyrrole biosynthetic process | 23 | 11 | 3.41 | 0.00018 | 120d_0FG_120d_0CK |
| GO:0033013 | BP | tetrapyrrole metabolic process | 28 | 11 | 4.66 | 0.00355 | 0FG_0CK |
| GO:0033013 | BP | tetrapyrrole metabolic process | 28 | 13 | 4.15 | 6.70E-05 | 120d_0FG_120d_0CK |
| GO:0033013 | BP | tetrapyrrole metabolic process | 28 | 9 | 3.23 | 0.00316 | 120d_2FG_120d_2CK |
| GO:0006412 | BP | translation | 493 | 178 | 81.99 | 6.90E-27 | 0FG_0CK |
| GO:0006412 | BP | translation | 493 | 141 | 69.65 | 9.40E-18 | 2FG_2CK |
| GO:0006412 | BP | translation | 493 | 150 | 60.13 | 1.90E-28 | 120d_4FG_120d_4CK |
| GO:0006414 | BP | translational elongation | 26 | 13 | 4.32 | 8.70E-05 | 0FG_0CK |
| GO:0006414 | BP | translational elongation | 26 | 11 | 3.17 | 0.00011 | 120d_4FG_120d_4CK |
| GO:0055085 | BP | transmembrane transport | 715 | 50 | 35.27 | 0.00749 | 120d_0PG_120d_0CK |

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|---|---|---|---|---|---|---|---|
| GO:0043039 | BP | tRNA aminoacylation | 60 | 18 | 9.98 | 0.00712 | 0FG_0CK |
| GO:0043039 | BP | tRNA aminoacylation | 60 | 17 | 8.48 | 0.00308 | 2FG_2CK |
| GO:0006418 | BP | tRNA aminoacylation for protein translat... | 57 | 18 | 9.48 | 0.00392 | 0FG_0CK |
| GO:0006418 | BP | tRNA aminoacylation for protein translat... | 57 | 17 | 8.05 | 0.00168 | 2FG_2CK |
| GO:0071944 | CC | cell periphery | 202 | 14 | 5.21 | 0.00061 | 0PG_0CK |
| GO:0071944 | CC | cell periphery | 202 | 13 | 5.74 | 0.0045 | 120d_2PG_120d_2CK |
| GO:0005618 | CC | cell wall | 130 | 12 | 3.36 | 0.00011 | 0PG_0CK |
| GO:0009507 | CC | chloroplast | 23 | 15 | 3.92 | 3.30E-07 | 0FG_0CK |
| GO:0009507 | CC | chloroplast | 23 | 13 | 3.31 | 2.90E-06 | 2FG_2CK |
| GO:0009507 | CC | chloroplast | 23 | 10 | 2.93 | 0.00025 | 120d_4FG_120d_4CK |
| GO:0009507 | CC | chloroplast | 23 | 13 | 3.09 | 1.30E-06 | 120d_0FG_120d_0CK |
| GO:0009507 | CC | chloroplast | 23 | 10 | 2.43 | 5.10E-05 | 120d_2FG_120d_2CK |
| GO:0005737 | CC | cytoplasm | 908 | 254 | 154.71 | 8.30E-21 | 0FG_0CK |
| GO:0005737 | CC | cytoplasm | 908 | 207 | 130.68 | 1.10E-14 | 2FG_2CK |
| GO:0005737 | CC | cytoplasm | 908 | 208 | 115.78 | 4.80E-22 | 120d_4FG_120d_4CK |
| GO:0044444 | CC | cytoplasmic part | 720 | 208 | 122.68 | 2.40E-18 | 0FG_0CK |
| GO:0044444 | CC | cytoplasmic part | 720 | 172 | 103.62 | 6.00E-14 | 2FG_2CK |
| GO:0044444 | CC | cytoplasmic part | 720 | 186 | 91.81 | 4.50E-26 | 120d_4FG_120d_4CK |
| GO:0030312 | CC | external encapsulating structure | 145 | 12 | 3.74 | 0.00031 | 0PG_0CK |
| GO:0030312 | CC | external encapsulating structure | 145 | 10 | 4.12 | 0.0078 | 120d_2PG_120d_2CK |
| GO:0019898 | CC | extrinsic component of membrane | 16 | 11 | 2.73 | 6.30E-06 | 0FG_0CK |
| GO:0019898 | CC | extrinsic component of membrane | 16 | 11 | 2.3 | 1.10E-06 | 2FG_2CK |
| GO:0019898 | CC | extrinsic component of membrane | 16 | 11 | 2.04 | 3.20E-07 | 120d_4FG_120d_4CK |
| GO:0019898 | CC | extrinsic component of membrane | 16 | 14 | 2.15 | 5.00E-11 | 120d_0FG_120d_0CK |
| GO:0019898 | CC | extrinsic component of membrane | 16 | 11 | 1.69 | 4.40E-08 | 120d_2FG_120d_2CK |
| GO:0016021 | CC | integral component of membrane | 837 | 53 | 33.32 | 0.00019 | 120d_0PG_120d_0CK |
| GO:0016021 | CC | integral component of membrane | 837 | 137 | 112.41 | 0.00399 | 120d_0FG_120d_0CK |
| GO:0005622 | CC | intracellular | 2596 | 479 | 442.32 | 0.00197 | 0FG_0CK |
| GO:0043232 | CC | intracellular non-membrane-bounded organ... | 528 | 159 | 89.96 | 1.40E-15 | 0FG_0CK |
| GO:0043232 | CC | intracellular non-membrane-bounded organ... | 528 | 124 | 75.99 | 1.80E-09 | 2FG_2CK |
| GO:0043232 | CC | intracellular non-membrane-bounded organ... | 528 | 139 | 67.33 | 1.10E-19 | 120d_4FG_120d_4CK |
| GO:0043229 | CC | intracellular organelle | 1450 | 281 | 247.06 | 0.00251 | 0FG_0CK |
| GO:0043229 | CC | intracellular organelle | 1450 | 222 | 184.9 | 0.00029 | 120d_4FG_120d_4CK |
| GO:0044424 | CC | intracellular part | 1942 | 397 | 330.89 | 1.00E-07 | 0FG_0CK |
| GO:0044424 | CC | intracellular part | 1942 | 325 | 279.49 | 6.70E-05 | 2FG_2CK |
| GO:0044424 | CC | intracellular part | 1942 | 301 | 247.63 | 1.20E-06 | 120d_4FG_120d_4CK |
| GO:0031224 | CC | intrinsic component of membrane | 877 | 54 | 34.91 | 0.00033 | 120d_0PG_120d_0CK |
| GO:0031224 | CC | intrinsic component of membrane | 877 | 141 | 117.78 | 0.00688 | 120d_0FG_120d_0CK |
| GO:0032991 | CC | macromolecular complex | 994 | 245 | 169.36 | 2.20E-12 | 0FG_0CK |
| GO:0032991 | CC | macromolecular complex | 994 | 205 | 143.06 | 6.70E-10 | 2FG_2CK |
| GO:0032991 | CC | macromolecular complex | 994 | 214 | 126.75 | 4.50E-19 | 120d_4FG_120d_4CK |

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|---|---|---|---|---|---|---|---|
| GO:0016020 | CC | membrane | 2087 | 106 | 83.08 | 0.00034 | 120d_0PG_120d_0CK |
| GO:0016020 | CC | membrane | 2087 | 339 | 280.28 | 2.10E-07 | 120d_0FG_120d_0CK |
| GO:0016020 | CC | membrane | 2087 | 74 | 59.34 | 0.0058 | 120d_2PG_120d_2CK |
| GO:0016020 | CC | membrane | 2087 | 261 | 220.48 | 5.70E-05 | 120d_2FG_120d_2CK |
| GO:0044425 | CC | membrane part | 1078 | 57 | 42.91 | 0.0091 | 120d_0PG_120d_0CK |
| GO:0044425 | CC | membrane part | 1078 | 186 | 144.77 | 2.40E-05 | 120d_0FG_120d_0CK |
| GO:0044425 | CC | membrane part | 1078 | 145 | 113.88 | 0.00034 | 120d_2FG_120d_2CK |
| GO:0005740 | CC | mitochondrial envelope | 66 | 17 | 8.42 | 0.00296 | 120d_4FG_120d_4CK |
| GO:0031966 | CC | mitochondrial membrane | 53 | 14 | 6.76 | 0.00528 | 120d_4FG_120d_4CK |
| GO:0044455 | CC | mitochondrial membrane part | 21 | 8 | 2.68 | 0.00296 | 120d_4FG_120d_4CK |
| GO:0044429 | CC | mitochondrial part | 74 | 19 | 9.44 | 0.00179 | 120d_4FG_120d_4CK |
| GO:0005739 | CC | mitochondrion | 84 | 22 | 10.71 | 0.0006 | 120d_4FG_120d_4CK |
| GO:0043228 | CC | non-membrane-bounded organelle | 528 | 159 | 89.96 | 1.40E-15 | 0FG_0CK |
| GO:0043228 | CC | non-membrane-bounded organelle | 528 | 124 | 75.99 | 1.80E-09 | 2FG_2CK |
| GO:0043228 | CC | non-membrane-bounded organelle | 528 | 139 | 67.33 | 1.10E-19 | 120d_4FG_120d_4CK |
| GO:0043226 | CC | organelle | 1450 | 281 | 247.06 | 0.00251 | 0FG_0CK |
| GO:0043226 | CC | organelle | 1450 | 222 | 184.9 | 0.00029 | 120d_4FG_120d_4CK |
| GO:1990204 | CC | oxidoreductase complex | 28 | 13 | 4.77 | 0.00028 | 0FG_0CK |
| GO:1990204 | CC | oxidoreductase complex | 28 | 16 | 4.03 | 1.60E-07 | 2FG_2CK |
| GO:1990204 | CC | oxidoreductase complex | 28 | 15 | 3.57 | 2.40E-07 | 120d_4FG_120d_4CK |
| GO:1990204 | CC | oxidoreductase complex | 28 | 18 | 3.76 | 5.70E-10 | 120d_0FG_120d_0CK |
| GO:1990204 | CC | oxidoreductase complex | 28 | 16 | 2.96 | 1.70E-09 | 120d_2FG_120d_2CK |
| GO:0034357 | CC | photosynthetic membrane | 52 | 34 | 8.86 | 7.50E-15 | 0FG_0CK |
| GO:0034357 | CC | photosynthetic membrane | 52 | 5 | 0.61 | 0.00032 | 2PG_2CK |
| GO:0034357 | CC | photosynthetic membrane | 52 | 37 | 7.48 | 1.50E-20 | 2FG_2CK |
| GO:0034357 | CC | photosynthetic membrane | 52 | 34 | 6.63 | 7.40E-19 | 120d_4FG_120d_4CK |
| GO:0034357 | CC | photosynthetic membrane | 52 | 36 | 6.98 | 2.00E-20 | 120d_0FG_120d_0CK |
| GO:0034357 | CC | photosynthetic membrane | 52 | 33 | 5.49 | 2.50E-20 | 120d_2FG_120d_2CK |
| GO:0009521 | CC | photosystem | 49 | 32 | 8.35 | 5.00E-14 | 0FG_0CK |
| GO:0009521 | CC | photosystem | 49 | 5 | 0.58 | 0.00024 | 2PG_2CK |
| GO:0009521 | CC | photosystem | 49 | 35 | 7.05 | 1.40E-19 | 2FG_2CK |
| GO:0009521 | CC | photosystem | 49 | 32 | 6.25 | 8.60E-18 | 120d_4FG_120d_4CK |
| GO:0009521 | CC | photosystem | 49 | 34 | 6.58 | 2.20E-19 | 120d_0FG_120d_0CK |
| GO:0009521 | CC | photosystem | 49 | 32 | 5.18 | 2.60E-20 | 120d_2FG_120d_2CK |
| GO:0009522 | CC | photosystem I | 16 | 12 | 2.73 | 5.20E-07 | 0FG_0CK |
| GO:0009522 | CC | photosystem I | 16 | 3 | 0.19 | 0.00078 | 2PG_2CK |
| GO:0009522 | CC | photosystem I | 16 | 13 | 2.3 | 3.80E-09 | 2FG_2CK |
| GO:0009522 | CC | photosystem I | 16 | 10 | 2.04 | 4.10E-06 | 120d_4FG_120d_4CK |
| GO:0009522 | CC | photosystem I | 16 | 10 | 2.15 | 6.70E-06 | 120d_0FG_120d_0CK |
| GO:0009522 | CC | photosystem I | 16 | 10 | 1.69 | 7.00E-07 | 120d_2FG_120d_2CK |
| GO:0009523 | CC | photosystem II | 30 | 20 | 5.11 | 1.90E-09 | 0FG_0CK |
| GO:0009523 | CC | photosystem II | 30 | 22 | 4.32 | 4.10E-13 | 2FG_2CK |
| GO:0009523 | CC | photosystem II | 30 | 22 | 3.83 | 3.20E-14 | 120d_4FG_120d_4CK |
| GO:0009523 | CC | photosystem II | 30 | 24 | 4.03 | 2.10E-16 | 120d_0FG_120d_0CK |

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|---|---|---|---|---|---|---|---|
| GO:0009523 | CC | photosystem II | 30 | 22 | 3.17 | 5.60E-16 | 120d_2FG_120d_2CK |
| GO:0009654 | CC | photosystem II oxygen evolving complex | 20 | 12 | 3.41 | 1.80E-05 | 0FG_0CK |
| GO:0009654 | CC | photosystem II oxygen evolving complex | 20 | 14 | 2.88 | 2.40E-08 | 2FG_2CK |
| GO:0009654 | CC | photosystem II oxygen evolving complex | 20 | 14 | 2.55 | 4.80E-09 | 120d_4FG_120d_4CK |
| GO:0009654 | CC | photosystem II oxygen evolving complex | 20 | 16 | 2.69 | 2.70E-11 | 120d_0FG_120d_0CK |
| GO:0009654 | CC | photosystem II oxygen evolving complex | 20 | 14 | 2.11 | 3.80E-10 | 120d_2FG_120d_2CK |
| GO:0009536 | CC | plastid | 30 | 18 | 5.11 | 1.40E-07 | 0FG_0CK |
| GO:0009536 | CC | plastid | 30 | 16 | 4.32 | 5.80E-07 | 2FG_2CK |
| GO:0009536 | CC | plastid | 30 | 11 | 3.83 | 0.00073 | 120d_4FG_120d_4CK |
| GO:0009536 | CC | plastid | 30 | 5 | 1.19 | 0.00599 | 120d_0PG_120d_0CK |
| GO:0009536 | CC | plastid | 30 | 16 | 4.03 | 2.20E-07 | 120d_0FG_120d_0CK |
| GO:0009536 | CC | plastid | 30 | 4 | 0.85 | 0.0096 | 120d_2PG_120d_2CK |
| GO:0009536 | CC | plastid | 30 | 13 | 3.17 | 3.80E-06 | 120d_2FG_120d_2CK |
| GO:0000502 | CC | proteasome complex | 33 | 16 | 4.43 | 1.20E-06 | 120d_0FG_120d_0CK |
| GO:0005839 | CC | proteasome core complex | 29 | 16 | 3.89 | 1.20E-07 | 120d_0FG_120d_0CK |
| GO:0005839 | CC | proteasome core complex | 29 | 8 | 3.06 | 0.00845 | 120d_2FG_120d_2CK |
| GO:0019773 | CC | proteasome core complex, alpha-subunit c... | 15 | 8 | 2.01 | 0.00027 | 120d_0FG_120d_0CK |
| GO:0045259 | CC | proton-transporting ATP synthase complex | 23 | 10 | 2.93 | 0.00025 | 120d_4FG_120d_4CK |
| GO:0045261 | CC | proton-transporting ATP synthase complex... | 15 | 6 | 1.91 | 0.00758 | 120d_4FG_120d_4CK |
| GO:0016469 | CC | proton-transporting two-sector ATPase co... | 64 | 18 | 8.16 | 0.00075 | 120d_4FG_120d_4CK |
| GO:0030529 | CC | ribonucleoprotein complex | 366 | 141 | 62.36 | 6.60E-25 | 0FG_0CK |
| GO:0030529 | CC | ribonucleoprotein complex | 366 | 113 | 52.67 | 2.20E-17 | 2FG_2CK |
| GO:0030529 | CC | ribonucleoprotein complex | 366 | 132 | 46.67 | < 1e-30 | 120d_4FG_120d_4CK |
| GO:0044391 | CC | ribosomal subunit | 21 | 9 | 3.58 | 0.00484 | 0FG_0CK |
| GO:0044391 | CC | ribosomal subunit | 21 | 8 | 3.02 | 0.0063 | 2FG_2CK |
| GO:0005840 | CC | ribosome | 342 | 140 | 58.27 | 6.50E-28 | 0FG_0CK |
| GO:0005840 | CC | ribosome | 342 | 111 | 49.22 | 6.20E-19 | 2FG_2CK |
| GO:0005840 | CC | ribosome | 342 | 131 | 43.61 | < 1e-30 | 120d_4FG_120d_4CK |
| GO:0009579 | CC | thylakoid | 54 | 36 | 9.2 | 4.60E-16 | 0FG_0CK |
| GO:0009579 | CC | thylakoid | 54 | 5 | 0.64 | 0.00039 | 2PG_2CK |
| GO:0009579 | CC | thylakoid | 54 | 39 | 7.77 | 5.50E-22 | 2FG_2CK |
| GO:0009579 | CC | thylakoid | 54 | 36 | 6.89 | 2.50E-20 | 120d_4FG_120d_4CK |
| GO:0009579 | CC | thylakoid | 54 | 38 | 7.25 | 6.80E-22 | 120d_0FG_120d_0CK |
| GO:0009579 | CC | thylakoid | 54 | 35 | 5.7 | 5.90E-22 | 120d_2FG_120d_2CK |
| GO:0042651 | CC | thylakoid membrane | 24 | 15 | 4.09 | 7.50E-07 | 0FG_0CK |
| GO:0042651 | CC | thylakoid membrane | 24 | 17 | 3.45 | 5.20E-10 | 2FG_2CK |
| GO:0042651 | CC | thylakoid membrane | 24 | 17 | 3.06 | 7.30E-11 | 120d_4FG_120d_4CK |
| GO:0042651 | CC | thylakoid membrane | 24 | 19 | 3.22 | 4.70E-13 | 120d_0FG_120d_0CK |
| GO:0042651 | CC | thylakoid membrane | 24 | 16 | 2.54 | 6.30E-11 | 120d_2FG_120d_2CK |
| GO:0044436 | CC | thylakoid part | 54 | 36 | 9.2 | 4.60E-16 | 0FG_0CK |
| GO:0044436 | CC | thylakoid part | 54 | 5 | 0.64 | 0.00039 | 2PG_2CK |
| GO:0044436 | CC | thylakoid part | 54 | 39 | 7.77 | 5.50E-22 | 2FG_2CK |
| GO:0044436 | CC | thylakoid part | 54 | 36 | 6.89 | 2.50E-20 | 120d_4FG_120d_4CK |

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|---|---|---|---|---|---|---|---|
| GO:0044436 | CC | thylakoid part | 54 | 38 | 7.25 | 6.80E-22 | 120d_0FG_120d_0CK |
| GO:0044436 | CC | thylakoid part | 54 | 35 | 5.7 | 5.90E-22 | 120d_2FG_120d_2CK |
| GO:0051537 | MF | 2 iron, 2 sulfur cluster binding | 17 | 7 | 2.5 | 0.00737 | 0FG_0CK |
| GO:0051537 | MF | 2 iron, 2 sulfur cluster binding | 17 | 8 | 2.08 | 0.00043 | 2FG_2CK |
| GO:0051537 | MF | 2 iron, 2 sulfur cluster binding | 17 | 9 | 1.76 | 1.50E-05 | 120d_4FG_120d_4CK |
| GO:0051537 | MF | 2 iron, 2 sulfur cluster binding | 17 | 6 | 1.69 | 0.00445 | 120d_2FG_120d_2CK |
| GO:0016832 | MF | aldehyde-lyase activity | 13 | 7 | 1.91 | 0.00111 | 0FG_0CK |
| GO:0016832 | MF | aldehyde-lyase activity | 13 | 7 | 1.59 | 0.00035 | 2FG_2CK |
| GO:0016832 | MF | aldehyde-lyase activity | 13 | 7 | 1.35 | 0.00012 | 120d_4FG_120d_4CK |
| GO:0016832 | MF | aldehyde-lyase activity | 13 | 4 | 0.55 | 0.00163 | 120d_0PG_120d_0CK |
| GO:0016832 | MF | aldehyde-lyase activity | 13 | 7 | 1.67 | 0.00048 | 120d_0FG_120d_0CK |
| GO:0016832 | MF | aldehyde-lyase activity | 13 | 7 | 1.29 | 9.30E-05 | 120d_2FG_120d_2CK |
| GO:0031420 | MF | alkali metal ion binding | 17 | 6 | 1.76 | 0.00558 | 120d_4FG_120d_4CK |
| GO:0031420 | MF | alkali metal ion binding | 17 | 6 | 1.69 | 0.00445 | 120d_2FG_120d_2CK |
| GO:0003905 | MF | alkylbase DNA N-glycosylase activity | 10 | 3 | 0.29 | 0.00258 | 0PG_0CK |
| GO:0016597 | MF | amino acid binding | 39 | 7 | 1.64 | 0.00106 | 120d_0PG_120d_0CK |
| GO:0016597 | MF | amino acid binding | 39 | 10 | 3.87 | 0.00388 | 120d_2FG_120d_2CK |
| GO:0004812 | MF | aminoacyl-tRNA ligase activity | 59 | 18 | 8.67 | 0.0015 | 0FG_0CK |
| GO:0004812 | MF | aminoacyl-tRNA ligase activity | 59 | 17 | 7.2 | 0.00049 | 2FG_2CK |
| GO:0016209 | MF | antioxidant activity | 160 | 14 | 6.72 | 0.00758 | 120d_0PG_120d_0CK |
| GO:0016887 | MF | ATPase activity | 360 | 62 | 46.19 | 0.00913 | 120d_0FG_120d_0CK |
| GO:0043492 | MF | ATPase activity, coupled to movement of ... | 97 | 24 | 14.26 | 0.00618 | 0FG_0CK |
| GO:0043492 | MF | ATPase activity, coupled to movement of ... | 97 | 21 | 11.84 | 0.00601 | 2FG_2CK |
| GO:0043492 | MF | ATPase activity, coupled to movement of ... | 97 | 22 | 12.45 | 0.00505 | 120d_0FG_120d_0CK |
| GO:0042626 | MF | ATPase activity, coupled to transmembran... | 97 | 24 | 14.26 | 0.00618 | 0FG_0CK |
| GO:0042626 | MF | ATPase activity, coupled to transmembran... | 97 | 21 | 11.84 | 0.00601 | 2FG_2CK |
| GO:0044769 | MF | ATPase activity, coupled to transmembran... | 28 | 8 | 2.91 | 0.00615 | 120d_4FG_120d_4CK |
| GO:0042626 | MF | ATPase activity, coupled to transmembran... | 97 | 22 | 12.45 | 0.00505 | 120d_0FG_120d_0CK |
| GO:0005509 | MF | calcium ion binding | 56 | 17 | 8.23 | 0.00213 | 0FG_0CK |
| GO:0005509 | MF | calcium ion binding | 56 | 19 | 6.84 | 1.90E-05 | 2FG_2CK |
| GO:0005509 | MF | calcium ion binding | 56 | 17 | 5.81 | 3.30E-05 | 120d_4FG_120d_4CK |
| GO:0005509 | MF | calcium ion binding | 56 | 18 | 7.19 | 0.00014 | 120d_0FG_120d_0CK |
| GO:0005509 | MF | calcium ion binding | 56 | 16 | 5.55 | 7.20E-05 | 120d_2FG_120d_2CK |
| GO:0019200 | MF | carbohydrate kinase activity | 12 | 6 | 1.76 | 0.00417 | 0FG_0CK |
| GO:0019200 | MF | carbohydrate kinase activity | 12 | 5 | 1.25 | 0.00507 | 120d_4FG_120d_4CK |
| GO:0016830 | MF | carbon-carbon lyase activity | 81 | 30 | 11.91 | 5.70E-07 | 0FG_0CK |
| GO:0016830 | MF | carbon-carbon lyase activity | 81 | 28 | 9.89 | 1.40E-07 | 2FG_2CK |
| GO:0016830 | MF | carbon-carbon lyase activity | 81 | 19 | 8.41 | 0.00051 | 120d_4FG_120d_4CK |
| GO:0016830 | MF | carbon-carbon lyase activity | 81 | 25 | 10.39 | 1.70E-05 | 120d_0FG_120d_0CK |
| GO:0016830 | MF | carbon-carbon lyase activity | 81 | 21 | 8.03 | 2.90E-05 | 120d_2FG_120d_2CK |
| GO:0016840 | MF | carbon-nitrogen lyase activity | 22 | 7 | 2.28 | 0.00536 | 120d_4FG_120d_4CK |
| GO:0016840 | MF | carbon-nitrogen lyase activity | 22 | 5 | 0.92 | 0.00187 | 120d_0PG_120d_0CK |
| GO:0031406 | MF | carboxylic acid binding | 39 | 7 | 1.64 | 0.00106 | 120d_0PG_120d_0CK |
| GO:0031406 | MF | carboxylic acid binding | 39 | 10 | 3.87 | 0.00388 | 120d_2FG_120d_2CK |

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|---|---|---|---|---|---|---|---|
| GO:0016831 | MF | carboxy-lyase activity | 48 | 14 | 7.06 | 0.00751 | 0FG_0CK |
| GO:0016831 | MF | carboxy-lyase activity | 48 | 13 | 5.86 | 0.00401 | 2FG_2CK |
| GO:0003824 | MF | catalytic activity | 7941 | 1256 | 1167.48 | 3.10E-05 | 0FG_0CK |
| GO:0003824 | MF | catalytic activity | 7941 | 109 | 92.02 | 0.0064 | 2PG_2CK |
| GO:0003824 | MF | catalytic activity | 7941 | 1094 | 969.56 | 5.00E-10 | 2FG_2CK |
| GO:0003824 | MF | catalytic activity | 7941 | 915 | 824.07 | 8.70E-07 | 120d_4FG_120d_4CK |
| GO:0003824 | MF | catalytic activity | 7941 | 406 | 333.64 | 3.30E-09 | 120d_0PG_120d_0CK |
| GO:0003824 | MF | catalytic activity | 7941 | 1211 | 1018.91 | 1.00E-20 | 120d_0FG_120d_0CK |
| GO:0003824 | MF | catalytic activity | 7941 | 249 | 218.48 | 0.00153 | 120d_2PG_120d_2CK |
| GO:0003824 | MF | catalytic activity | 7941 | 935 | 787.57 | 9.50E-16 | 120d_2FG_120d_2CK |
| GO:0043169 | MF | cation binding | 1895 | 36 | 21.96 | 0.0018 | 2PG_2CK |
| GO:0043169 | MF | cation binding | 1895 | 248 | 187.94 | 1.20E-06 | 120d_2FG_120d_2CK |
| GO:0008324 | MF | cation transmembrane transporter activit... | 224 | 38 | 23.25 | 0.0016 | 120d_4FG_120d_4CK |
| GO:0019829 | MF | cation-transporting ATPase activity | 28 | 8 | 2.91 | 0.00615 | 120d_4FG_120d_4CK |
| GO:0051087 | MF | chaperone binding | 20 | 6 | 0.59 | 1.70E-05 | 0PG_0CK |
| GO:0008061 | MF | chitin binding | 12 | 2 | 0.14 | 0.0082 | 2PG_2CK |
| GO:0050662 | MF | coenzyme binding | 298 | 61 | 43.81 | 0.004 | 0FG_0CK |
| GO:0050662 | MF | coenzyme binding | 298 | 59 | 36.38 | 0.00011 | 2FG_2CK |
| GO:0050662 | MF | coenzyme binding | 298 | 47 | 30.92 | 0.00233 | 120d_4FG_120d_4CK |
| GO:0050662 | MF | coenzyme binding | 298 | 59 | 38.24 | 0.00041 | 120d_0FG_120d_0CK |
| GO:0050662 | MF | coenzyme binding | 298 | 50 | 29.55 | 0.00014 | 120d_2FG_120d_2CK |
| GO:0048037 | MF | cofactor binding | 419 | 88 | 61.6 | 0.00027 | 0FG_0CK |
| GO:0048037 | MF | cofactor binding | 419 | 85 | 51.16 | 1.30E-06 | 2FG_2CK |
| GO:0048037 | MF | cofactor binding | 419 | 76 | 43.48 | 8.10E-07 | 120d_4FG_120d_4CK |
| GO:0048037 | MF | cofactor binding | 419 | 85 | 53.76 | 9.40E-06 | 120d_0FG_120d_0CK |
| GO:0048037 | MF | cofactor binding | 419 | 21 | 11.53 | 0.00618 | 120d_2PG_120d_2CK |
| GO:0048037 | MF | cofactor binding | 419 | 73 | 41.56 | 1.20E-06 | 120d_2FG_120d_2CK |
| GO:0004129 | MF | cytochrome-c oxidase activity | 11 | 6 | 1.14 | 0.00036 | 120d_4FG_120d_4CK |
| GO:0051213 | MF | dioxygenase activity | 189 | 8 | 2.19 | 0.0016 | 2PG_2CK |
| GO:0051213 | MF | dioxygenase activity | 189 | 12 | 5.2 | 0.00617 | 120d_2PG_120d_2CK |
| GO:0019104 | MF | DNA N-glycosylase activity | 12 | 3 | 0.35 | 0.00452 | 0PG_0CK |
| GO:0009055 | MF | electron carrier activity | 522 | 15 | 6.05 | 0.0011 | 2PG_2CK |
| GO:0009055 | MF | electron carrier activity | 522 | 83 | 54.17 | 4.80E-05 | 120d_4FG_120d_4CK |
| GO:0009055 | MF | electron carrier activity | 522 | 27 | 14.36 | 0.0013 | 120d_2PG_120d_2CK |
| GO:0009055 | MF | electron carrier activity | 522 | 88 | 51.77 | 4.10E-07 | 120d_2FG_120d_2CK |
| GO:0004332 | MF | fructose-bisphosphate aldolase activity | 11 | 7 | 1.62 | 0.00028 | 0FG_0CK |
| GO:0004332 | MF | fructose-bisphosphate aldolase activity | 11 | 7 | 1.34 | 8.40E-05 | 2FG_2CK |
| GO:0004332 | MF | fructose-bisphosphate aldolase activity | 11 | 7 | 1.14 | 2.90E-05 | 120d_4FG_120d_4CK |
| GO:0004332 | MF | fructose-bisphosphate aldolase activity | 11 | 4 | 0.46 | 0.0008 | 120d_0PG_120d_0CK |
| GO:0004332 | MF | fructose-bisphosphate aldolase activity | 11 | 7 | 1.41 | 0.00012 | 120d_0FG_120d_0CK |
| GO:0004332 | MF | fructose-bisphosphate aldolase activity | 11 | 7 | 1.09 | 2.10E-05 | 120d_2FG_120d_2CK |
| GO:0004372 | MF | glycine hydroxymethyltransferase activit... | 10 | 5 | 1.47 | 0.00903 | 0FG_0CK |
| GO:0031072 | MF | heat shock protein binding | 128 | 28 | 15.63 | 0.00143 | 2FG_2CK |
| GO:0020037 | MF | heme binding | 470 | 14 | 5.45 | 0.0012 | 2PG_2CK |

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|---|---|---|---|---|---|---|---|
| GO:0020037 | MF | heme binding | 470 | 38 | 19.75 | 8.90E-05 | 120d_0PG_120d_0CK |
| GO:0020037 | MF | heme binding | 470 | 30 | 12.93 | 1.80E-05 | 120d_2PG_120d_2CK |
| GO:0020037 | MF | heme binding | 470 | 71 | 46.61 | 0.0002 | 120d_2FG_120d_2CK |
| GO:0015002 | MF | heme-copper terminal oxidase activity | 11 | 6 | 1.14 | 0.00036 | 120d_4FG_120d_4CK |
| GO:0015078 | MF | hydrogen ion transmembrane transporter a... | 113 | 26 | 11.73 | 7.30E-05 | 120d_4FG_120d_4CK |
| GO:0016820 | MF | hydrolase activity, acting on acid anhyd... | 105 | 27 | 15.44 | 0.00214 | 0FG_0CK |
| GO:0016820 | MF | hydrolase activity, acting on acid anhyd... | 105 | 23 | 12.82 | 0.00357 | 2FG_2CK |
| GO:0016820 | MF | hydrolase activity, acting on acid anhyd... | 105 | 20 | 10.9 | 0.00527 | 120d_4FG_120d_4CK |
| GO:0016820 | MF | hydrolase activity, acting on acid anhyd... | 105 | 23 | 13.47 | 0.00658 | 120d_0FG_120d_0CK |
| GO:0016798 | MF | hydrolase activity, acting on glycosyl b... | 473 | 27 | 13.87 | 0.00078 | 0PG_0CK |
| GO:0004553 | MF | hydrolase activity, hydrolyzing O-glycos... | 448 | 24 | 13.14 | 0.00343 | 0PG_0CK |
| GO:0016836 | MF | hydro-lyase activity | 37 | 11 | 3.84 | 0.00097 | 120d_4FG_120d_4CK |
| GO:0016836 | MF | hydro-lyase activity | 37 | 7 | 1.55 | 0.00077 | 120d_0PG_120d_0CK |
| GO:0016836 | MF | hydro-lyase activity | 37 | 10 | 3.67 | 0.00255 | 120d_2FG_120d_2CK |
| GO:0042802 | MF | identical protein binding | 92 | 8 | 2.7 | 0.00558 | 0PG_0CK |
| GO:0022890 | MF | inorganic cation transmembrane transport... | 198 | 37 | 20.55 | 0.00028 | 120d_4FG_120d_4CK |
| GO:0016860 | MF | intramolecular oxidoreductase activity | 23 | 8 | 2.81 | 0.00438 | 2FG_2CK |
| GO:0016860 | MF | intramolecular oxidoreductase activity | 23 | 5 | 0.97 | 0.00231 | 120d_0PG_120d_0CK |
| GO:0016860 | MF | intramolecular oxidoreductase activity | 23 | 8 | 2.95 | 0.00596 | 120d_0FG_120d_0CK |
| GO:0016861 | MF | intramolecular oxidoreductase activity, ... | 20 | 5 | 0.84 | 0.00118 | 120d_0PG_120d_0CK |
| GO:0016861 | MF | intramolecular oxidoreductase activity, ... | 20 | 7 | 2.57 | 0.0096 | 120d_0FG_120d_0CK |
| GO:0015075 | MF | ion transmembrane transporter activity | 344 | 55 | 35.7 | 0.00075 | 120d_4FG_120d_4CK |
| GO:0005506 | MF | iron ion binding | 378 | 15 | 4.38 | 3.50E-05 | 2PG_2CK |
| GO:0005506 | MF | iron ion binding | 378 | 64 | 46.15 | 0.004 | 2FG_2CK |
| GO:0005506 | MF | iron ion binding | 378 | 66 | 39.23 | 1.50E-05 | 120d_4FG_120d_4CK |
| GO:0005506 | MF | iron ion binding | 378 | 32 | 15.88 | 0.00014 | 120d_0PG_120d_0CK |
| GO:0005506 | MF | iron ion binding | 378 | 68 | 48.5 | 0.00227 | 120d_0FG_120d_0CK |
| GO:0005506 | MF | iron ion binding | 378 | 27 | 10.4 | 6.30E-06 | 120d_2PG_120d_2CK |
| GO:0005506 | MF | iron ion binding | 378 | 78 | 37.49 | 2.30E-10 | 120d_2FG_120d_2CK |
| GO:0051536 | MF | iron-sulfur cluster binding | 80 | 21 | 11.76 | 0.00489 | 0FG_0CK |
| GO:0051536 | MF | iron-sulfur cluster binding | 80 | 20 | 9.77 | 0.00122 | 2FG_2CK |
| GO:0051536 | MF | iron-sulfur cluster binding | 80 | 21 | 8.3 | 4.70E-05 | 120d_4FG_120d_4CK |
| GO:0016853 | MF | isomerase activity | 146 | 40 | 21.46 | 4.80E-05 | 0FG_0CK |
| GO:0016853 | MF | isomerase activity | 146 | 31 | 17.83 | 0.00137 | 2FG_2CK |
| GO:0016853 | MF | isomerase activity | 146 | 15 | 6.13 | 0.00124 | 120d_0PG_120d_0CK |
| GO:0016853 | MF | isomerase activity | 146 | 32 | 18.73 | 0.00152 | 120d_0FG_120d_0CK |
| GO:0016874 | MF | ligase activity | 288 | 55 | 36.95 | 0.0015 | 120d_0FG_120d_0CK |
| GO:0016876 | MF | ligase activity, forming aminoacyl-tRNA ... | 61 | 18 | 8.97 | 0.00227 | 0FG_0CK |
| GO:0016876 | MF | ligase activity, forming aminoacyl-tRNA ... | 61 | 17 | 7.45 | 0.00075 | 2FG_2CK |
| GO:0016875 | MF | ligase activity, forming carbon-oxygen b... | 61 | 18 | 8.97 | 0.00227 | 0FG_0CK |
| GO:0016875 | MF | ligase activity, forming carbon-oxygen b... | 61 | 17 | 7.45 | 0.00075 | 2FG_2CK |
| GO:0016829 | MF | lyase activity | 223 | 52 | 32.79 | 0.00039 | 0FG_0CK |
| GO:0016829 | MF | lyase activity | 223 | 53 | 27.23 | 1.10E-06 | 2FG_2CK |
| GO:0016829 | MF | lyase activity | 223 | 42 | 23.14 | 9.50E-05 | 120d_4FG_120d_4CK |

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|---|---|---|---|---|---|---|---|
| GO:0016829 | MF | lyase activity | 223 | 22 | 9.37 | 0.00018 | 120d_0PG_120d_0CK |
| GO:0016829 | MF | lyase activity | 223 | 46 | 28.61 | 0.00068 | 120d_0FG_120d_0CK |
| GO:0016829 | MF | lyase activity | 223 | 14 | 6.14 | 0.00357 | 120d_2PG_120d_2CK |
| GO:0016829 | MF | lyase activity | 223 | 43 | 22.12 | 1.50E-05 | 120d_2FG_120d_2CK |
| GO:0051540 | MF | metal cluster binding | 80 | 21 | 11.76 | 0.00489 | 0FG_0CK |
| GO:0051540 | MF | metal cluster binding | 80 | 20 | 9.77 | 0.00122 | 2FG_2CK |
| GO:0051540 | MF | metal cluster binding | 80 | 21 | 8.3 | 4.70E-05 | 120d_4FG_120d_4CK |
| GO:0046872 | MF | metal ion binding | 1884 | 36 | 21.83 | 0.0016 | 2PG_2CK |
| GO:0046872 | MF | metal ion binding | 1884 | 246 | 186.85 | 1.60E-06 | 120d_2FG_120d_2CK |
| GO:0015077 | MF | monovalent inorganic cation transmembran... | 161 | 32 | 16.71 | 0.00023 | 120d_4FG_120d_4CK |
| GO:0051287 | MF | NAD binding | 43 | 13 | 6.32 | 0.00709 | 0FG_0CK |
| GO:0051287 | MF | NAD binding | 43 | 15 | 5.25 | 0.0001 | 2FG_2CK |
| GO:0051287 | MF | NAD binding | 43 | 13 | 4.46 | 0.00028 | 120d_4FG_120d_4CK |
| GO:0051287 | MF | NAD binding | 43 | 13 | 4.26 | 0.00018 | 120d_2FG_120d_2CK |
| GO:0004576 | MF | oligosaccharyl transferase activity | 12 | 6 | 1.47 | 0.00158 | 2FG_2CK |
| GO:0043177 | MF | organic acid binding | 39 | 7 | 1.64 | 0.00106 | 120d_0PG_120d_0CK |
| GO:0043177 | MF | organic acid binding | 39 | 10 | 3.87 | 0.00388 | 120d_2FG_120d_2CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 308 | 237.44 | 2.30E-07 | 0FG_0CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 40 | 18.71 | 2.50E-06 | 2PG_2CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 288 | 197.18 | 2.40E-12 | 2FG_2CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 287 | 167.6 | 7.60E-22 | 120d_4FG_120d_4CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 112 | 67.85 | 5.00E-08 | 120d_0PG_120d_0CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 305 | 207.22 | 1.60E-13 | 120d_0FG_120d_0CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 79 | 44.43 | 2.40E-07 | 120d_2PG_120d_2CK |
| GO:0016491 | MF | oxidoreductase activity | 1615 | 275 | 160.17 | 4.60E-21 | 120d_2FG_120d_2CK |
| GO:0016675 | MF | oxidoreductase activity, acting on a hem... | 11 | 6 | 1.14 | 0.00036 | 120d_4FG_120d_4CK |
| GO:0016676 | MF | oxidoreductase activity, acting on a hem... | 11 | 6 | 1.14 | 0.00036 | 120d_4FG_120d_4CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 40 | 22.79 | 0.0002 | 0FG_0CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 31 | 18.92 | 0.00364 | 2FG_2CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 37 | 16.09 | 9.40E-07 | 120d_4FG_120d_4CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 14 | 6.51 | 0.00576 | 120d_0PG_120d_0CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 37 | 19.89 | 0.00011 | 120d_0FG_120d_0CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 11 | 4.26 | 0.00376 | 120d_2PG_120d_2CK |
| GO:0016614 | MF | oxidoreductase activity, acting on CH-OH... | 155 | 37 | 15.37 | 3.10E-07 | 120d_2FG_120d_2CK |
| GO:0016679 | MF | oxidoreductase activity, acting on diphe... | 12 | 5 | 1.25 | 0.00507 | 120d_4FG_120d_4CK |
| GO:0016705 | MF | oxidoreductase activity, acting on paire... | 517 | 18 | 5.99 | 3.20E-05 | 2PG_2CK |
| GO:0016706 | MF | oxidoreductase activity, acting on paire... | 156 | 6 | 1.81 | 0.0097 | 2PG_2CK |
| GO:0016705 | MF | oxidoreductase activity, acting on paire... | 517 | 72 | 53.65 | 0.00576 | 120d_4FG_120d_4CK |
| GO:0016705 | MF | oxidoreductase activity, acting on paire... | 517 | 36 | 21.72 | 0.00211 | 120d_0PG_120d_0CK |
| GO:0016717 | MF | oxidoreductase activity, acting on paire... | 15 | 6 | 1.92 | 0.00789 | 120d_0FG_120d_0CK |
| GO:0016705 | MF | oxidoreductase activity, acting on paire... | 517 | 35 | 14.22 | 9.10E-07 | 120d_2PG_120d_2CK |
| GO:0016705 | MF | oxidoreductase activity, acting on paire... | 517 | 82 | 51.27 | 1.20E-05 | 120d_2FG_120d_2CK |
| GO:0016717 | MF | oxidoreductase activity, acting on paire... | 15 | 7 | 1.49 | 0.00029 | 120d_2FG_120d_2CK |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GO:0016701 | MF | oxidoreductase activity, acting on singl... | 44 | 12 | 5.37 | 0.00527 | 2FG_2CK |
| GO:0016701 | MF | oxidoreductase activity, acting on singl... | 44 | 12 | 4.57 | 0.00134 | 120d_4FG_120d_4CK |
| GO:0016701 | MF | oxidoreductase activity, acting on singl... | 44 | 12 | 5.65 | 0.00783 | 120d_0FG_120d_0CK |
| GO:0016701 | MF | oxidoreductase activity, acting on singl... | 44 | 13 | 4.36 | 0.00023 | 120d_2FG_120d_2CK |
| GO:0016620 | MF | oxidoreductase activity, acting on the a... | 30 | 11 | 4.41 | 0.00248 | 0FG_0CK |
| GO:0016903 | MF | oxidoreductase activity, acting on the a... | 44 | 14 | 6.47 | 0.00316 | 0FG_0CK |
| GO:0016620 | MF | oxidoreductase activity, acting on the a... | 30 | 9 | 3.11 | 0.00258 | 120d_4FG_120d_4CK |
| GO:0016903 | MF | oxidoreductase activity, acting on the a... | 44 | 13 | 4.57 | 0.00037 | 120d_4FG_120d_4CK |
| GO:0016620 | MF | oxidoreductase activity, acting on the a... | 30 | 8 | 2.98 | 0.00735 | 120d_2FG_120d_2CK |
| GO:0016903 | MF | oxidoreductase activity, acting on the a... | 44 | 11 | 4.36 | 0.0031 | 120d_2FG_120d_2CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 39 | 20.73 | 4.70E-05 | 0FG_0CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 30 | 17.22 | 0.00157 | 2FG_2CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 34 | 14.63 | 2.00E-06 | 120d_4FG_120d_4CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 14 | 5.92 | 0.00246 | 120d_0PG_120d_0CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 34 | 18.09 | 0.00017 | 120d_0FG_120d_0CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 11 | 3.88 | 0.0018 | 120d_2PG_120d_2CK |
| GO:0016616 | MF | oxidoreductase activity, acting on the C... | 141 | 35 | 13.98 | 2.30E-07 | 120d_2FG_120d_2CK |
| GO:0016638 | MF | oxidoreductase activity, acting on the C... | 18 | 6 | 1.79 | 0.00613 | 120d_2FG_120d_2CK |
| GO:0008443 | MF | phosphofructokinase activity | 12 | 6 | 1.76 | 0.00417 | 0FG_0CK |
| GO:0008443 | MF | phosphofructokinase activity | 12 | 5 | 1.25 | 0.00507 | 120d_4FG_120d_4CK |
| GO:0030955 | MF | potassium ion binding | 17 | 6 | 1.76 | 0.00558 | 120d_4FG_120d_4CK |
| GO:0030955 | MF | potassium ion binding | 17 | 6 | 1.69 | 0.00445 | 120d_2FG_120d_2CK |
| GO:0015405 | MF | P-P-bond-hydrolysis-driven transmembrane... | 115 | 28 | 16.91 | 0.00418 | 0FG_0CK |
| GO:0015399 | MF | primary active transmembrane transporter... | 115 | 28 | 16.91 | 0.00418 | 0FG_0CK |
| GO:0046933 | MF | proton-transporting ATP synthase activit... | 22 | 8 | 2.28 | 0.00111 | 120d_4FG_120d_4CK |
| GO:0030170 | MF | pyridoxal phosphate binding | 93 | 23 | 13.67 | 0.00729 | 0FG_0CK |
| GO:0030170 | MF | pyridoxal phosphate binding | 93 | 20 | 11.35 | 0.0078 | 2FG_2CK |
| GO:0030170 | MF | pyridoxal phosphate binding | 93 | 20 | 9.65 | 0.00118 | 120d_4FG_120d_4CK |
| GO:0030170 | MF | pyridoxal phosphate binding | 93 | 21 | 11.93 | 0.00639 | 120d_0FG_120d_0CK |
| GO:0030170 | MF | pyridoxal phosphate binding | 93 | 17 | 9.22 | 0.00941 | 120d_2FG_120d_2CK |
| GO:0004743 | MF | pyruvate kinase activity | 17 | 6 | 1.76 | 0.00558 | 120d_4FG_120d_4CK |
| GO:0004743 | MF | pyruvate kinase activity | 17 | 6 | 1.69 | 0.00445 | 120d_2FG_120d_2CK |
| GO:0019843 | MF | rRNA binding | 14 | 7 | 2.06 | 0.00195 | 0FG_0CK |
| GO:0004252 | MF | serine-type endopeptidase activity | 126 | 10 | 3.7 | 0.00397 | 0PG_0CK |
| GO:0003735 | MF | structural constituent of ribosome | 342 | 140 | 50.28 | < 1e-30 | 0FG_0CK |
| GO:0003735 | MF | structural constituent of ribosome | 342 | 111 | 41.76 | 2.20E-23 | 2FG_2CK |
| GO:0003735 | MF | structural constituent of ribosome | 342 | 131 | 35.49 | < 1e-30 | 120d_4FG_120d_4CK |
| GO:0005198 | MF | structural molecule activity | 392 | 156 | 57.63 | < 1e-30 | 0FG_0CK |
| GO:0005198 | MF | structural molecule activity | 392 | 122 | 47.86 | 8.40E-24 | 2FG_2CK |
| GO:0005198 | MF | structural molecule activity | 392 | 137 | 40.68 | < 1e-30 | 120d_4FG_120d_4CK |
| GO:0022891 | MF | substrate-specific transmembrane transpo... | 362 | 57 | 37.57 | 0.00089 | 120d_4FG_120d_4CK |
| GO:0046906 | MF | tetrapyrrole binding | 473 | 14 | 5.48 | 0.0012 | 2PG_2CK |
| GO:0046906 | MF | tetrapyrrole binding | 473 | 38 | 19.87 | 0.0001 | 120d_0PG_120d_0CK |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GO:0046906 | MF | tetrapyrrole binding | 473 | 30 | 13.01 | 2.00E-05 | 120d_2PG_120d_2CK |
| GO:0046906 | MF | tetrapyrrole binding | 473 | 71 | 46.91 | 0.00025 | 120d_2FG_120d_2CK |
| GO:0004298 | MF | threonine-type endopeptidase activity | 29 | 16 | 3.72 | 6.60E-08 | 120d_0FG_120d_0CK |
| GO:0004298 | MF | threonine-type endopeptidase activity | 29 | 8 | 2.88 | 0.00589 | 120d_2FG_120d_2CK |
| GO:0070003 | MF | threonine-type peptidase activity | 29 | 16 | 3.72 | 6.60E-08 | 120d_0FG_120d_0CK |
| GO:0070003 | MF | threonine-type peptidase activity | 29 | 8 | 2.88 | 0.00589 | 120d_2FG_120d_2CK |
| GO:0046912 | MF | transferase activity, transferring acyl ... | 11 | 6 | 1.34 | 0.00088 | 2FG_2CK |
| GO:0046912 | MF | transferase activity, transferring acyl ... | 11 | 6 | 1.14 | 0.00036 | 120d_4FG_120d_4CK |
| GO:0016746 | MF | transferase activity, transferring acyl ... | 272 | 49 | 34.9 | 0.00838 | 120d_0FG_120d_0CK |
| GO:0016758 | MF | transferase activity, transferring hexos... | 345 | 58 | 42.12 | 0.00689 | 2FG_2CK |
| GO:0016769 | MF | transferase activity, transferring nitro... | 47 | 12 | 5.74 | 0.00924 | 2FG_2CK |
| GO:0016769 | MF | transferase activity, transferring nitro... | 47 | 11 | 4.88 | 0.00749 | 120d_4FG_120d_4CK |
| GO:0046914 | MF | transition metal ion binding | 1509 | 28 | 17.49 | 0.0084 | 2PG_2CK |
| GO:0046914 | MF | transition metal ion binding | 1509 | 182 | 149.66 | 0.00239 | 120d_2FG_120d_2CK |
| GO:0022857 | MF | transmembrane transporter activity | 586 | 87 | 60.81 | 0.00036 | 120d_4FG_120d_4CK |
| GO:0005215 | MF | transporter activity | 811 | 122 | 84.16 | 1.30E-05 | 120d_4FG_120d_4CK |
| GO:0005215 | MF | transporter activity | 811 | 53 | 34.07 | 0.00092 | 120d_0PG_120d_0CK |
| GO:0005215 | MF | transporter activity | 811 | 38 | 22.31 | 0.00096 | 120d_2PG_120d_2CK |

**Note:** “CK”indicates control, “PG”indicates partial girdled, and “FG” indicates fully girdled. “0”indicates 0hr, “2” indicates 2hr and “4”indicates 4hr. “120d”indicates 120-day old leaf, others not labeld with days came from 45-day old leaf.

## Supplemental Table S4. Genes annotated to photosynthesis, N-metabolism and tetrapyrrole synthesis pathways. The extent of differential expression is measured in terms of log2 fold change of treatment vs. control.

| Table Class | Cassava ID | Mapman Category | Short Description | PG0 | FG0 | PG2 | FG2 | PG4 | FG4 | PG0 | FG0 | PG2 | FG2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | 120 day | | | | | | 45 day | | | |
| Light Reaction | cassava4.1_028060m.g | PS.lightreaction.ATP synthase | ATP synthase subunit alpha | -1.78 | -1.02 | -0.94 | -0.45 | -0.15 | -2.65 | 0.55 | -2.27 | -0.45 | -1.77 |
| | cassava4.1_014114m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 6 | -1.41 | -2.41 | -0.81 | -1.83 | -0.09 | -1.89 | -0.91 | -2.00 | -0.72 | -1.93 |
| | cassava4.1_013714m.g | PS.lightreaction.photosystem II.LHC-II | light harvesting complex photosystem II | -1.33 | -3.17 | -0.60 | -3.56 | -0.13 | -4.56 | -0.92 | -3.18 | -1.20 | -3.90 |
| | cassava4.1_010721m.g | PS.lightreaction.cyclic electron flow-chlororespiration | NDH-dependent cyclic electron flow 1 | -1.29 | -4.78 | -0.91 | -4.45 | 0.05 | -3.55 | -0.68 | -2.43 | -0.48 | -2.17 |
| | cassava4.1_017367m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II reaction center PSB28 protein | -1.29 | -2.65 | -0.95 | -2.18 | -0.36 | -1.30 | -0.75 | -1.84 | -0.68 | -1.77 |
| | cassava4.1_015252m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | PsbP-like protein 2 | -1.18 | -2.58 | -0.83 | -2.64 | -0.07 | -2.42 | -0.56 | -1.56 | -0.54 | -1.78 |
| | cassava4.1_013294m.g | PS.lightreaction.photosystem II.LHC-II | light harvesting complex photosystem II | -1.04 | -3.86 | 0.06 | -3.04 | 0.09 | -2.67 | -0.72 | -2.45 | -0.42 | -2.60 |
| | cassava4.1_015152m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | PsbP-like protein 1 | -1.03 | -2.97 | -0.53 | -2.28 | -0.39 | -2.95 | -0.51 | -2.61 | -0.63 | -2.41 |
| | cassava4.1_010832m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase | ferredoxin-NADP(+)-oxidoreductase 2 | -1.03 | -3.21 | -0.65 | -2.64 | -0.17 | -3.00 | -0.90 | -2.69 | -1.14 | -3.44 |
| | cassava4.1_017708m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I P subunit | -1.02 | -4.00 | -0.37 | -3.02 | -0.09 | -4.06 | -0.65 | -3.38 | -1.15 | -3.80 |
| | cassava4.1_012195m.g | PS.lightreaction.photosystem I.LHC-I | light-harvesting chlorophyll-protein complex I subunit A4 | -0.99 | -3.74 | -0.06 | -2.20 | 0.14 | -1.97 | -0.52 | -1.79 | -0.33 | -1.93 |
| | cassava4.1_012460m.g | PS.lightreaction.photosystem II.LHC-II | light-harvesting chlorophyll-protein complex II subunit B1 | -0.97 | -5.16 | 0.09 | -2.62 | 0.07 | -2.03 | -0.93 | -1.94 | -0.32 | -1.94 |
| | cassava4.1_019328m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II subunit X | -0.97 | -3.65 | -0.72 | -3.15 | 0.03 | -2.36 | -0.27 | -2.53 | -0.72 | -2.38 |
| | cassava4.1_011470m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II subunit O-2 | -0.88 | -3.07 | -0.29 | -2.54 | 0.00 | -2.59 | -0.66 | -2.56 | -0.75 | -2.74 |
| | cassava4.1_011539m.g | PS.lightreaction.photosystem II.PSII polypeptide | photosystem II subunit O-2 | -0.88 | -2.69 | -0.27 | -2.54 | -0.06 | -2.76 | -0.64 | -2.32 | -0.91 | -2.99 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | subunits | | | | | | | | | | | |
| | cassava4.1_014055m.g | PS.lightreaction.photosystem II.LHC-II | photosystem II light harvesting complex gene 2.1 | -0.86 | -3.85 | -0.32 | -2.62 | -0.08 | -2.74 | -0.76 | -2.36 | -0.84 | -2.42 |
| | cassava4.1_009836m.g | PS.lightreaction.ATP synthase.gamma chain | ATPase, F1 complex, gamma subunit protein | -0.85 | -2.26 | -0.75 | -2.61 | -0.24 | -2.50 | -0.66 | -2.37 | -1.08 | -2.93 |
| | cassava4.1_017705m.g | PS.lightreaction.other electron carrier (ox/red).plastocyanin | Cupredoxin superfamily protein | -0.85 | -3.18 | -0.50 | -2.90 | -0.09 | -2.35 | -0.81 | -2.15 | -1.10 | -2.72 |
| | cassava4.1_018500m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin | 2Fe-2S ferredoxin-like superfamily protein | -0.84 | -4.02 | -0.99 | -3.76 | 0.06 | -2.71 | -0.39 | -3.14 | -1.00 | -3.32 |
| | cassava4.1_013980m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 5 | -0.84 | -2.47 | -0.39 | -2.20 | 0.11 | -1.98 | -0.38 | -1.04 | -0.25 | -0.79 |
| | cassava4.1_015521m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II subunit Q-2 | -0.84 | -2.62 | -0.16 | -2.82 | -0.01 | -3.03 | -0.64 | -2.29 | -0.77 | -2.74 |
| | cassava4.1_017374m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I P subunit | -0.83 | -2.49 | -0.24 | -2.92 | -0.01 | -3.17 | -0.40 | -2.42 | -0.72 | -2.90 |
| | cassava4.1_030348m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit l | -0.83 | -2.98 | -0.11 | -2.59 | 0.00 | -2.57 | -0.66 | -2.33 | -0.90 | -2.72 |
| | cassava4.1_014559m.g | PS.lightreaction.photosystem I.LHC-I | light-harvesting chlorophyll-protein complex I subunit A4 | -0.81 | -3.94 | -0.03 | -2.65 | 0.04 | -2.03 | -0.20 | -1.54 | -0.28 | -2.01 |
| | cassava4.1_018914m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II reaction center W | -0.81 | -2.88 | -0.93 | -2.71 | 0.01 | -2.24 | -0.34 | -1.80 | -0.66 | -2.34 |
| | cassava4.1_014926m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 1 | -0.81 | -3.93 | 0.03 | -2.55 | -0.01 | -1.91 | -0.53 | -1.94 | -0.10 | -1.74 |
| | cassava4.1_017909m.g | PS.lightreaction.NADH DH | NAD(P)H:plastoquinone dehydrogenase complex subunit O | -0.80 | -1.58 | -0.39 | -0.74 | 0.02 | -0.72 | -0.49 | -0.92 | -0.39 | -0.57 |
| | cassava4.1_019060m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit K | -0.79 | -3.38 | -0.48 | -3.14 | 0.02 | -3.22 | -0.60 | -2.42 | -1.17 | -3.22 |
| | cassava4.1_010341m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase | ferredoxin-NADP(+)-oxidoreductase 2 | -0.78 | -3.02 | -0.77 | -3.76 | -0.13 | -3.37 | -0.45 | -2.29 | -1.05 | -3.53 |
| | cassava4.1_017061m.g | PS.lightreaction.NADH DH | inorganic carbon transport protein-related | -0.77 | -2.42 | -0.73 | -2.59 | -0.24 | -3.31 | -0.57 | -1.62 | -0.92 | -2.36 |
| | cassava4.1_010324m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase | ferredoxin-NADP(+)-oxidoreductase 1 | -0.77 | -2.08 | -0.39 | -2.19 | 0.03 | -2.08 | -0.50 | -1.85 | -0.81 | -2.51 |
| | cassava4.1_017065m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | PsbQ-like 2 | -0.76 | -2.18 | -0.80 | -3.17 | 0.09 | -2.78 | -0.42 | -1.44 | -0.76 | -2.22 |
| | cassava4.1_014170m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | -0.75 | -1.19 | -0.24 | -0.96 | 0.01 | -1.61 | -0.33 | -0.96 | -0.07 | -0.84 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_017073m.g | PS.lightreaction.photosystem I.LHC-I | one-helix protein 2 | -0.75 | -1.47 | -0.15 | -1.45 | -0.07 | -1.04 | -0.32 | -1.70 | -0.92 | -2.52 |
| | cassava4.1_012896m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | -0.75 | -1.60 | -0.35 | -0.67 | -0.27 | -0.66 | -0.80 | -0.49 | 0.08 | 0.28 |
| | cassava4.1_015488m.g | PS.lightreaction.cytochrome b6/f.iron sulfur subunit | photosynthetic electron transfer C | -0.74 | -2.03 | -0.42 | -1.72 | -0.05 | -1.83 | -0.77 | -1.98 | -0.88 | -2.24 |
| | cassava4.1_019108m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit K | -0.73 | -3.55 | -0.17 | -3.16 | 0.04 | -3.16 | -0.60 | -2.27 | -1.22 | -3.25 |
| | cassava4.1_015604m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | PsbQ-like 1 | -0.73 | -1.80 | -0.87 | -1.94 | 0.09 | -1.48 | -0.56 | 0.56 | -0.09 | 0.63 |
| | cassava4.1_014868m.g | PS.lightreaction.ATP synthase.delta chain | ATP synthase delta-subunit gene | -0.72 | -2.38 | -0.55 | -1.95 | -0.08 | -1.92 | -0.73 | -2.01 | -0.95 | -2.54 |
| | cassava4.1_015015m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | PsbP-like protein 1 | -0.71 | -1.85 | -0.63 | -1.60 | 0.11 | -1.79 | -0.38 | -1.27 | -0.53 | -1.33 |
| | cassava4.1_014216m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II subunit P-1 | -0.70 | -2.03 | -0.08 | -2.04 | 0.01 | -2.75 | -0.73 | -2.05 | -0.78 | -2.51 |
| | cassava4.1_014117m.g | PS.lightreaction.photosystem II.LHC-II | light-harvesting chlorophyll B-binding protein 3 | -0.69 | -4.02 | -0.11 | -2.35 | 0.06 | -2.03 | -0.74 | -1.83 | -0.47 | -2.33 |
| | cassava4.1_015490m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit F | -0.68 | -2.28 | -0.21 | -2.40 | 0.07 | -2.45 | -0.67 | -2.13 | -0.86 | -2.55 |
| | cassava4.1_008115m.g | PS.lightreaction.NADH DH | unknow | -0.68 | -0.63 | -0.13 | -0.57 | -0.09 | -1.03 | -0.04 | 0.10 | -0.02 | -0.23 |
| | cassava4.1_014906m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 1 | -0.68 | -3.19 | -0.13 | -2.28 | -0.08 | -1.34 | -0.42 | -1.60 | -0.53 | -2.08 |
| | cassava4.1_014115m.g | PS.lightreaction.ATP synthase.subunit B_ (ATPX) | ATPase, F0 complex, subunit B/B', bacterial/chloroplast | -0.67 | -2.46 | -0.49 | -1.64 | -0.04 | -1.74 | -0.58 | -1.81 | -0.88 | -1.67 |
| | cassava4.1_018335m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit O | -0.63 | -2.45 | -0.11 | -2.70 | 0.03 | -3.21 | -0.70 | -2.46 | -0.81 | -2.88 |
| | cassava4.1_014010m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II subunit P-1 | -0.62 | -1.94 | -0.07 | -1.68 | -0.08 | -1.22 | -0.80 | -1.01 | -0.51 | -1.31 |
| | cassava4.1_017616m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) | -0.61 | -3.27 | -0.69 | -3.38 | 0.08 | -2.49 | -0.34 | -2.34 | -1.08 | -3.04 |
| | cassava4.1_015083m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | unclear | -0.61 | -2.30 | -0.63 | -2.14 | -0.13 | -1.82 | -0.49 | -2.37 | -0.80 | -2.14 |
| | cassava4.1_011842m.g | PS.lightreaction.cyclic electron flow-chlororespiration | PGR5-LIKE A | -0.60 | -1.80 | -0.25 | -2.07 | -0.06 | -1.97 | -0.18 | -1.80 | -0.88 | -2.53 |
| | cassava4.1_013916m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 2 | -0.60 | -3.24 | 0.15 | -3.21 | 0.01 | -2.78 | -0.64 | -2.45 | -0.71 | -2.91 |
| | cassava4.1_020972m.g | PS.lightreaction.ATP synthase.subunit B_ (ATPX) | Ubiquitin-like superfamily protein | -0.59 | -1.98 | -0.52 | -1.77 | 0.00 | -1.40 | -0.48 | -1.57 | -0.74 | -1.83 |
| | cassava4.1_016312m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit D-1 | -0.58 | -2.28 | -0.16 | -2.10 | 0.04 | -1.56 | -0.88 | -1.54 | -0.68 | -2.07 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_013735m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | Chlorophyll A-B binding family protein | -0.57 | -2.92 | -0.25 | -3.28 | 0.01 | -3.37 | -0.21 | -1.70 | -0.86 | -2.97 |
| | cassava4.1_015240m.g | PS.lightreaction.NADH DH | subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex | -0.57 | -1.48 | -0.55 | -1.85 | -0.10 | -1.82 | -0.63 | -0.94 | -0.97 | -2.14 |
| | cassava4.1_018584m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit H-1 | -0.54 | -2.43 | -0.24 | -2.26 | 0.12 | -2.59 | -0.66 | -1.74 | -1.12 | -2.61 |
| | cassava4.1_016411m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit D-1 | -0.54 | -1.51 | -0.25 | -1.87 | 0.05 | -1.92 | -0.76 | -1.59 | -0.93 | -2.29 |
| | cassava4.1_013872m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | -0.52 | -3.34 | -0.07 | -1.53 | 0.15 | -1.39 | 0.44 | -1.44 | -0.45 | -1.58 |
| | cassava4.1_018544m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit E-2 | -0.52 | -2.16 | -0.16 | -2.33 | 0.06 | -2.15 | -0.63 | -1.90 | -0.73 | -2.55 |
| | cassava4.1_019040m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II reaction center W | -0.52 | -2.25 | -0.42 | -2.71 | 0.07 | -2.40 | -0.48 | -2.00 | -0.92 | -2.53 |
| | cassava4.1_010951m.g | PS.lightreaction.photosystem II.LHC-II | Chlorophyll A-B binding family protein | -0.50 | -1.73 | -0.01 | -1.86 | 0.07 | -1.87 | -0.47 | -1.82 | -0.81 | -2.53 |
| | cassava4.1_026492m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | Photosystem II reaction center PsbP family protein | -0.49 | -1.11 | -0.09 | -0.60 | -0.16 | -0.88 | -0.41 | -1.13 | -0.72 | -1.19 |
| | cassava4.1_016712m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II BY | -0.48 | -1.69 | -0.24 | -1.96 | -0.04 | -1.67 | -0.53 | -1.36 | -1.15 | -2.34 |
| | cassava4.1_018917m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II reaction center W | -0.48 | -2.08 | -0.32 | -2.14 | 0.01 | -1.72 | -0.34 | -1.56 | -0.84 | -2.20 |
| | cassava4.1_015547m.g | PS.lightreaction.NADH DH | oxidoreductases, acting on NADH or NADPH, quinone or similar compound as acceptor | -0.44 | -1.90 | -0.68 | -1.77 | 0.05 | -2.06 | -0.75 | -0.96 | -0.85 | -1.86 |
| | cassava4.1_030615m.g | PS.lightreaction.ATP synthase.chloroplastic subunit a | ATPase, F0 complex, subunit A protein | -0.43 | -0.49 | -0.11 | -0.09 | 0.46 | -0.35 | 0.10 | -2.20 | -0.32 | -1.59 |
| | cassava4.1_016692m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | low psii accumulation2 | -0.42 | -0.67 | -0.05 | -0.37 | 0.23 | -0.72 | -0.85 | -0.64 | -0.66 | -1.03 |
| | cassava4.1_018334m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | photosystem I subunit G | -0.38 | -1.68 | -0.23 | -2.02 | 0.00 | -1.61 | -0.39 | -1.59 | -0.70 | -2.01 |
| | cassava4.1_013957m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 2 | -0.37 | -2.64 | -0.14 | -2.68 | 0.08 | -2.53 | -0.63 | -1.72 | -0.89 | -2.68 |
| | cassava4.1_016854m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II BY | -0.37 | -1.81 | -0.13 | -2.11 | 0.03 | -1.83 | -0.46 | -1.36 | -1.34 | -2.59 |
| | cassava4.1_018756m.g | PS.lightreaction.photosystem II.PSII polypeptide | photosystem II subunit R | -0.36 | -1.80 | -0.24 | -1.92 | -0.05 | -2.05 | -0.48 | -1.42 | -1.22 | -2.90 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | subunits | | | | | | | | | | | |
| | cassava4.1_013684m.g | PS.lightreaction.photosystem I.LHC-I | photosystem I light harvesting complex gene 3 | -0.36 | -2.84 | -0.32 | -2.82 | 0.04 | -2.15 | -0.41 | -2.00 | -0.78 | -2.57 |
| | cassava4.1_018388m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin | 2Fe-2S ferredoxin-like superfamily protein | -0.35 | -1.09 | -0.71 | -1.20 | -0.34 | -0.84 | -0.32 | -1.53 | -0.51 | -1.32 |
| | cassava4.1_019355m.g | PS.lightreaction.cyclic electron flow-chlororespiration | proton gradient regulation 5 | -0.34 | -1.94 | 0.13 | -0.03 | -0.02 | -0.32 | -0.26 | -0.05 | -0.83 | -1.61 |
| | cassava4.1_004476m.g | PS.lightreaction.state transition | STT7 homolog STN7 | -0.32 | -1.32 | -0.08 | -1.20 | 0.04 | -1.24 | 0.12 | -1.84 | -0.68 | -2.04 |
| | cassava4.1_019321m.g | PS.lightreaction.cyclic electron flow-chlororespiration | proton gradient regulation 5 | -0.29 | -2.37 | -0.10 | -1.31 | 0.03 | -1.78 | -0.17 | -0.50 | -1.02 | -2.22 |
| | cassava4.1_017598m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II family protein | -0.28 | -1.62 | -0.17 | -1.23 | 0.11 | -1.36 | -0.85 | -1.41 | -0.71 | -1.66 |
| | cassava4.1_004477m.g | PS.lightreaction.state transition | STT7 homolog STN7 | -0.25 | -1.61 | -0.25 | -2.00 | 0.00 | -2.42 | -0.17 | -1.94 | -0.71 | -2.63 |
| | cassava4.1_012618m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin oxireductase | FAD/NAD(P)-binding oxidoreductase | -0.24 | -0.96 | -0.19 | -0.66 | 0.01 | -0.32 | -0.35 | -1.17 | -0.56 | -1.53 |
| | cassava4.1_013632m.g | PS.lightreaction.photosystem II.LHC-II | light harvesting complex photosystem II subunit 6 | -0.21 | -1.85 | -0.22 | -1.95 | 0.10 | -1.71 | -0.70 | -1.00 | -0.90 | -2.00 |
| | cassava4.1_031236m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II reaction center protein A | -0.15 | -0.97 | -1.38 | -1.02 | 0.36 | -0.11 | -0.45 | -1.01 | -0.94 | -1.63 |
| | cassava4.1_016776m.g | PS.lightreaction.other electron carrier (ox/red).ferredoxin | NDH-dependent cyclic electron flow 1 | -0.09 | -0.33 | -0.60 | -1.79 | -0.25 | -2.48 | -0.60 | -0.52 | -0.91 | -0.86 |
| | cassava4.1_027296m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | Photosystem I, PsaA/PsaB protein | -0.04 | -0.42 | -1.97 | -0.82 | -0.14 | -1.31 | -0.53 | -2.52 | -0.10 | -1.97 |
| | cassava4.1_013335m.g | PS.lightreaction.cyclic electron flow-chlororespiration | post-illumination chlorophyll fluorescence increase | -0.03 | -1.60 | -0.03 | -2.39 | 0.11 | -2.90 | -0.16 | -1.29 | -0.71 | -2.74 |
| | cassava4.1_018830m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II subunit R | 0.28 | -0.12 | -0.06 | -1.59 | 0.27 | -1.41 | -0.24 | -0.38 | -0.92 | -2.73 |
| | cassava4.1_025967m.g | PS.lightreaction.ATP synthase | ATP synthase protein I -related | 0.31 | 0.18 | 0.17 | -1.60 | 0.03 | -2.22 | 0.00 | -0.64 | -0.48 | -1.71 |
| | cassava4.1_029388m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | Photosystem I, PsaA/PsaB protein | 0.34 | -0.01 | -1.34 | -0.31 | -0.55 | -1.28 | -0.46 | -2.15 | -0.11 | -2.27 |
| | cassava4.1_020912m.g | PS.lightreaction.ATP synthase.chloroplastic subunit a | ATPase, F0 complex, subunit A protein | 0.35 | 0.29 | -0.91 | -0.66 | 0.91 | -0.48 | -0.29 | -2.27 | -0.43 | -1.84 |
| | cassava4.1_022954m.g | PS.lightreaction.photosystem I.PSI polypeptide subunits | Photosystem I, PsaA/PsaB protein | 0.48 | -1.13 | -0.05 | -0.66 | -0.16 | -1.20 | -0.10 | -1.78 | 0.05 | -2.08 |
| | cassava4.1_031110m.g | PS.lightreaction.photosystem II.PSII polypeptide subunits | photosystem II reaction center protein D | 0.49 | 0.38 | -0.65 | -0.40 | -1.05 | -0.77 | 0.62 | -2.04 | -0.47 | -2.67 |
| Calvin Cycle | cassava4.1_029431m.g | PS.calvin cycle.Rib5P Isomerase | NagB/RpiA/CoA transferase-like superfamily protein | -1.53 | -2.32 | -0.73 | -2.55 | -0.03 | -3.17 | -1.05 | -2.51 | -0.93 | -2.97 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_017243m.g | PS.calvin cycle.rubisco small subunit | Ribulose bisphosphate carboxylase (small chain) family protein | -1.48 | -2.83 | -0.71 | -2.14 | -0.13 | -3.06 | -1.31 | -2.70 | -0.82 | -2.71 |
| | cassava4.1_030397m.g | PS.calvin cycle.FBPase | high cyclic electron flow 1 | -1.46 | -3.28 | 0.45 | -0.61 | 0.36 | -2.44 | -1.10 | -3.65 | -0.94 | -2.08 |
| | cassava4.1_012057m.g | PS.calvin cycle.TPI | triosephosphate isomerase | -1.39 | -1.73 | -0.39 | -0.79 | -0.29 | -0.58 | -1.15 | -1.48 | -0.74 | -0.61 |
| | cassava4.1_011197m.g | PS.calvin cycle.FBPase | Inositol monophosphatase family protein | -1.36 | -3.76 | -0.89 | -3.04 | -0.37 | -3.56 | -0.19 | -3.54 | -0.76 | -3.53 |
| | cassava4.1_007468m.g | PS.calvin cycle.GAP | glyceraldehyde-3-phosphate dehydrogenase B subunit | -1.24 | -5.51 | -0.65 | -5.32 | -0.11 | -5.90 | -0.49 | -4.58 | -0.91 | -5.38 |
| | cassava4.1_010561m.g | PS.calvin cycle.aldolase | Aldolase superfamily protein | -1.17 | -4.18 | -0.72 | -4.45 | -0.10 | -4.50 | -0.84 | -3.41 | -1.18 | -4.14 |
| | cassava4.1_006492m.g | PS.calvin cycle.rubisco interacting | Rubisco methyltransferase family protein | -1.15 | -2.17 | -0.72 | -0.95 | -0.07 | -1.77 | -0.88 | -0.73 | 0.09 | -0.49 |
| | cassava4.1_006605m.g | PS.calvin cycle.phosphoglycerate kinase | Phosphoglycerate kinase family protein | -1.07 | -3.08 | -0.44 | -2.95 | -0.34 | -3.22 | -0.49 | -2.47 | -0.96 | -3.34 |
| | cassava4.1_008668m.g | PS.calvin cycle.FBPase | high cyclic electron flow 1 | -1.07 | -3.35 | -0.55 | -3.05 | -0.02 | -3.81 | -0.82 | -2.46 | -0.91 | -3.01 |
| | cassava4.1_008849m.g | PS.calvin cycle.PRK | phosphoribulokinase | -1.04 | -3.22 | -0.58 | -2.94 | -0.11 | -3.41 | -0.52 | -2.56 | -0.97 | -3.10 |
| | cassava4.1_014454m.g | PS.calvin cycle.TPI | triosephosphate isomerase | -1.01 | -2.70 | -0.35 | -1.79 | -0.28 | -1.66 | -0.55 | -2.79 | -0.88 | -2.74 |
| | cassava4.1_008960m.g | PS.calvin cycle.GAP | glyceraldehyde 3-phosphate dehydrogenase A subunit | -0.88 | -2.75 | -0.56 | -2.14 | -0.09 | -2.04 | -0.77 | -2.27 | -0.91 | -2.55 |
| | cassava4.1_017170m.g | PS.calvin cycle.rubisco small subunit | Ribulose bisphosphate carboxylase (small chain) family protein | -0.88 | -3.08 | -0.49 | -2.78 | -0.09 | -3.52 | -0.52 | -2.63 | -0.82 | -2.77 |
| | cassava4.1_014243m.g | PS.calvin cycle.FBPase | Inositol monophosphatase family protein | -0.87 | -3.71 | -0.43 | -2.52 | -0.20 | -3.82 | -0.19 | -2.93 | -0.50 | -3.12 |
| | cassava4.1_012016m.g | PS.calvin cycle.TPI | triosephosphate isomerase | -0.83 | -1.29 | -0.23 | -0.79 | -0.15 | -1.06 | -0.77 | -1.58 | -0.87 | -1.50 |
| | cassava4.1_006803m.g | PS.calvin cycle.rubisco interacting | rubisco activase | -0.81 | -3.62 | -0.69 | -3.00 | -0.31 | -3.54 | -0.45 | -2.90 | -0.84 | -3.52 |
| | cassava4.1_002307m.g | PS.calvin cycle.transketolase | Transketolase | -0.80 | -2.18 | -0.27 | -1.06 | -0.06 | -0.56 | -0.38 | -1.47 | -0.68 | -1.60 |
| | cassava4.1_008965m.g | PS.calvin cycle.GAP | glyceraldehyde 3-phosphate dehydrogenase A subunit | -0.78 | -2.98 | -0.47 | -2.20 | -0.15 | -2.36 | -0.67 | -2.44 | -0.82 | -2.60 |
| | cassava4.1_013583m.g | PS | acclimation of photosynthesis to environment | -0.74 | -2.09 | -0.29 | -1.71 | 0.11 | -1.72 | -0.42 | -1.71 | -0.93 | -2.30 |
| | cassava4.1_009395m.g | PS.calvin cycle.seduheptulose bisphosphatase | sedoheptulose-bisphosphatase | -0.73 | -2.57 | -0.52 | -1.88 | 0.03 | -2.07 | -0.37 | -1.59 | -0.77 | -2.15 |
| | cassava4.1_008894m.g | PS.calvin cycle.PRK | phosphoribulokinase | -0.71 | -1.81 | -0.36 | -1.65 | -0.02 | -2.00 | -0.64 | -1.41 | -0.94 | -2.35 |
| | cassava4.1_007476m.g | PS.calvin cycle.GAP | glyceraldehyde-3-phosphate dehydrogenase B subunit | -0.68 | -1.58 | -0.33 | -1.23 | -0.10 | -1.57 | -0.45 | -1.95 | -0.55 | -1.93 |
| | cassava4.1_006183m.g | PS.calvin cycle.GAP | aldehyde dehydrogenase 11A3 | -0.63 | -2.11 | -0.19 | -0.53 | -0.03 | 0.13 | -0.10 | -0.48 | -0.71 | -0.82 |
| | cassava4.1_009163m.g | PS.calvin cycle.aldolase | fructose-bisphosphate aldolase 2 | -0.57 | -2.44 | -0.23 | -2.35 | -0.01 | -3.18 | 0.07 | -2.81 | -0.25 | -2.84 |
| | cassava4.1_009140m.g | PS.calvin cycle.aldolase | fructose-bisphosphate aldolase 2 | -0.55 | -2.12 | -0.62 | -2.29 | 0.09 | -2.07 | -0.47 | -2.20 | -0.50 | -2.67 |
| | cassava4.1_006596m.g | PS.calvin cycle.phosphoglycerate kinase | Phosphoglycerate kinase family protein | -0.51 | -1.28 | -0.27 | -0.93 | 0.05 | -0.85 | -0.50 | -1.40 | -0.76 | -2.00 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_009143m.g | PS.calvin cycle.aldolase | fructose-bisphosphate aldolase 2 | -0.51 | -2.79 | -0.47 | -2.20 | -0.03 | -1.77 | -0.18 | -1.58 | -0.62 | -2.17 |
| | cassava4.1_017330m.g | PS.calvin cycle.rubisco large subunit | ribulose-bisphosphate carboxylases | -0.47 | -0.25 | -1.21 | -0.37 | 0.11 | -0.06 | -1.09 | -1.99 | -0.83 | -2.31 |
| | cassava4.1_013479m.g | PS.calvin cycle.RPE | D-ribulose-5-phosphate-3-epimerase | -0.45 | -1.70 | -0.32 | -1.86 | -0.08 | -2.41 | -0.31 | -1.90 | -0.97 | -2.82 |
| | cassava4.1_006796m.g | PS.calvin cycle.rubisco interacting | rubisco activase | -0.31 | -2.06 | -0.27 | -2.60 | -0.12 | -2.21 | 1.45 | -1.09 | -0.29 | -2.37 |
| | cassava4.1_033564m.g | PS.calvin cycle.rubisco interacting | P-loop containing nucleoside triphosphate hydrolases superfamily protein | -0.29 | -1.46 | -0.06 | -0.88 | 0.03 | -1.90 | 0.39 | -2.44 | -0.52 | -2.20 |
| | cassava4.1_009003m.g | PS.calvin cycle.phosphoglycerate kinase | phosphoglycerate kinase | -0.07 | -0.16 | 0.02 | -0.10 | -0.13 | 0.06 | -0.23 | 0.08 | -0.69 | -1.08 |
| | cassava4.1_019184m.g | PS.calvin cycle | CP12 domain-containing protein 2 | 0.37 | 0.01 | 0.00 | -1.28 | 0.16 | -1.55 | -0.35 | -0.61 | -0.79 | -1.77 |
| | cassava4.1_023305m.g | PS.calvin cycle.rubisco large subunit | ribulose-bisphosphate carboxylases | 0.67 | -0.34 | -1.78 | -0.56 | -0.03 | -0.72 | -1.03 | -1.53 | -0.32 | -2.29 |
| Photorespiration | cassava4.1_005710m.g | PS.photorespiration.serine hydroxymethyltransferase | serine transhydroxymethyltransferase 1 | -1.25 | -3.78 | -0.61 | -4.50 | 0.01 | -4.10 | -0.12 | -3.73 | -0.92 | -4.28 |
| | cassava4.1_005814m.g | PS.photorespiration.serine hydroxymethyltransferase | serine transhydroxymethyltransferase 1 | -1.16 | -3.56 | -0.34 | -2.81 | 0.05 | -3.22 | -0.33 | -2.73 | -0.70 | -2.98 |
| | cassava4.1_008994m.g | PS.photorespiration.aminotransferases peroxisomal | alanine:glyoxylate aminotransferase | -1.05 | -3.36 | -0.77 | -3.49 | -0.09 | -3.05 | -0.19 | -2.29 | -0.57 | -2.68 |
| | cassava4.1_017913m.g | PS.photorespiration.glycine cleavage.H protein | Single hybrid motif superfamily protein | -0.98 | -2.64 | -1.00 | -2.60 | -0.10 | -2.30 | -0.69 | -1.75 | -1.05 | -2.30 |
| | cassava4.1_009477m.g | PS.photorespiration.hydroxypyruvate reductase | hydroxypyruvate reductase | -0.88 | -2.85 | -0.51 | -2.71 | -0.04 | -2.81 | -0.33 | -2.24 | -0.81 | -2.88 |
| | cassava4.1_011790m.g | PS.photorespiration | formyltetrahydrofolate deformylase, putative | -0.72 | -2.09 | -0.23 | -1.09 | -0.05 | -1.99 | -0.39 | -1.87 | -0.56 | -1.86 |
| | cassava4.1_008989m.g | PS.photorespiration.aminotransferases peroxisomal | alanine:glyoxylate aminotransferase | -0.69 | -2.17 | -0.67 | -2.37 | 0.00 | -1.82 | -0.13 | -1.84 | -0.57 | -2.53 |
| | cassava4.1_010145m.g | PS.photorespiration.glycolate oxydase | Aldolase-type TIM barrel family protein | -0.67 | -2.98 | -0.33 | -2.89 | 0.06 | -2.87 | -0.06 | -1.82 | -0.54 | -2.51 |
| | cassava4.1_010148m.g | PS.photorespiration.glycolate oxydase | Aldolase-type TIM barrel family protein | -0.64 | -2.37 | -0.52 | -2.10 | -0.14 | -1.88 | -0.27 | -1.99 | -0.74 | -2.48 |
| | cassava4.1_006274m.g | PS.photorespiration.glycerate kinase | P-loop containing nucleoside triphosphate hydrolases superfamily protein | -0.54 | -1.45 | -0.10 | -1.45 | 0.05 | -1.83 | -0.19 | -1.64 | -0.61 | -2.16 |
| | cassava4.1_012207m.g | PS.photorespiration.hydroxypyruvate reductase | D-isomer specific 2-hydroxyacid dehydrogenase family protein | -0.42 | -2.01 | 0.14 | -2.17 | 0.15 | -2.58 | -0.46 | -1.42 | -0.58 | -2.18 |
| | cassava4.1_004233m.g | nitrite reductase 1 | N-metabolism.nitrate metabolism.nitrite reductase | -2.35 | -3.89 | -0.98 | -0.68 | -0.31 | -2.51 | -1.02 | -3.32 | -0.51 | -1.51 |
| | cassava4.1_009848m.g | FMN-linked oxidoreductases superfamily protein | N-metabolism.misc | -1.18 | -1.61 | -0.16 | -0.46 | 0.12 | -0.41 | -0.26 | -2.46 | -0.37 | -1.36 |
| | cassava4.1_008019m.g | glutamine synthetase 2 | N-metabolism.ammonia metabolism.glutamine synthetase | -1.05 | -2.83 | -0.45 | -2.12 | -0.22 | -2.78 | -0.85 | -2.59 | -0.71 | -2.54 |
| | cassava4.1_000214m.g | glutamate synthase 1 | N-metabolism.ammonia metabolism.glutamate synthase | -0.99 | -2.47 | -0.27 | -2.31 | -0.37 | -2.45 | 0.10 | -2.91 | -0.78 | -3.14 |
| | cassava4.1_031400m.g | nitrate reductase 1 | N-metabolism.nitrate metabolism.NR | -0.98 | -2.84 | -0.45 | -1.49 | -0.15 | -3.11 | -0.49 | -3.61 | -0.40 | -2.09 |
| | cassava4.1_007225m.g | nitrate reductase 1 | N-metabolism.nitrate metabolism.NR | -0.84 | -2.80 | -0.64 | -1.31 | 0.00 | -2.69 | -0.62 | -3.58 | -0.29 | -1.46 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | cassava4.1_003338m.g | nitroreductase family protein | N-metabolism.misc | -0.60 | -1.13 | -0.73 | -1.46 | -0.11 | -0.79 | 0.21 | -0.74 | -0.41 | -1.26 |
|  | cassava4.1_009228m.g | sulfite oxidase | N-metabolism.nitrate metabolism.NR | -0.52 | -1.65 | -0.06 | -1.16 | -0.23 | -0.79 | 0.19 | -2.88 | -0.64 | -2.49 |
|  | cassava4.1_000040m.g | NADH-dependent glutamate synthase 1 | N-metabolism.ammonia metabolism.glutamate synthase | -0.30 | -2.18 | -0.20 | -2.68 | -0.36 | -2.31 | 0.53 | -1.75 | -1.09 | -3.48 |
|  | cassava4.1_010581m.g | glutamine synthase clone R1 | N-metabolism.ammonia metabolism.glutamine synthetase | -0.26 | 0.09 | -0.03 | 0.94 | -0.09 | 1.32 | -0.83 | -0.62 | -0.31 | -0.33 |
|  | cassava4.1_000038m.g | NADH-dependent glutamate synthase 1 | N-metabolism.ammonia metabolism.glutamate synthase | 0.09 | 0.02 | 0.51 | 0.81 | -0.38 | 0.89 | 0.97 | 0.24 | 0.24 | 0.81 |
|  | cassava4.1_001290m.g | signalling.in sugar and nutrient physiology | glutamate receptor 5 | 0.22 | 0.80 | 0.64 | 0.83 | 0.12 | 0.08 | 0.27 | 0.86 | 0.44 | 0.88 |
|  | cassava4.1_010597m.g | glutamine synthase clone R1 | N-metabolism.ammonia metabolism.glutamine synthetase | 0.29 | 0.27 | 0.01 | 0.19 | -0.30 | -0.07 | -1.14 | -0.59 | -0.15 | -0.51 |
| Tetrapyrrole Synthesis | cassava4.1_028676m.g | tetrapyrrole synthesis.uroporphyrin-III C-methyltransferase | urophorphyrin methylase 1 | -1.89 | -1.78 | 0.44 | 1.49 | -0.40 | 0.16 | -1.40 | -2.91 | 0.13 | -0.44 |
|  | cassava4.1_010226m.g | tetrapyrrole synthesis.uroporphyrin-III C-methyltransferase | urophorphyrin methylase 1 | -1.53 | -2.13 | 0.22 | 0.45 | -0.70 | -0.50 | -0.75 | -2.86 | -0.84 | -1.25 |
|  | cassava4.1_027491m.g | tetrapyrrole synthesis.ALA dehydratase | Aldolase superfamily protein | -0.97 | -2.63 | 0.19 | -1.67 | 0.04 | -2.49 | -0.88 | -2.32 | -0.57 | -2.29 |
|  | cassava4.1_031984m.g | tetrapyrrole synthesis.uroporphyrinogen III synthase | uroporphyrinogen-III synthase family protein | -0.95 | -1.60 | -0.62 | -0.86 | -0.36 | -1.83 | 0.02 | -1.67 | -0.04 | -1.13 |
|  | cassava4.1_013789m.g | tetrapyrrole synthesis.regulation | enzyme binding;tetrapyrrole binding | -0.92 | -3.38 | -0.56 | -2.41 | 0.09 | -1.99 | -0.02 | -1.70 | -0.40 | -2.54 |
|  | cassava4.1_000280m.g | tetrapyrrole synthesis.magnesium chelatase | magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH) | -0.91 | -2.90 | -0.16 | -2.19 | -0.12 | -2.38 | -0.14 | -2.19 | -0.58 | -2.66 |
|  | cassava4.1_002247m.g | tetrapyrrole synthesis.magnesium chelatase | ALBINA 1 | -0.74 | -1.35 | -0.41 | -1.00 | -0.09 | -1.72 | -0.25 | -1.02 | 0.04 | -0.22 |
|  | cassava4.1_005000m.g | tetrapyrrole synthesis.glu-tRNA synthetase | Amidase family protein | -0.73 | -1.70 | -0.42 | -1.29 | -0.02 | -0.77 | -0.61 | -0.74 | -0.40 | -0.86 |
|  | cassava4.1_008391m.g | tetrapyrrole synthesis.magnesium chelatase | P-loop containing nucleoside triphosphate hydrolases superfamily protein | -0.72 | -1.50 | -0.30 | -1.04 | -0.09 | -1.33 | -1.00 | -1.08 | -0.64 | -1.09 |
|  | cassava4.1_004598m.g | tetrapyrrole synthesis.glu-tRNA synthetase | GLU-ADT subunit B | -0.72 | -1.24 | -0.01 | -0.44 | -0.18 | -0.78 | -0.68 | -1.22 | -0.37 | -0.82 |
|  | cassava4.1_008382m.g | tetrapyrrole synthesis.magnesium chelatase | magnesium chelatase i2 | -0.69 | -1.46 | 0.12 | -0.68 | 0.16 | -1.51 | -0.57 | 0.65 | -0.16 | 0.19 |
|  | cassava4.1_008691m.g | tetrapyrrole synthesis.magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase | dicarboxylate diiron protein, putative (Crd1) | -0.64 | -2.84 | -0.25 | -2.29 | 0.04 | -2.36 | -0.49 | -1.80 | -0.87 | -2.33 |
|  | cassava4.1_009378m.g | tetrapyrrole synthesis.uroporphyrinogen decarboxylase | Uroporphyrinogen decarboxylase | -0.61 | -1.30 | -0.01 | -1.24 | 0.07 | -1.91 | -0.66 | -0.97 | -0.50 | -1.08 |
|  | assava4.1_009000m.g | tetrapyrrole synthesis.coproporphyrinogen III oxidase | Coproporphyrinogen III oxidase | -0.59 | -0.85 | -0.18 | -0.46 | -0.10 | -0.29 | -0.64 | -0.70 | -0.16 | -0.43 |
|  | cassava4.1_008036m.g | tetrapyrrole synthesis.ALA dehydratase | Aldolase superfamily protein | -0.56 | -1.17 | -0.03 | -0.82 | -0.05 | -0.81 | -0.43 | -0.78 | -0.41 | -0.78 |
|  | cassava4.1_008914m.g | tetrapyrrole synthesis.protochlorophyllide reductase | protochlorophyllide oxidoreductase C | -0.55 | -2.06 | -0.28 | -2.33 | 0.00 | -1.76 | 0.39 | -1.58 | -0.46 | -1.93 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_006730m.g | tetrapyrrole synthesis.GSA | glutamate-1-semialdehyde 2,1-aminomutase 2 | -0.52 | -1.49 | -0.08 | -1.06 | 0.02 | -0.91 | -0.83 | -0.43 | -0.37 | -0.52 |
| | cassava4.1_005258m.g | tetrapyrrole synthesis.chlorophyll b synthase | Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain | -0.49 | -2.33 | -0.19 | -1.90 | 0.14 | -2.25 | -0.12 | -1.93 | -0.52 | -2.15 |
| | cassava4.1_004918m.g | tetrapyrrole synthesis.glu-tRNA reductase | Glutamyl-tRNA reductase family protein | -0.48 | -0.76 | 1.04 | 1.07 | 0.35 | 0.52 | -0.65 | -1.12 | -0.30 | -0.51 |
| | cassava4.1_013127m.g | tetrapyrrole synthesis.heme oxygenase | Plant haem oxygenase (decyclizing) family protein | -0.47 | -0.73 | -0.42 | -0.94 | -0.09 | -0.51 | 0.00 | -1.76 | -0.85 | -2.11 |
| | cassava4.1_009920m.g | tetrapyrrole synthesis.chlorophyll synthase | UbiA prenyltransferase family protein | -0.46 | -0.43 | -0.21 | -0.55 | -0.10 | -0.80 | -0.28 | -1.05 | -0.09 | -0.73 |
| | cassava4.1_007874m.g | tetrapyrrole synthesis.ferrochelatase | ferrochelatase 2 | -0.36 | -1.53 | -0.23 | -0.89 | 0.00 | -0.74 | 0.10 | -0.47 | -0.33 | -0.74 |
| | cassava4.1_011961m.g | tetrapyrrole synthesis.magnesium protoporphyrin IX methyltransferase | magnesium-protoporphyrin IX methyltransferase | -0.35 | -2.00 | 0.16 | -2.31 | -0.04 | -2.35 | -0.66 | -1.26 | -0.26 | -1.23 |
| | cassava4.1_017765m.g | tetrapyrrole synthesis.uroporphyrinogen III synthase | uroporphyrinogen-III synthase family protein | -0.31 | -1.19 | -0.10 | -0.95 | 0.06 | -1.90 | -0.38 | -1.96 | -0.94 | -1.90 |
| | cassava4.1_008498m.g | tetrapyrrole synthesis.divinyl chlorophyllide-a 8-vinyl-reductase | NAD(P)-binding Rossmann-fold superfamily protein | -0.29 | -0.83 | 0.49 | -0.42 | -0.10 | -1.36 | 0.19 | -0.93 | -0.61 | -1.56 |
| | cassava4.1_009063m.g | tetrapyrrole synthesis.protochlorophyllide reductase | protochlorophyllide oxidoreductase A | 0.54 | -0.30 | 0.42 | -1.38 | 0.04 | -2.21 | -0.88 | 0.10 | 0.08 | -0.58 |

## Supplemental Table S5. Genes annotated to glycolysis, TCA, mitochondrial electron transport and flavonoid biosynthetic pathway.

## The extent of differential expression is measured in terms of log2 fold change of treatment vs. control.

| Table Class | Cassava ID | Mapman Category | Short Description | PG0 | FG0 | PG2 | FG2 | PG4 | FG4 | PG0 | FG0 | PG2 | FG2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | 120 day | | | | | | 45 day | | | |
| Glycolysis | cassava4.1_006973m.g | glycolysis.cytosolic branch.UGPase | UDP-glucose pyrophosphorylase 2 | -0.46 | -0.20 | -0.35 | -0.01 | -0.31 | 0.07 | -0.48 | -0.78 | -0.77 | -0.99 |
| | cassava4.1_006979m.g | glycolysis.cytosolic branch.UGPase | UDP-glucose pyrophosphorylase 2 | 0.90 | 2.14 | 0.73 | 1.79 | 0.30 | 2.29 | 0.20 | 1.60 | 0.42 | 1.77 |
| | cassava4.1_003757m.g | glycolysis.cytosolic branch.phosphofructokinase (PFK) | Phosphofructokinase family protein | 0.13 | 0.66 | 0.26 | 0.64 | 0.00 | 0.95 | 0.03 | 0.80 | -0.20 | 0.67 |
| | cassava4.1_003814m.g | glycolysis.cytosolic branch.phosphofructokinase (PFK) | Phosphofructokinase family protein | 0.25 | 0.61 | 0.12 | 1.13 | 0.14 | 2.18 | -0.81 | 1.48 | 0.24 | 1.72 |
| | cassava4.1_004602m.g | glycolysis.cytosolic branch.phosphofructokinase (PFK) | Phosphofructokinase family protein | -0.12 | 0.03 | 0.06 | 0.41 | 0.09 | 0.96 | -0.57 | 1.01 | -0.02 | 0.88 |
| | cassava4.1_014454m.g | glycolysis.cytosolic branch.triosephosphate isomerase (TPI) | triosephosphate isomerase | -1.01 | -2.70 | -0.35 | -1.79 | -0.28 | -1.66 | -0.55 | -2.79 | -0.88 | -2.74 |
| | cassava4.1_008220m.g | glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH) | glyceraldehyde-3-phosphate dehydrogenase of plastid 2 | 1.59 | 2.68 | 1.64 | 2.64 | 0.34 | 2.92 | 0.63 | 2.27 | 0.65 | 2.01 |
| | cassava4.1_008225m.g | glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH) | glyceraldehyde-3-phosphate dehydrogenase of plastid 2 | 1.95 | 3.75 | 0.65 | 2.33 | -0.18 | 3.72 | -1.18 | 3.27 | 2.05 | 4.67 |
| | cassava4.1_011176m.g | glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH) | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | 0.31 | 1.01 | -0.17 | 0.37 | -0.13 | 0.89 | 0.19 | 0.72 | -0.22 | 0.29 |
| | cassava4.1_011340m.g | glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH) | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | -0.02 | 0.50 | -0.06 | 0.44 | -0.02 | 0.88 | -0.60 | 0.43 | -0.37 | 0.29 |
| | cassava4.1_007673m.g | glycolysis.cytosolic branch.enolase | Enolase | 0.22 | 0.34 | 0.24 | 0.75 | 0.16 | 1.08 | 0.31 | 1.04 | 0.03 | 0.70 |
| | cassava4.1_006316m.g | glycolysis.cytosolic branch.pyruvate kinase (PK) | Pyruvate kinase family protein | 0.29 | 1.19 | 0.75 | 2.61 | 0.05 | 2.03 | 0.22 | 0.67 | 0.70 | 2.41 |
| | cassava4.1_005850m.g | glycolysis.cytosolic branch.pyruvate kinase (PK) | Pyruvate kinase family protein | 0.30 | 0.80 | 0.53 | 1.25 | -0.14 | 1.66 | -0.40 | 0.61 | -0.31 | 0.72 |
| | cassava4.1_005893m.g | glycolysis.cytosolic branch.pyruvate kinase (PK) | Pyruvate kinase family protein | 1.27 | 1.82 | 0.35 | 1.49 | 0.18 | 1.08 | -0.44 | 2.10 | -0.17 | 0.52 |
| | cassava4.1_000725m.g | glycolysis.cytosolic branch.phospho-enol-pyruvate carboxylase (PEPC) | phosphoenolpyruvate carboxylase 4 | 0.08 | -0.05 | -0.05 | -0.73 | 0.09 | -0.31 | 0.30 | -0.98 | -0.05 | -0.56 |
| | cassava4.1_001047m.g | glycolysis.cytosolic branch.phospho-enol-pyruvate carboxylase (PEPC) | phosphoenolpyruvate carboxylase 1 | -0.88 | -1.80 | -0.22 | -1.18 | -0.07 | -0.96 | -0.12 | -2.21 | -0.53 | -1.84 |
| | cassava4.1_003792m.g | glycolysis.plastid branch.phosphoglucomutase (PGM) | phosphoglucosamine mutase family protein | 0.38 | 1.30 | 0.60 | 1.05 | 0.00 | 0.42 | 0.14 | 1.30 | 0.26 | 0.87 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_006414m.g | glycolysis.plastid branch.glucose-6-phosphate isomerase | phosphoglucose isomerase 1 | 1.55 | 2.39 | 1.14 | 1.65 | 0.25 | 0.64 | -0.42 | 1.63 | 0.12 | 1.28 |
| | cassava4.1_005217m.g | glycolysis.plastid branch.phosphofructokinase (PFK) | phosphofructokinase 5 | 1.12 | 1.68 | 0.88 | 1.78 | 0.23 | 2.05 | -0.03 | 2.01 | -0.07 | 1.77 |
| | cassava4.1_005438m.g | glycolysis.plastid branch.phosphofructokinase (PFK) | phosphofructokinase 4 | 0.43 | 0.64 | 0.15 | 0.25 | 0.20 | 0.55 | -0.49 | 1.22 | 0.26 | 0.91 |
| | cassava4.1_005418m.g | glycolysis.plastid branch.pyruvate kinase (PK) | Pyruvate kinase family protein | 0.66 | 1.11 | -0.14 | 1.01 | 0.07 | 1.41 | 0.14 | 1.15 | -0.27 | 0.24 |
| | cassava4.1_004396m.g | glycolysis.plastid branch.pyruvate kinase (PK) | plastidic pyruvate kinase beta subunit 1 | 0.00 | 1.36 | 0.39 | 1.87 | -0.10 | 2.37 | -0.68 | 0.43 | 0.23 | 1.52 |
| | cassava4.1_004405m.g | glycolysis.plastid branch.pyruvate kinase (PK) | plastidic pyruvate kinase beta subunit 1 | 0.25 | 1.14 | 0.08 | 0.91 | 0.23 | 1.49 | -0.31 | 1.28 | 0.59 | 1.86 |
| | cassava4.1_006316m.g | glycolysis.plastid branch.pyruvate kinase (PK) | Pyruvate kinase family protein | 0.29 | 1.19 | 0.75 | 2.61 | 0.05 | 2.03 | 0.22 | 0.67 | 0.70 | 2.41 |
| | cassava4.1_006063m.g | glycolysis.unclear/dually targeted.phosphoglycerate mutase | phosphoglycerate/bisphosphoglycerate mutase family protein | -0.01 | -1.07 | 0.57 | -0.38 | 0.06 | -0.38 | 0.33 | 0.10 | -0.44 | -0.94 |
| | cassava4.1_011851m.g | glycolysis.unclear/dually targeted.phosphoglycerate mutase | Phosphoglycerate mutase family protein | -0.19 | 0.24 | -0.28 | -1.10 | 0.01 | -1.09 | 0.69 | 0.51 | -0.15 | -0.75 |
| TCA | cassava4.1_007404m.g | TCA / org transformation.TCA.pyruvate DH.E1 | pyruvate dehydrogenase complex E1 alpha subunit | 0.39 | 0.78 | 0.61 | 1.23 | 0.08 | 1.09 | -0.35 | 0.37 | -0.24 | 0.86 |
| | cassava4.1_007540m.g | TCA / org transformation.TCA.pyruvate DH.E1 | pyruvate dehydrogenase complex E1 alpha subunit | 0.48 | 1.00 | 0.34 | 1.07 | -0.12 | 1.74 | -0.31 | 1.07 | -0.08 | 0.81 |
| | cassava4.1_010116m.g | TCA / org transformation.TCA.pyruvate DH.E1 | Transketolase family protein | 0.66 | 1.23 | 0.48 | 1.30 | 0.14 | 0.83 | -0.15 | 0.44 | -0.05 | 0.75 |
| | cassava4.1_010442m.g | TCA / org transformation.TCA.pyruvate DH.E1 | Transketolase family protein | 0.36 | 0.97 | 0.08 | 0.55 | 0.17 | 0.86 | 0.17 | 1.05 | -0.11 | 0.70 |
| | cassava4.1_004839m.g | TCA / org transformation.TCA.pyruvate DH.E2 | Dihydrolipoamide acetyltransferase, long form protein | 0.21 | 0.63 | 0.73 | 1.08 | 0.02 | 1.02 | -0.01 | 0.96 | 0.03 | 0.95 |
| | cassava4.1_004864m.g | TCA / org transformation.TCA.pyruvate DH.E2 | Dihydrolipoamide acetyltransferase, long form protein | 0.42 | 0.99 | 0.58 | 1.26 | 0.16 | 1.51 | 0.26 | 0.97 | 0.14 | 0.94 |
| | cassava4.1_006906m.g | TCA / org transformation.TCA.pyruvate DH.E2 | 2-oxoacid dehydrogenases acyltransferase family protein | -0.20 | 0.55 | 0.10 | 0.52 | 0.18 | 1.10 | -0.75 | 0.56 | -0.09 | 0.63 |
| | cassava4.1_004342m.g | TCA / org transformation.TCA.pyruvate DH.E3 | lipoamide dehydrogenase 1 | 0.13 | 0.84 | 0.15 | 0.91 | 0.16 | 0.87 | -0.53 | 0.94 | 0.24 | 1.48 |
| | cassava4.1_005856m.g | TCA / org transformation.TCA.pyruvate DH.E3 | mitochondrial lipoamide dehydrogenase 1 | -0.84 | -1.72 | -0.49 | -0.93 | -0.25 | -0.36 | -0.50 | -1.53 | -0.70 | -1.41 |
| | cassava4.1_006853m.g | TCA / org transformation.TCA.CS | Citrate synthase family protein | 0.33 | 0.84 | 0.07 | 0.78 | 0.02 | 0.98 | -0.01 | 0.30 | 0.22 | 0.80 |
| | cassava4.1_012522m.g | TCA / org transformation.TCA.CS | citrate synthase 5 | 1.05 | 1.55 | 0.51 | 0.85 | 0.11 | 1.21 | -0.40 | 1.14 | 0.46 | 1.23 |
| | cassava4.1_000903m.g | TCA / org transformation.TCA.aconitase | aconitase 3 | 0.69 | 1.54 | 0.62 | 1.52 | -0.02 | 1.43 | 0.27 | 0.57 | -0.13 | 0.60 |
| | cassava4.1_000908m.g | TCA / org transformation.TCA.aconitase | aconitase 3 | 0.47 | 0.90 | 0.35 | 0.68 | 0.06 | 0.87 | 0.29 | 0.96 | -0.03 | 0.47 |
| | cassava4.1_001348m.g | TCA / org transformation.TCA.aconitase | aconitase 1 | 1.23 | 2.37 | 0.83 | 1.66 | -0.06 | 1.18 | 0.33 | 2.29 | 0.70 | 2.14 |
| | cassava4.1_005842m.g | TCA / org transformation.TCA.aconitase | isopropyl malate isomerase large subunit 1 | -0.64 | -0.63 | 0.03 | 0.06 | 0.04 | 0.17 | -0.49 | -0.95 | -0.29 | -0.61 |
| | cassava4.1_005859m.g | TCA / org transformation.TCA.aconitase | isopropyl malate isomerase large subunit 1 | -0.40 | -1.15 | -0.10 | -0.48 | -0.22 | -0.01 | -0.60 | -1.77 | -0.89 | -1.61 |
| | cassava4.1_033921m.g | TCA / org transformation.TCA.aconitase | aconitase 3 | -0.36 | 1.59 | -1.73 | -0.89 | -0.93 | 2.23 | 2.08 | 2.78 | 0.17 | 2.85 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | cassava4.1_007405m.g | TCA / org transformation.TCA.IDH | Isocitrate/isopropylmalate dehydrogenase family protein | -0.24 | 0.17 | 0.13 | 0.63 | 0.32 | 1.11 | -0.40 | 1.87 | 0.21 | 1.84 |
|  | cassava4.1_009195m.g | TCA / org transformation.TCA.IDH | cytosolic NADP+-dependent isocitrate dehydrogenase | 1.58 | 2.52 | 0.97 | 2.08 | 0.18 | 2.63 | -0.23 | 1.87 | 0.56 | 2.60 |
|  | cassava4.1_009952m.g | TCA / org transformation.TCA.IDH | isocitrate dehydrogenase III | 0.68 | 0.43 | 0.47 | 0.68 | 0.05 | 0.83 | -0.26 | 0.58 | 0.00 | 0.90 |
|  | cassava4.1_008387m.g | TCA / org transformation.TCA.succinyl-CoA ligase | ATP citrate lyase (ACL) family protein | 0.25 | 0.56 | 0.21 | 0.85 | -0.04 | 1.22 | -0.17 | 0.41 | -0.03 | 0.53 |
|  | cassava4.1_010959m.g | TCA / org transformation.TCA.succinyl-CoA ligase | Succinyl-CoA ligase, alpha subunit | 0.41 | 0.85 | 0.19 | 0.89 | 0.14 | 1.11 | -0.38 | 1.17 | 0.53 | 1.58 |
|  | cassava4.1_034079m.g | TCA / org transformation.TCA.succinyl-CoA ligase | Succinyl-CoA ligase, alpha subunit | 0.20 | 0.67 | -0.06 | 0.55 | 0.53 | 1.41 | -0.70 | 1.42 | -0.13 | 1.29 |
|  | cassava4.1_003519m.g | TCA / org transformation.TCA.succinate dehydrogenase | succinate dehydrogenase 1-1 | -0.41 | -0.23 | -0.23 | -0.02 | -0.07 | 0.88 | -0.04 | -0.03 | -0.19 | 0.21 |
|  | cassava4.1_013361m.g | TCA / org transformation.TCA.succinate dehydrogenase | succinate dehydrogenase 2-2 | 0.65 | 0.76 | 0.41 | 0.78 | 0.19 | 1.20 | -0.22 | 1.24 | 0.23 | 0.86 |
|  | cassava4.1_034460m.g | TCA / org transformation.TCA.malate DH | malate dehydrogenase | 0.57 | 0.77 | 0.02 | 0.46 | 0.08 | 1.44 | -1.19 | 1.01 | -0.62 | 0.76 |
|  | cassava4.1_013362m.g | TCA / org transformation.TCA.succinate dehydrogenase | succinate dehydrogenase 2-2 | 0.75 | 1.51 | 0.12 | 0.50 | 0.09 | 1.34 | 0.69 | 1.40 | -0.38 | 0.73 |
|  | cassava4.1_011133m.g | TCA / org transformation.TCA.malate DH | Lactate/malate dehydrogenase family protein | -0.02 | 0.10 | 0.25 | 0.63 | 0.13 | 1.04 | -0.36 | 0.30 | -0.43 | 0.13 |
| mitochondrial electron transport | cassava4.1_010822m.g | mitochondrial electron transport / ATP synthesis.alternative oxidase | alternative oxidase 2 | -0.41 | -0.90 | -0.19 | -0.58 | -0.04 | -0.40 | 0.08 | -0.56 | -0.49 | -0.72 |
|  | cassava4.1_027944m.g | mitochondrial electron transport / ATP synthesis.cytochrome c | transmembrane protein G1P-related 1 | -0.37 | -0.03 | 0.13 | 0.25 | 0.30 | 1.39 | -0.97 | 0.52 | -0.94 | -0.02 |
|  | cassava4.1_010184m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.type II.mitochondrial | NAD(P)H dehydrogenase C1 | -0.33 | -1.00 | -0.57 | -0.62 | 0.08 | -0.55 | -0.39 | -0.69 | -0.34 | -0.86 |
|  | cassava4.1_016672m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.complex I | NADPH:quinone oxidoreductase | -0.21 | -1.50 | -0.44 | -1.10 | -0.13 | -0.25 | -0.20 | -0.25 | -0.46 | -0.32 |
|  | cassava4.1_013530m.g | mitochondrial electron transport / ATP synthesis.cytochrome c reductase | Ubiquinol-cytochrome C reductase iron-sulfur subunit | -0.06 | 0.01 | -0.05 | 0.25 | 0.04 | 0.93 | -0.45 | -0.60 | -0.62 | -0.21 |
|  | cassava4.1_017064m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | cytochrome C oxidase 6B | -0.05 | -0.15 | -0.13 | 0.16 | -0.02 | 0.90 | -0.33 | 0.77 | -0.01 | 0.56 |
|  | cassava4.1_002356m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH-ubiquinone dehydrogenase, mitochondrial, putative | 0.04 | -0.08 | 0.12 | 0.12 | 0.09 | 0.86 | -0.03 | 0.23 | -0.20 | 0.03 |
|  | cassava4.1_012361m.g | mitochondrial electron transport / ATP synthesis.cytochrome c reductase | Ubiquinol-cytochrome C reductase iron-sulfur subunit | 0.05 | 0.13 | 0.11 | 0.35 | 0.00 | 1.22 | -0.02 | 0.22 | -0.28 | 0.16 |
|  | cassava4.1_004343m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.type II.external | NAD(P)H dehydrogenase B1 | 0.11 | -0.03 | 0.17 | -0.23 | -0.01 | -0.21 | 0.17 | -0.31 | -0.38 | -0.77 |
|  | cassava4.1_013140m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | unknow | 0.11 | 0.08 | 0.06 | -0.49 | 0.20 | -1.11 | -0.38 | 0.11 | -0.32 | -0.37 |
|  | cassava4.1_004630m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | ATP synthase alpha/beta family protein | 0.13 | 0.32 | 0.16 | 0.52 | 0.10 | 1.03 | -0.51 | 0.56 | -0.03 | 0.68 |
|  | cassava4.1_016028m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial | 0.14 | -0.10 | 0.08 | 0.33 | 0.03 | 1.14 | -0.01 | -0.09 | -0.16 | 0.23 |
|  | cassava4.1_013120m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.complex I | prohibitin 6 | 0.15 | 0.68 | 0.20 | 0.82 | 0.18 | 1.12 | -0.69 | 1.61 | -0.10 | 1.16 |
|  | cassava4.1_017764m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | Rubredoxin-like superfamily protein | 0.16 | 0.01 | 0.19 | 0.57 | 0.03 | 0.98 | -0.20 | 0.22 | 0.18 | 0.85 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_017840m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH-ubiquinone oxidoreductase-related | 0.17 | 0.78 | 0.10 | 0.88 | 0.28 | 1.34 | -0.25 | 1.51 | -0.19 | 1.41 |
| | cassava4.1_019324m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | Mitochondrial ATP synthase subunit G protein | 0.19 | 0.85 | 0.46 | 0.91 | 0.15 | 1.41 | -0.14 | 0.81 | -0.10 | 0.51 |
| | cassava4.1_014720m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.complex I.carbonic anhydrase | gamma carbonic anhydrase like 1 | 0.19 | 0.22 | 0.15 | 0.42 | -0.09 | 1.10 | -0.23 | 1.19 | 0.25 | 1.20 |
| | cassava4.1_004726m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | ATP synthase alpha/beta family protein | 0.20 | 0.53 | 0.23 | 0.63 | 0.01 | 0.97 | -0.07 | 0.38 | -0.08 | 0.38 |
| | cassava4.1_014473m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH-ubiquinone oxidoreductase 24 kDa subunit, putative | 0.23 | 0.28 | 0.22 | 0.58 | 0.22 | 0.92 | -0.31 | 0.79 | 0.06 | 0.82 |
| | cassava4.1_012332m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH-ubiquinone oxidoreductase 24 kDa subunit, putative | 0.24 | 0.52 | 0.28 | 0.55 | -0.26 | 0.60 | -0.45 | 0.59 | 0.05 | 0.89 |
| | cassava4.1_020733m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | ATP synthase epsilon chain, mitochondrial | 0.25 | 0.53 | 0.10 | 0.66 | 0.20 | 1.21 | -0.24 | 1.19 | 0.09 | 1.24 |
| | cassava4.1_019319m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | Mitochondrial ATP synthase subunit G protein | 0.27 | 0.76 | 0.36 | 0.95 | 0.02 | 1.03 | -0.43 | 0.29 | 0.00 | 0.39 |
| | cassava4.1_016505m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | electron transport SCO1/SenC family protein | 0.28 | 1.11 | 0.02 | 0.54 | 0.00 | 0.79 | -0.26 | 2.22 | 0.44 | 1.67 |
| | cassava4.1_013823m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.complex I.carbonic anhydrase | gamma carbonic anhydrase 1 | 0.29 | 0.52 | 0.40 | 0.55 | -0.14 | 0.91 | -0.31 | 0.76 | -0.12 | 0.61 |
| | cassava4.1_014599m.g | mitochondrial electron transport / ATP synthesis.electron transfer flavoprotein | electron transfer flavoprotein beta | 0.29 | 0.87 | -0.09 | 0.26 | 0.19 | 0.32 | 0.36 | 1.71 | -0.04 | 0.80 |
| | cassava4.1_017212m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | cytochrome C oxidase 6B | 0.29 | 0.88 | 0.28 | 1.03 | -0.26 | 1.05 | -1.02 | 0.76 | 0.47 | 1.75 |
| | cassava4.1_019654m.g | mitochondrial electron transport / ATP synthesis.cytochrome c | cytochrome c-2 | 0.31 | 0.55 | 0.77 | 1.50 | 0.05 | 1.84 | 0.05 | 1.79 | 0.10 | 1.30 |
| | cassava4.1_020694m.g | mitochondrial electron transport / ATP synthesis.cytochrome c reductase | Cytochrome b-c1 complex, subunit 8 protein | 0.31 | 0.50 | 0.18 | 0.61 | 0.09 | 1.10 | -0.46 | 0.68 | -0.21 | 0.55 |
| | cassava4.1_006409m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | ATPase, V1 complex, subunit B protein | 0.32 | 0.86 | 0.45 | 1.01 | 0.19 | 0.75 | -0.72 | 0.69 | -0.14 | 0.78 |
| | cassava4.1_017771m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | ATP synthase D chain, mitochondrial | 0.33 | 0.91 | 0.31 | 0.77 | 0.10 | 1.06 | -0.13 | 0.86 | -0.26 | 0.57 |
| | cassava4.1_006064m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.type II.internal matrix | alternative NAD(P)H dehydrogenase 2 | 0.33 | 0.28 | 0.50 | 0.56 | -0.06 | 0.02 | 0.19 | 0.54 | 0.57 | 1.26 |
| | cassava4.1_019945m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | cytochrome c oxidase-related | 0.40 | 0.40 | 0.06 | 0.56 | -0.03 | 1.29 | -0.61 | 0.68 | -0.22 | 0.87 |
| | cassava4.1_013108m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.complex I | prohibitin 1 | 0.41 | 0.83 | 0.20 | 0.68 | 0.17 | 1.04 | -0.78 | 2.39 | 0.29 | 2.03 |
| | cassava4.1_014824m.g | mitochondrial electron transport / ATP synthesis.uncoupling protein | plant uncoupling mitochondrial protein 1 | 0.43 | 1.05 | 0.10 | 0.94 | 0.43 | 1.26 | -0.23 | 1.37 | -0.08 | 1.07 |
| | cassava4.1_020696m.g | mitochondrial electron transport / ATP synthesis.cytochrome c reductase | ubiquinol-cytochrome C reductase UQCRX/QCR9-like family protein | 0.43 | 0.68 | 0.39 | 0.90 | -0.06 | 0.81 | -0.58 | 0.78 | 0.12 | 1.15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_016521m.g | mitochondrial electron transport / ATP synthesis.F1-ATPase | ATPase, F1 complex, delta/epsilon subunit | 0.45 | 0.75 | 0.25 | 0.67 | 0.17 | 1.50 | -0.16 | 0.67 | -0.24 | 0.50 |
| | cassava4.1_019932m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH-ubiquinone oxidoreductase B18 subunit, putative | 0.47 | 0.59 | 0.20 | 0.76 | 0.10 | 1.16 | -0.49 | 0.83 | -0.06 | 1.14 |
| | cassava4.1_013697m.g | mitochondrial electron transport / ATP synthesis.cytochrome c reductase | Ubiquinol-cytochrome C reductase iron-sulfur subunit | 0.47 | 0.80 | 0.58 | 0.70 | 0.23 | 1.35 | -0.70 | 0.79 | -0.01 | 1.01 |
| | cassava4.1_019624m.g | mitochondrial electron transport / ATP synthesis.cytochrome c | cytochrome c-2 | 0.49 | 0.70 | 0.64 | 1.30 | -0.15 | 1.98 | -0.98 | 0.33 | -0.21 | 0.92 |
| | cassava4.1_010295m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | Surfeit locus 1 cytochrome c oxidase biogenesis protein | 0.54 | 0.91 | 0.03 | 0.74 | 0.04 | 1.07 | 0.18 | 1.42 | -0.39 | 1.13 |
| | cassava4.1_005184m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.type II.internal matrix | alternative NAD(P)H dehydrogenase 1 | 0.63 | 0.83 | 0.18 | 0.86 | -0.04 | 1.31 | -1.26 | 0.78 | -0.56 | 1.20 |
| | cassava4.1_010697m.g | mitochondrial electron transport / ATP synthesis.electron transfer flavoprotein | electron transfer flavoprotein alpha | 0.68 | 1.39 | 0.07 | 0.42 | 0.04 | 1.04 | -0.17 | 1.30 | 0.17 | 1.09 |
| | cassava4.1_004741m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.type II.external | NAD(P)H dehydrogenase B2 | 0.70 | 0.30 | -0.18 | -0.14 | 0.06 | 0.80 | 0.03 | 1.86 | -0.76 | -1.18 |
| | cassava4.1_019695m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | NADH:ubiquinone oxidoreductase, 17.2kDa subunit | 0.74 | 0.44 | -0.29 | 1.05 | 0.09 | 1.30 | 0.33 | 1.39 | 1.09 | 2.14 |
| | cassava4.1_009351m.g | transport.metabolite transporters at the mitochondrial membrane | ADP/ATP carrier 2 | 0.37 | 0.51 | 0.51 | 0.89 | 0.19 | 0.90 | -0.93 | 0.04 | -0.10 | 0.59 |
| | cassava4.1_009354m.g | transport.metabolite transporters at the mitochondrial membrane | ADP/ATP carrier 2 | 0.10 | 0.40 | 0.84 | 1.56 | 0.07 | 1.81 | -0.65 | 0.37 | -0.12 | 1.03 |
| | cassava4.1_011745m.g | transport.metabolite transporters at the mitochondrial membrane | uncoupling protein 5 | 0.38 | -1.46 | 1.75 | 1.08 | 0.41 | 0.44 | -2.26 | 0.12 | 0.62 | -0.48 |
| | cassava4.1_023265m.g | mitochondrial electron transport / ATP synthesis.electron transfer flavoprotein | electron-transfer flavoprotein:ubiquinone oxidoreductase | 0.80 | 1.67 | 0.52 | 0.56 | 0.00 | 0.40 | 0.68 | 1.28 | 0.44 | 0.80 |
| | cassava4.1_017914m.g | mitochondrial electron transport / ATP synthesis.cytochrome c oxidase | Rubredoxin-like superfamily protein | 0.81 | 0.75 | 0.85 | 1.22 | 0.08 | 1.42 | -0.01 | 1.34 | 0.57 | 1.60 |
| | cassava4.1_014864m.g | mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear | DERLIN-1 | 0.85 | 0.79 | 0.48 | 0.50 | -0.10 | -0.02 | 1.63 | 1.17 | 0.35 | 0.37 |
| Flavonoid Biosynthetic | cassava4.1_004658m.g | 4CL3; 4-coumarate-CoA ligase | 4-coumarate:CoA ligase 3 | 0.27 | 1.03 | 1.04 | 3.06 | -0.39 | 4.68 | -0.15 | 0.91 | -0.12 | 2.48 |
| | cassava4.1_000031m.g | lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation.homomeric Enzyme | acetyl-CoA carboxylase 1 (ACC1) | 0.82 | 2.10 | 0.61 | 2.16 | 0.23 | 2.20 | 1.30 | 1.60 | 0.43 | 1.85 |
| | cassava4.1_000041m.g | lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation.homomeric Enzyme | acetyl-CoA carboxylase 1 (ACC1) | 0.47 | 1.49 | 0.67 | 1.92 | -0.11 | 2.21 | 0.92 | 0.34 | -0.07 | 0.76 |
| | cassava4.1_010685m.g | secondary metabolism.flavonoids.dihydroflavonols.dihydroflavonol 4-reductase | dihydroflavonol 4-reductase (DFR) | 2.65 | 4.49 | 4.37 | 6.95 | 0.50 | 7.40 | -2.31 | 6.64 | 4.10 | 9.30 |
| | cassava4.1_010212m.g | hormone metabolism.ethylene.synthesis-degradation | flavanone 3-hydroxylase (F3H) | 3.44 | 5.05 | 4.32 | 6.42 | 0.20 | 7.71 | -1.61 | 5.35 | 2.87 | 7.69 |
| | cassava4.1_011534m.g | hormone metabolism.ethylene.synthesis-degradation | flavonol synthase 1 (FLS1) | 1.37 | 2.75 | 2.59 | 4.59 | 0.17 | 4.60 | -1.49 | 3.55 | 1.09 | 5.63 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_010809m.g | hormone metabolism.ethylene.synthesis-degradation | leucoanthocyanidin dioxygenase (LDOX) | 2.38 | 3.20 | 4.43 | 6.31 | 0.34 | 7.60 | -3.74 | 5.40 | 3.36 | 8.59 |
| | cassava4.1_008985m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 111 (MYB111) | 0.98 | 0.80 | 1.32 | 0.68 | -0.78 | 1.73 | 0.32 | 2.04 | 1.28 | 2.27 |
| | cassava4.1_009295m.g | secondary metabolism.flavonoids.chalcones | TRANSPARENT TESTA 4 (TT4) | 1.62 | 4.03 | 2.37 | 5.46 | 0.40 | 7.37 | -1.77 | 3.38 | 0.61 | 5.50 |
| | cassava4.1_009206m.g | secondary metabolism.flavonoids.chalcones | TRANSPARENT TESTA 4 (TT4) | 2.51 | 4.35 | 3.43 | 5.94 | -0.08 | 7.97 | -3.30 | 2.01 | 1.86 | 6.09 |
| | cassava4.1_009402m.g | secondary metabolism.flavonoids.chalcones | TRANSPARENT TESTA 4 (TT4) | 3.06 | 4.46 | 5.26 | 7.21 | 0.46 | 7.99 | -4.08 | 5.66 | 3.89 | 9.29 |
| | cassava4.1_007396m.g | secondary metabolism.flavonoids.chalcones | TRANSPARENT TESTA 5 (TT5) | 1.03 | 2.27 | 1.20 | 3.03 | 0.22 | 3.56 | -0.77 | 1.59 | 0.38 | 3.56 |
| | cassava4.1_005974m.g | misc.cytochrome P450 | TRANSPARENT TESTA 7 (TT7); | 1.93 | 2.73 | 4.94 | 6.92 | 0.33 | 7.79 | -0.59 | 7.22 | 3.54 | 8.89 |
| | cassava4.1_005668m.g | misc.cytochrome P450 | TRANSPARENT TESTA 7 (TT7); | 2.19 | 3.84 | 1.94 | 4.34 | 0.22 | 4.54 | -1.83 | 1.75 | 0.96 | 4.59 |
| cytochrome B5 | cassava4.1_018938m.g | cytochrome | cytochrome B5 isoform E | 1.27 | 2.19 | 0.34 | 0.76 | 0.08 | 1.14 | 0.37 | -0.21 | -0.33 | 0.27 |
| | cassava4.1_018863m.g | cytochrome | cytochrome B5 isoform B | -0.15 | 0.04 | 0.09 | 0.78 | -0.03 | 0.92 | -0.45 | -0.31 | -0.59 | -0.42 |
| | cassava4.1_018955m.g | cytochrome | cytochrome B5 isoform B | 0.61 | 1.02 | 0.44 | 1.10 | 0.29 | 0.98 | -1.22 | 0.58 | -0.31 | 1.12 |
| | cassava4.1_018882m.g | cytochrome | cytochrome B5 isoform B | 0.31 | 0.63 | 0.21 | 0.64 | -0.28 | 1.38 | -0.79 | 0.34 | -0.53 | 0.57 |
| | cassava4.1_018854m.g | cytochrome | cytochrome B5 isoform B | 0.94 | 1.65 | 0.89 | 1.30 | 0.14 | 2.17 | -1.38 | 0.52 | -0.22 | 0.53 |
| | cassava4.1_027275m.g | cytochrome | cytochrome B5 isoform D | 2.85 | 4.14 | 4.58 | 6.77 | 0.61 | 8.35 | -3.19 | 4.41 | 2.94 | 7.91 |

**Supplemental Table S6. Genes annotated to starch and sucrose metabolism related genes. The extent of differential expression is measured in terms of log2 fold change of treatment vs. control.**

| Cassava ID | Mapman Category | Short Description | PG0 | FG0 | PG2 | FG2 | PG4 | FG4 | PG0 | FG0 | PG2 | FG2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 120 day | | | | | | 45 day | | | |
| cassava4.1_005409m.g | major CHO metabolism.synthesis.starch.AGPase | glucose-1-phosphate adenylyltransferase | 2.31 | 3.39 | 1.70 | 2.76 | 0.32 | 2.01 | 0.24 | 3.35 | 0.84 | 2.53 |
| cassava4.1_005518m.g | major CHO metabolism.synthesis.starch.AGPase | glucose-1-phosphate adenylyltransferase | 2.71 | 3.05 | 2.11 | 2.82 | 0.31 | 1.22 | -0.77 | 4.41 | 1.46 | 3.81 |
| cassava4.1_021267m.g | major CHO metabolism.synthesis.starch.AGPase | highly similar to ( 674) AT1G27680 \| Symbols: APL2 \| APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase | 0.03 | 0.53 | 0.90 | 1.59 | -0.23 | 1.05 | -0.36 | 1.92 | -0.03 | 2.26 |
| cassava4.1_005507m.g | major CHO metabolism.synthesis.starch.AGPase | highly similar to ( 855) AT5G19220 \| Symbols: ADG2, APL1 \| APL1 (ADP GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT 1); glucose-1-phosphate adenylyltransferase | -0.91 | -2.90 | -0.19 | -2.72 | -0.02 | -3.77 | -0.30 | -2.39 | -0.62 | -2.70 |
| cassava4.1_002278m.g | major CHO metabolism.synthesis.starch.starch synthase | nearly identical (1009) AT3G01180 \| Symbols: AtSS2 \| AtSS2 (starch synthase 2); transferase, transferring glycosyl groups | -0.07 | -1.64 | 0.03 | -1.41 | -0.12 | -0.89 | 0.03 | -1.26 | -0.43 | -1.66 |
| cassava4.1_003884m.g | major CHO metabolism.synthesis.starch.starch synthase | highly similar to ( 894) AT1G32900 \| Symbols: \| starch synthase, putative | -0.97 | -2.77 | -0.01 | -1.37 | -0.05 | -1.30 | -0.69 | -2.18 | -0.75 | -2.68 |
| cassava4.1_004619m.g | major CHO metabolism.synthesis.starch.starch synthase | highly similar to ( 885) AT5G24300 \| Symbols: SSI1, SSI, ATSS1 \| SSI1 (SUPPRESSOR OF SALICYLIC ACID INSENSITIVITY 1); starch synthase/ transferase, transferring glycosyl groups | -0.28 | -0.12 | -0.35 | -0.84 | -0.13 | -0.72 | 0.20 | -0.33 | -0.22 | -0.59 |
| cassava4.1_001595m.g | major CHO metabolism.synthesis.starch.starch branching | highly similar to ( 832) AT5G03650 \| Symbols: SBE2.2 \| SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | 0.29 | 0.88 | 0.69 | 0.97 | 0.14 | 1.17 | -0.33 | 1.72 | 0.44 | 1.79 |
| cassava4.1_001686m.g | major CHO metabolism.synthesis.starch.starch branching | nearly identical (1303) AT5G03650 \| Symbols: SBE2.2 \| SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | 0.54 | 0.71 | 0.84 | 1.05 | 0.17 | 0.11 | 0.42 | 1.71 | 0.26 | 1.08 |
| cassava4.1_003773m.g | major CHO metabolism.synthesis.starch.starch branching | nearly identical (1128) AT5G03650 \| Symbols: SBE2.2 \| SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | 0.91 | 1.42 | 1.05 | 1.23 | 0.30 | 0.24 | 0.40 | 3.40 | 0.95 | 2.50 |
| cassava4.1_001096m.g | major CHO metabolism.degradation.starch.starch phosphorylase | nearly identical (1369) AT3G29320 \| Symbols: \| glucan phosphorylase, putative | -0.51 | -1.13 | 0.24 | -0.55 | -0.13 | -1.71 | -0.56 | 0.01 | -0.19 | 0.37 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cassava4.1_001626m.g | major CHO metabolism.degradation.starch.starch phosphorylase | nearly identical (1470) AT3G46970 \| Symbols: ATPHS2, PHS2 \| PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups | 1.46 | 2.17 | 1.48 | 2.15 | 0.27 | 1.10 | 0.01 | 3.01 | 0.71 | 2.66 |
| cassava4.1_002466m.g | major CHO metabolism.degradation.starch.starch phosphorylase | highly similar to ( 778) AT3G29320 \| Symbols: \| glucan phosphorylase, putative | 1.23 | 2.09 | 0.71 | 1.42 | 0.35 | 0.98 | -0.86 | 2.88 | 0.77 | 2.93 |
| cassava4.1_002614m.g | major CHO metabolism.degradation.starch.starch phosphorylase | highly similar to ( 764) AT3G29320 \| Symbols: \| glucan phosphorylase, putative | 0.69 | 1.54 | 0.76 | 1.07 | 0.36 | 1.00 | 0.06 | 3.77 | 0.67 | 3.12 |
| cassava4.1_004717m.g | major CHO metabolism.degradation.starch.starch phosphorylase | highly similar to ( 739) AT3G29320 \| Symbols: \| glucan phosphorylase, putative | 0.97 | 1.94 | 1.17 | 1.54 | 0.30 | 1.02 | -0.18 | 3.45 | 0.33 | 2.64 |
| cassava4.1_000266m.g | major CHO metabolism.degradation.starch.glucan water dikinase | nearly identical (1917) AT1G10760 \| Symbols: SEX1, SOP1, SOP, GWD1, GWD \| SEX1 (STARCH EXCESS 1); alpha-glucan, water dikinase | 0.44 | 1.31 | 0.79 | 1.82 | 0.08 | 1.53 | 0.26 | 1.29 | 0.82 | 1.72 |
| cassava4.1_000497m.g | major CHO metabolism.degradation.starch.glucan water dikinase | nearly identical (1490) AT5G26570 \| Symbols: PWD, OK1, ATGWD3 \| ATGWD3; carbohydrate kinase/ catalytic/ phosphoglucan, water dikinase | 0.24 | 0.69 | 0.15 | -0.28 | 0.06 | -0.54 | 0.51 | 0.86 | 0.18 | -0.13 |
| cassava4.1_006053m.g | major CHO metabolism.degradation.starch.starch cleavage | highly similar to ( 627) AT5G11720 \| Symbols: \| alpha-glucosidase 1 (AGLU1) | 0.52 | 0.93 | -0.20 | 0.26 | 0.32 | 1.93 | 1.18 | 2.60 | 1.44 | 2.90 |
| cassava4.1_001362m.g | major CHO metabolism.degradation.starch.starch cleavage.alpha amylase | nearly identical (1236) AT1G69830 \| Symbols: ATAMY3, AMY3 \| AMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase | 0.70 | 1.27 | -0.63 | -0.31 | -0.12 | -0.95 | 0.60 | 0.15 | -0.27 | -0.47 |
| cassava4.1_008754m.g | major CHO metabolism.degradation.starch.starch cleavage.alpha amylase | highly similar to ( 708) AT1G76130 \| Symbols: ATAMY2, AMY2 \| AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion binding / catalytic/ cation binding | 0.81 | 1.47 | 0.41 | 1.18 | -0.08 | 1.47 | -0.66 | 0.85 | -0.57 | 0.50 |
| cassava4.1_004345m.g | major CHO metabolism.degradation.starch.starch cleavage.beta amylase | highly similar to ( 876) AT3G23920 \| Symbols: BAM1, BMY7, TR-BAMY \| BAM1 (BETA-AMYLASE 1); beta-amylase | -0.12 | -1.15 | -0.12 | -1.58 | -0.09 | -0.50 | 0.99 | 0.08 | -0.42 | -1.12 |
| cassava4.1_005239m.g | major CHO metabolism.degradation.starch.starch cleavage.beta amylase | highly similar to ( 582) AT5G18670 \| Symbols: BMY3, BAM9 \| BMY3; beta-amylase/ catalytic/ cation binding | -0.53 | -1.42 | -0.50 | -0.53 | -0.01 | -0.05 | 0.34 | -1.18 | -1.00 | -1.80 |
| cassava4.1_032401m.g | major CHO metabolism.degradation.starch.starch cleavage.beta amylase | moderately similar to ( 376) AT4G17090 \| Symbols: CT-BMY, BAM3, BMY8 \| CT-BMY (CHLOROPLAST BETA-AMYLASE); | 1.26 | 1.94 | 2.31 | 3.67 | 0.49 | 1.89 | 1.48 | 3.47 | 0.04 | 2.71 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | beta-amylase | | | | | | | | | | |
| cassava4.1_034364m.g | major CHO metabolism.degradation.starch.starch cleavage.beta amylase | moderately similar to ( 332) AT4G17090 \| Symbols: CT-BMY, BAM3, BMY8 \| CT-BMY (CHLOROPLAST BETA-AMYLASE) | -0.66 | -2.41 | -0.36 | -1.30 | -0.07 | -1.25 | -0.65 | -1.33 | -0.59 | -2.20 |
| cassava4.1_008825m.g | transport.metabolite transporters at the envelope membrane | highly similar to ( 573) AT5G46110 \| Symbols: APE2, TPT \| APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT 2) | -0.64 | -2.09 | -0.28 | -1.28 | -0.06 | -1.55 | -0.38 | -1.88 | -0.61 | -1.85 |
| cassava4.1_000732m.g | major CHO metabolism.synthesis.sucrose.SPS | nearly identical (1669) AT5G20280 \| Symbols: ATSPS1F \| ATSPS1F (sucrose phosphate synthase 1F) | 0.08 | 1.35 | 0.12 | 0.15 | 0.05 | -0.06 | 0.44 | -0.22 | -0.05 | -0.21 |
| cassava4.1_000827m.g | major CHO metabolism.synthesis.sucrose.SPS | nearly identical (1521) AT4G10120 \| Symbols: ATSPS4F \| ATSPS4F; transferase, transferring glycosyl groups | -0.20 | -0.52 | 0.00 | -0.13 | 0.18 | -1.18 | 0.45 | 0.94 | 0.62 | 0.72 |
| cassava4.1_000839m.g | major CHO metabolism.synthesis.sucrose.SPS | nearly identical (1527) AT4G10120 \| Symbols: ATSPS4F \| ATSPS4F; transferase, transferring glycosyl groups | -0.84 | -2.25 | -0.43 | -1.12 | -0.26 | -1.93 | -0.34 | -2.64 | -0.11 | -2.10 |
| cassava4.1_024105m.g | major CHO metabolism.synthesis.sucrose.SPS | nearly identical (1583) AT1G04920 \| Symbols: ATSPS3F \| ATSPS3F (sucrose phosphate synthase 3F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | -0.20 | -2.22 | 0.00 | -1.85 | -0.30 | -3.28 | 0.41 | -2.17 | -0.35 | -2.22 |
| cassava4.1_008177m.g | major CHO metabolism.synthesis.sucrose.SPP | highly similar to ( 621) AT2G35840 \| Symbols: \| sucrose-phosphatase 1 (SPP1) | 0.23 | 0.14 | 0.18 | 0.50 | 0.14 | 0.66 | -0.08 | 0.89 | -0.45 | 0.20 |
| cassava4.1_008254m.g | major CHO metabolism.synthesis.sucrose.SPP | highly similar to ( 626) AT2G35840 \| Symbols: \| sucrose-phosphatase 1 (SPP1) | -0.29 | -0.23 | 0.31 | 0.40 | -0.05 | -0.11 | -0.23 | -1.15 | -0.54 | -1.03 |
| cassava4.1_004111m.g | transport.sugars.sucrose | highly similar to ( 620) AT1G22710 \| Symbols: SUC2, SUT1, ATSUC2 \| SUC2 (SUCROSE-PROTON SYMPORTER 2) | 0.80 | 1.66 | -0.18 | -0.35 | -0.13 | 0.77 | -0.13 | 0.24 | -0.30 | -0.25 |
| cassava4.1_006202m.g | transport.sugars.sucrose | highly similar to ( 628) AT1G09960 \| Symbols: SUT4, ATSUT4, suc4 \| SUT4 (SUCROSE TRANSPORTER 4) | 0.71 | 0.94 | 0.09 | 0.80 | 0.02 | 0.78 | 0.09 | 0.76 | -0.08 | 0.15 |
| cassava4.1_006880m.g | transport.sugars.sucrose | highly similar to ( 609) AT1G09960 \| Symbols: SUT4, ATSUT4, suc4 \| SUT4 (SUCROSE TRANSPORTER 4) | -0.69 | -1.23 | -0.32 | -0.29 | 0.12 | 0.41 | 0.33 | 0.59 | 0.30 | 0.16 |
| cassava4.1_007460m.g | transport.sugars.sucrose | highly similar to ( 536) AT1G22710 \| Symbols: SUC2, SUT1, ATSUC2 \| SUC2 (SUCROSE-PROTON SYMPORTER 2) | 0.55 | 0.93 | -0.18 | 0.46 | -0.18 | 1.64 | 0.29 | 0.83 | -0.63 | 0.71 |
| cassava4.1_021570m.g | transport.sugars | MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen | 1.87 | 2.84 | 0.08 | 1.09 | 0.74 | 2.50 | 0.26 | 2.17 | 1.74 | 2.78 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter | | | | | | | | | | |
| cassava4.1_002913m.g | major CHO metabolism.degradation.sucrose.invertases.neutral | highly similar to ( 980) AT3G06500 \| Symbols: \| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | 0.44 | 0.51 | 1.09 | 1.68 | 0.28 | 1.44 | 0.67 | 0.66 | -0.49 | 0.85 |
| cassava4.1_005201m.g | major CHO metabolism.degradation.sucrose.invertases.neutral | nearly identical (1003) AT4G09510 \| Symbols: CINV2 \| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | 0.69 | 1.01 | 0.89 | 1.23 | -0.02 | 0.94 | -0.10 | 1.05 | 0.47 | 1.82 |
| cassava4.1_002971m.g | major CHO metabolism.degradation.sucrose.invertases.neutral | highly similar to ( 961) AT1G56560 \| Symbols: \| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | -0.41 | -1.13 | -0.10 | -0.49 | -0.03 | -0.79 | -0.01 | -1.44 | -0.50 | -1.11 |
| cassava4.1_003155m.g | major CHO metabolism.degradation.sucrose.invertases.neutral | highly similar to ( 903) AT5G22510 \| Symbols: \| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | -0.30 | -0.71 | 0.03 | -0.57 | -0.05 | -0.47 | 0.00 | -1.52 | -0.72 | -1.61 |
| cassava4.1_001840m.g | major CHO metabolism.degradation.sucrose.Susy | nearly identical (1488) AT4G02280 \| Symbols: SUS3, ATSUS3 \| SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | 0.96 | 1.95 | 0.15 | 0.45 | 0.22 | 0.77 | 1.60 | 3.03 | 0.72 | 1.89 |
| cassava4.1_001867m.g | major CHO metabolism.degradation.sucrose.Susy | nearly identical (1395) AT3G43190 \| Symbols: SUS4, ATSUS4 \| SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | -0.81 | -0.67 | -0.86 | -0.50 | -0.37 | -1.88 | -0.67 | -1.44 | -0.81 | -1.00 |
| cassava4.1_001871m.g | major CHO metabolism.degradation.sucrose.Susy | nearly identical (1416) AT3G43190 \| Symbols: SUS4, ATSUS4 \| SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | -0.07 | -0.19 | 0.38 | 0.58 | -0.05 | 0.36 | -1.10 | 0.50 | 0.96 | 1.16 |
| cassava4.1_001874m.g | major CHO metabolism.degradation.sucrose.Susy | nearly identical (1167) AT1G73370 \| Symbols: SUS6, ATSUS6 \| SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ sucrose synthase | 2.07 | 3.16 | 0.75 | 0.93 | 0.48 | 1.67 | 1.90 | 2.75 | 0.58 | 2.21 |
| cassava4.1_027790m.g | major CHO metabolism.degradation.sucrose.Susy | nearly identical (1178) AT1G73370 \| Symbols: SUS6, ATSUS6 \| SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ | 0.80 | 2.04 | 0.47 | 1.06 | -0.12 | 0.95 | -0.50 | -0.04 | 0.21 | 1.19 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | sucrose synthase | | | | | | | | | | |
| cassava4.1_005907m.g | major CHO metabolism.degradation.sucrose.hexokinase | highly similar to ( 627) AT1G50460 \| Symbols: HKL1 \| HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | 2.43 | 1.47 | 1.77 | 2.47 | 0.21 | 2.12 | 1.04 | 4.23 | 1.94 | 4.59 |
| cassava4.1_005952m.g | major CHO metabolism.degradation.sucrose.hexokinase | highly similar to ( 627) AT1G50460 \| Symbols: HKL1 \| HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | 0.58 | 0.15 | 0.39 | 0.36 | 0.08 | 0.94 | 0.19 | 0.06 | 0.18 | 0.86 |
| cassava4.1_006138m.g | major CHO metabolism.degradation.sucrose.hexokinase | highly similar to ( 754) AT4G29130 \| Symbols: ATHXK1, GIN2, HXK1 \| HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | 0.77 | 1.27 | 0.28 | 0.59 | 0.21 | 0.62 | 0.29 | 1.94 | 0.46 | 1.14 |

**Supplemental Table S7. Genes annotated to transcription factor and light signalling. The extent of differential expression is measured in terms of log2 fold change of treatment vs. control.**

| Cluster | Cassava ID | Mapman Category | Short Description | PG0 | FG0 | PG2 | FG2 | PG4 | FG4 | PG0 | FG0 | PG2 | FG2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | 120 day | | | | | | 45 day | | | |
| C1 | cassava4.1_013886m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | 1.04 | 0.54 | -0.39 | -1.43 | 0.12 | -0.22 | -0.45 | 0.62 | -0.22 | 0.69 |
| | cassava4.1_013880m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | ethylene-responsive element binding protein | 1.24 | 0.68 | 0.59 | -0.05 | 0.16 | 0.37 | 0.45 | 1.92 | 0.78 | 2.08 |
| | cassava4.1_010743m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 1.33 | 1.46 | 0.21 | 0.20 | 0.16 | 0.15 | 0.78 | 1.45 | 1.01 | 1.80 |
| | cassava4.1_009529m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | related to AP2 12 | 0.25 | 0.28 | -0.43 | -0.29 | 0.26 | 0.22 | -0.20 | 1.09 | 0.37 | 1.16 |
| | cassava4.1_011381m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | SET domain protein 20 | -0.03 | 0.07 | -0.55 | 0.38 | 0.12 | -0.01 | -1.28 | 1.00 | 0.43 | 1.69 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_014267m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | ethylene-responsive element binding protein | 0.25 | 2.40 | -1.99 | -0.64 | 0.53 | 0.80 | 0.97 | 3.06 | 1.66 | 1.79 |
| | cassava4.1_013174m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | heat shock factor 4 | 1.33 | 2.49 | -0.19 | 0.94 | 0.26 | 2.99 | 2.04 | 3.38 | 1.09 | 3.09 |
| | cassava4.1_009652m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | related to AP2 12 | 0.26 | 0.47 | 0.06 | 0.20 | 0.20 | 0.79 | 0.08 | 0.62 | -0.28 | 0.39 |
| | cassava4.1_034346m.g | RNA.regulation of transcription.GeBP like | DNA-binding storekeeper protein-related transcriptional regulator | 0.45 | 0.77 | -0.05 | 0.17 | 0.32 | 0.75 | -0.38 | 1.04 | -0.10 | 0.62 |
| | cassava4.1_002532m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | Serine/threonine-protein kinase WNK (With No Lysine)-related | 0.98 | 0.92 | 0.45 | 0.57 | 0.07 | 0.80 | 0.50 | 0.97 | 0.26 | 0.84 |
| | cassava4.1_006085m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger protein with CCT domain | 1.23 | 1.05 | 0.60 | 0.67 | -0.06 | 0.88 | 0.15 | 2.05 | -0.18 | 1.07 |
| | cassava4.1_011035m.g | RNA.regulation of transcription.Aux/IAA family | phytochrome-associated protein 1 | 1.96 | 2.16 | 0.35 | 0.73 | 0.19 | 1.84 | -0.48 | 4.07 | 0.76 | 2.43 |
| | cassava4.1_002962m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | SU(VAR)3-9 homolog 1 | 0.15 | 0.28 | -0.05 | 0.01 | -0.12 | 0.13 | 0.06 | 0.83 | 0.02 | 0.47 |
| | cassava4.1_013977m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | BIG PETAL P | -0.14 | -0.11 | -0.35 | -0.13 | 0.09 | 1.43 | -0.18 | 0.71 | 0.70 | 1.16 |
| | cassava4.1_025964m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.96 | -0.36 | -0.08 | 0.68 | 0.29 | 3.39 | -0.54 | 1.55 | 0.80 | 3.09 |
| | cassava4.1_012328m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | -0.21 | -0.09 | 0.02 | 0.47 | -0.08 | 1.18 | -0.07 | 0.52 | -0.18 | 0.62 |
| | cassava4.1_006932m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | NACL-inducible gene 1 | 0.63 | -1.07 | 0.03 | 0.64 | 0.35 | 1.54 | -1.76 | 0.69 | -0.25 | 0.46 |
| | cassava4.1_012221m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | Dof-type zinc finger DNA-binding family protein | 0.97 | 0.51 | 1.56 | 1.20 | 0.36 | 1.48 | -0.13 | 1.34 | 0.73 | 1.04 |
| | cassava4.1_010727m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | Plant-specific GATA-type zinc finger transcription factor family protein | 1.14 | 0.46 | 0.69 | 1.23 | 0.14 | 1.04 | -0.53 | 0.96 | 0.10 | 1.04 |
| | cassava4.1_018669m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 15 | 0.61 | 0.57 | 0.56 | 0.80 | 0.32 | 0.97 | -0.39 | 0.96 | -0.25 | 0.96 |
| | cassava4.1_027980m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | CONSTANS-like 9 | 0.34 | 0.55 | 0.83 | 1.42 | 0.16 | 1.18 | 0.36 | 1.57 | 0.12 | 0.94 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | cassava4.1_005340m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.65 | -0.19 | 1.38 | 1.40 | -0.05 | 1.44 | 0.27 | 2.74 | -0.19 | 0.97 |
|  | cassava4.1_016130m.g | RNA.regulation of transcription.MADS box transcription factor family | AGAMOUS-like 20 | -0.19 | -0.61 | 0.40 | 0.58 | -0.06 | 0.62 | -0.33 | 1.31 | -0.19 | 0.78 |
|  | cassava4.1_008985m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 111 | 0.98 | 0.80 | 1.32 | 0.68 | -0.78 | 1.73 | 0.32 | 2.04 | 1.28 | 2.27 |
|  | cassava4.1_008697m.g | RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family | AP2/B3-like transcriptional factor family protein | 0.78 | 0.82 | 0.65 | 1.07 | 0.09 | 1.51 | 0.73 | 2.37 | 0.72 | 2.13 |
|  | cassava4.1_013572m.g | RNA.regulation of transcription.Bromodomain proteins | DNA-binding bromodomain-containing protein | 0.03 | 0.21 | 0.10 | 0.81 | -0.26 | 0.63 | 0.03 | 1.23 | 0.05 | 1.05 |
|  | cassava4.1_022303m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 1.45 | 1.47 | 1.87 | 2.15 | 0.36 | 2.42 | 0.80 | 3.42 | 1.96 | 3.91 |
|  | cassava4.1_002844m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.65 | 1.68 | 1.38 | 3.24 | 0.39 | 3.03 | 0.13 | 3.37 | 0.96 | 5.32 |
|  | cassava4.1_019365m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | unknow | 0.71 | 1.08 | 0.52 | 1.33 | 0.20 | 1.64 | 0.05 | 2.30 | 0.70 | 2.59 |
|  | cassava4.1_028721m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 5 | -0.24 | -1.02 | 1.66 | 1.82 | 0.13 | 1.86 | -1.03 | 4.27 | 1.09 | 5.32 |
|  | cassava4.1_010068m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | AP2/B3 transcription factor family protein | 1.09 | 0.17 | 1.83 | 2.19 | -0.07 | 1.74 | -0.11 | 2.00 | 1.96 | 2.30 |
|  | cassava4.1_010829m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.56 | 0.29 | 1.19 | 1.69 | 0.39 | 1.91 | -0.56 | 1.27 | 0.81 | 2.96 |
|  | cassava4.1_016663m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.13 | -0.36 | 0.54 | 0.86 | 0.04 | 1.27 | -0.21 | 0.68 | 0.42 | 1.40 |
|  | cassava4.1_034118m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | Dof-type zinc finger DNA-binding family protein | 0.53 | 0.70 | 1.15 | 1.98 | -0.09 | 1.79 | -0.20 | 1.61 | 0.82 | 2.16 |
|  | cassava4.1_010892m.g | RNA.regulation of transcription.Aux/IAA family | phytochrome-associated protein 1 | 1.65 | 2.05 | 1.57 | 3.34 | 0.49 | 3.80 | -0.35 | 3.15 | 1.06 | 3.80 |
|  | cassava4.1_012643m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 5 | 3.75 | 5.04 | 4.53 | 6.13 | 0.24 | 6.73 | -1.99 | 6.15 | 2.00 | 7.93 |
|  | cassava4.1_004650m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | 1.88 | 1.13 | 2.42 | 3.08 | 0.75 | 1.79 | -0.05 | 5.28 | 1.56 | 3.65 |
|  | cassava4.1_000786m.g | RNA.regulation of transcription.CCAAT box binding factor family, DR1 | CCAAT-binding factor | 0.19 | 0.68 | 0.26 | 0.61 | -0.11 | 0.59 | -0.86 | 1.75 | 0.23 | 1.28 |
|  | cassava4.1_014347m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | WUSCHEL related homeobox 13 | 0.29 | 0.60 | 0.19 | 0.35 | -0.10 | 0.18 | -0.36 | 1.30 | 0.54 | 1.01 |
|  | cassava4.1_012390m.g | RNA.regulation of transcription.AP2/EREBP, | ethylene-responsive element binding | 1.26 | 1.35 | 0.87 | 1.50 | 0.17 | 0.20 | 0.02 | 1.80 | 0.82 | 1.56 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | APETALA2/Ethylene-responsive element binding protein family | protein | | | | | | | | | | |
| | cassava4.1_015101m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 5 | 5.68 | 4.89 | 2.96 | 4.06 | 0.50 | 3.91 | -0.60 | 6.02 | 3.05 | 8.07 |
| | cassava4.1_014074m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 4 | 4.71 | 5.65 | 4.06 | 6.04 | 0.52 | 5.36 | 0.22 | 8.73 | 4.14 | 8.64 |
| | cassava4.1_016153m.g | RNA.regulation of transcription.MYB-related transcription factor family | Duplicated homeodomain-like superfamily protein | 2.27 | 2.00 | 2.34 | 3.50 | 0.34 | 2.12 | 0.19 | 3.68 | 2.22 | 4.19 |
| | cassava4.1_029459m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 3 | -0.27 | 1.19 | -0.13 | 1.21 | -0.03 | 0.88 | 0.01 | 0.95 | 0.38 | 1.47 |
| | cassava4.1_014632m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | related to AP2 6l | 2.16 | 3.57 | 1.15 | 2.83 | 0.03 | 3.83 | 1.75 | 4.17 | 2.02 | 4.79 |
| | cassava4.1_024069m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | chromatin remodeling 31 | 1.61 | 1.88 | 0.53 | 1.95 | -0.48 | 1.13 | 0.72 | 2.51 | 0.87 | 2.83 |
| | cassava4.1_020908m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 5 | 0.63 | 2.04 | 0.83 | 2.64 | 0.12 | 1.39 | 0.34 | 3.58 | 0.87 | 6.10 |
| | cassava4.1_011594m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 5 | 0.41 | 1.12 | 0.02 | 1.65 | 0.25 | 0.82 | -0.02 | 1.62 | -0.38 | 3.26 |
| | cassava4.1_015395m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 4 | 1.44 | 2.43 | 1.28 | 3.10 | -0.43 | 2.32 | -0.73 | 2.46 | 2.08 | 6.80 |
| | cassava4.1_016832m.g | RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family | LOB domain-containing protein 1 | 0.52 | 2.53 | 0.60 | 2.78 | -0.02 | 2.25 | -1.22 | 1.55 | 1.35 | 2.41 |
| | cassava4.1_012667m.g | RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family | LOB domain-containing protein 41 | 1.05 | 3.60 | 3.24 | 5.84 | 0.72 | 5.36 | -0.99 | 3.75 | 2.25 | 3.02 |
| | cassava4.1_010104m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.82 | 2.09 | 0.41 | 1.18 | -0.36 | 1.59 | 0.30 | 1.19 | 0.27 | 1.62 |
| | cassava4.1_000036m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | transcription regulatory protein SNF2, putative | 1.91 | 3.64 | 1.21 | 2.82 | 0.37 | 4.18 | 0.66 | 2.52 | 1.17 | 3.10 |
| | cassava4.1_014014m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox protein 16 | 0.90 | 1.36 | -0.04 | 1.24 | -0.14 | 2.49 | -0.40 | 1.50 | 0.33 | 1.69 |
| | cassava4.1_005519m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-like zinc finger protein | 0.45 | 1.33 | 0.13 | 0.94 | 0.12 | 1.37 | -0.12 | 0.79 | 0.22 | 0.54 |
| | cassava4.1_028193m.g | RNA.regulation of transcription.MYB domain transcription factor family | MYB-like 102 | 0.47 | 1.21 | 0.04 | 0.90 | 0.20 | 1.97 | -0.01 | 1.24 | 0.02 | 0.31 |
| | cassava4.1_012780m.g | RNA.regulation of transcription.bZIP transcription factor family | basic leucine zipper 9 | 1.16 | 1.75 | 0.59 | 1.18 | -0.17 | 1.38 | 0.55 | 0.90 | 0.13 | 0.71 |
| | cassava4.1_028489m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | 1.12 | 2.02 | 0.85 | 1.76 | -0.08 | 2.05 | 0.09 | 1.07 | -0.28 | 0.68 |
| | cassava4.1_008256m.g | RNA.regulation of transcription.TCP transcription factor family | TCP family transcription factor | 0.46 | 0.90 | 0.21 | 0.58 | -0.05 | 0.72 | -0.43 | 0.35 | -0.04 | 0.14 |
| | cassava4.1_012542m.g | RNA.regulation of transcription.MYB-related transcription factor family | Duplicated homeodomain-like | 2.02 | 1.44 | 1.13 | 1.30 | 0.21 | 0.76 | -0.48 | 0.95 | 0.66 | 1.86 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | superfamily protein | | | | | | | | | | |
| | cassava4.1_011111m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 73 | 1.99 | 1.73 | 1.91 | 2.88 | 0.12 | 0.83 | -0.61 | 1.94 | 0.74 | 1.93 |
| | cassava4.1_008733m.g | RNA.regulation of transcription.PHOR1 | plant U-box 29 | 2.05 | 1.96 | 3.42 | 4.42 | 0.48 | 1.49 | -0.54 | 3.22 | 2.59 | 3.29 |
| | cassava4.1_014105m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 1 | -0.03 | 0.10 | 0.13 | 0.19 | -0.03 | 0.01 | -1.36 | -0.28 | -0.08 | -0.09 |
| | cassava4.1_033577m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger (C2H2 type) family protein | 0.02 | 0.27 | 0.26 | 0.29 | -0.12 | -0.04 | -1.20 | 0.09 | -0.28 | 0.24 |
| | cassava4.1_034350m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein r1 | 1.39 | 1.46 | 1.73 | 1.87 | 0.37 | 0.13 | -1.02 | 0.77 | 1.51 | 0.95 |
| | cassava4.1_011082m.g | RNA.regulation of transcription.TCP transcription factor family | TCP family transcription factor 4 | 0.93 | 0.42 | 0.77 | 1.11 | 0.23 | 0.38 | -1.04 | -0.43 | 0.41 | 0.70 |
| | cassava4.1_014713m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2 and C2HC zinc fingers superfamily protein | 1.15 | 1.82 | 2.69 | 3.45 | 0.38 | 1.40 | 1.99 | 3.23 | 1.28 | 0.89 |
| | cassava4.1_003495m.g | RNA.regulation of transcription.GRAS transcription factor family | SCARECROW-like 8 | 0.65 | 0.01 | 0.43 | 0.12 | 0.03 | 0.57 | 0.60 | 1.44 | -0.24 | -0.18 |
| | cassava4.1_019535m.g | RNA.regulation of transcription.General Transcription, TBP-binding protein | YEATS family protein | 0.00 | 0.79 | 0.32 | 0.50 | 0.18 | 0.97 | 0.60 | 1.73 | 0.06 | 0.60 |
| | cassava4.1_008339m.g | RNA.regulation of transcription.bZIP transcription factor family | G-box binding factor 3 | 0.99 | 0.99 | 0.17 | 0.27 | 0.05 | 1.45 | 1.71 | 3.83 | 0.30 | 1.14 |
| | cassava4.1_014981m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox 7 | 1.32 | 1.89 | 0.61 | 1.78 | 0.38 | 3.33 | 2.84 | 5.06 | 0.73 | 2.33 |
| | cassava4.1_007413m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2 and C2HC zinc fingers superfamily protein | 0.35 | 0.63 | -0.03 | -0.11 | 0.04 | -0.03 | 0.85 | 1.57 | 0.31 | 0.71 |
| | cassava4.1_009488m.g | RNA.regulation of transcription.C3H zinc finger family | CCCH-type zinc finger family protein | 0.81 | 0.51 | -0.39 | -1.01 | -0.05 | 0.10 | 1.34 | 2.25 | -0.47 | -0.25 |
| | cassava4.1_009450m.g | RNA.regulation of transcription.C3H zinc finger family | CCCH-type zinc finger family protein | 0.15 | -0.84 | -1.01 | -2.10 | -0.11 | -0.04 | 1.06 | 1.40 | -0.03 | -0.51 |
| | cassava4.1_012382m.g | RNA.regulation of transcription.CCAAT box binding factor family, HAP2 | nuclear factor Y, subunit A9 | -0.01 | -0.68 | -0.16 | -0.96 | 0.05 | 0.84 | 2.53 | 3.26 | -0.27 | 0.14 |
| | cassava4.1_004896m.g | RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family | TESMIN/TSO1-like CXC 2 | 0.38 | -0.01 | 0.30 | -0.25 | -0.44 | -0.19 | 1.69 | 1.24 | 0.43 | 0.31 |
| | cassava4.1_009750m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | heat shock transcription factor A2 | 1.73 | 1.70 | 1.42 | 1.23 | -0.11 | -1.22 | 3.62 | 3.26 | 1.25 | 1.21 |
| | cassava4.1_004528m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.31 | -0.69 | 0.13 | 0.30 | -0.05 | 0.21 | 0.44 | 1.01 | 0.17 | 0.27 |
| | cassava4.1_014707m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc-finger protein 2 | 0.42 | -0.04 | 1.20 | 0.28 | 0.48 | 0.19 | 0.80 | 2.20 | 1.10 | 1.15 |
| | cassava4.1_014662m.g | RNA.regulation of transcription.C2H2 zinc finger family | salt tolerance zinc finger | 0.67 | -0.31 | 1.47 | 0.33 | 0.21 | -0.08 | 0.25 | 2.08 | 0.82 | 0.84 |
| | cassava4.1_017982m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-type zinc finger family protein | 0.22 | -1.16 | 1.78 | 1.60 | 0.30 | 0.56 | 0.65 | 2.86 | 1.10 | 0.24 |
| | cassava4.1_014607m.g | RNA.regulation of transcription.C2H2 zinc finger family | salt tolerance zinc finger | 0.68 | -0.11 | 1.73 | 0.92 | 0.30 | -0.06 | 0.21 | 2.00 | 1.19 | -0.07 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_002960m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 16 | 0.76 | -0.59 | 0.20 | -0.55 | -0.11 | -0.01 | 0.37 | 0.91 | 0.34 | 0.44 |
| | cassava4.1_006005m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | related to AP2.7 | 0.90 | -0.53 | 0.23 | 0.01 | -0.11 | 0.09 | 0.66 | 1.52 | 0.15 | 1.18 |
| | cassava4.1_007184m.g | RNA.regulation of transcription.bZIP transcription factor family | Basic-leucine zipper (bZIP) transcription factor family protein | 0.24 | -0.54 | -0.11 | -0.14 | -0.22 | -0.16 | 0.39 | 1.38 | 0.56 | 0.73 |
| | cassava4.1_023048m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.01 | -0.70 | -0.09 | -0.84 | 0.02 | -0.19 | 0.14 | 1.31 | 0.00 | -0.03 |
| | cassava4.1_004069m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Duplicated homeodomain-like superfamily protein | -0.55 | -2.66 | -0.43 | -2.80 | -0.24 | -0.77 | 0.46 | 1.65 | 0.22 | 0.01 |
| C2 | cassava4.1_015506m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.18 | -0.21 | -0.11 | 0.14 | -0.31 | -1.68 | -0.42 | -0.11 | 0.58 | 0.29 |
| | cassava4.1_004906m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | RNA-binding (RRM/RBD/RNP motifs) family protein | 0.50 | 0.81 | 0.38 | 0.43 | -0.09 | -0.75 | 0.69 | 0.36 | 0.88 | 1.39 |
| | cassava4.1_033275m.g | RNA.regulation of transcription.LUG | LEUNIG_homolog | 1.03 | 0.50 | 0.88 | 1.08 | -0.49 | -0.51 | 0.38 | 0.77 | 0.89 | 1.83 |
| | cassava4.1_023141m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 73 | 1.55 | 1.27 | 1.62 | 2.34 | 0.39 | 1.15 | 0.92 | 1.34 | 1.96 | 2.53 |
| | cassava4.1_000393m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | 0.21 | 0.50 | 0.32 | 0.87 | -0.04 | 0.12 | 0.40 | 0.10 | 0.96 | 0.44 |
| | cassava4.1_004902m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-like zinc finger protein | -0.03 | 0.52 | 0.15 | 0.77 | -0.24 | -0.42 | -0.43 | -1.48 | 0.47 | 0.41 |
| | cassava4.1_006556m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | myb-like HTH transcriptional regulator family protein | 0.44 | 0.76 | 0.87 | 1.24 | 0.08 | -0.14 | 0.58 | -0.50 | 0.56 | 0.62 |
| | cassava4.1_000117m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | chromatin remodeling 5 | -0.01 | 0.52 | 0.22 | 0.39 | -0.50 | -0.77 | 0.79 | -0.70 | 0.29 | -0.04 |
| | cassava4.1_000114m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | chromatin remodeling 5 | 0.05 | 0.53 | 0.25 | 0.42 | -0.26 | -0.47 | 0.77 | -0.91 | 0.20 | 0.08 |
| | cassava4.1_000396m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger protein-related | -0.35 | -0.37 | 0.06 | 0.08 | -0.33 | -0.89 | 0.24 | -0.82 | 0.08 | -0.37 |
| | cassava4.1_000779m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | DNA/RNA helicase protein | -0.55 | -0.36 | 0.04 | -0.47 | -0.42 | -1.49 | 0.43 | -1.52 | -0.01 | -0.79 |
| | cassava4.1_001653m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | 0.38 | 0.27 | 0.36 | 0.25 | 0.00 | -0.17 | 0.86 | -0.41 | 0.46 | 0.04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_006759m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | BEL1-like homeodomain 6 | 0.14 | 0.68 | 0.07 | 0.64 | -0.36 | -0.73 | 0.46 | -1.53 | -0.11 | -0.82 |
| | cassava4.1_002618m.g | RNA.regulation of transcription.Nucleosome/chromatin assembly factor group | DDT domain-containing protein | -0.13 | 0.43 | 0.35 | 0.57 | -0.21 | -0.32 | 0.39 | -1.09 | 0.23 | -0.55 |
| | cassava4.1_012115m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | heat shock transcription factor A6B | 2.65 | 2.78 | 1.87 | 1.31 | -1.25 | 0.57 | 2.54 | 0.90 | 0.83 | 1.02 |
| | cassava4.1_002701m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | SNF2 domain-containing protein / helicase domain-containing protein | 0.55 | 1.18 | -0.05 | -0.11 | -0.01 | 0.41 | 0.32 | 0.35 | 0.07 | 0.22 |
| | cassava4.1_026051m.g | RNA.regulation of transcription.MADS box transcription factor family | AGAMOUS-like 19 | 0.39 | 0.89 | -0.58 | -0.62 | -0.01 | -0.06 | 0.30 | 0.08 | 0.03 | -0.06 |
| | cassava4.1_011766m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 31 | 0.93 | 1.77 | -0.26 | 0.42 | 0.33 | 1.14 | 0.60 | 1.17 | 0.16 | 0.59 |
| | cassava4.1_015207m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | 0.16 | 1.50 | 0.07 | 0.53 | 0.01 | 0.74 | 0.34 | 0.37 | -0.14 | 0.04 |
| | cassava4.1_005556m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-like zinc finger protein | 0.73 | 0.94 | 0.52 | 0.65 | 0.23 | 0.60 | 0.55 | 0.38 | 0.18 | 0.54 |
| | cassava4.1_011212m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | KNOTTED1-like homeobox gene 3 | 0.56 | 1.11 | 0.10 | 0.34 | -0.09 | 0.20 | 0.28 | 0.14 | 0.03 | 0.20 |
| | cassava4.1_008671m.g | RNA.regulation of transcription.bZIP transcription factor family | Basic-leucine zipper (bZIP) transcription factor family protein | 0.36 | 1.00 | 0.02 | 0.10 | -0.02 | 0.28 | 0.61 | 0.45 | -0.06 | -0.07 |
| | cassava4.1_000870m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | SET domain protein 16 | 0.45 | 0.93 | 0.05 | 0.44 | 0.11 | -0.09 | 0.50 | 0.42 | 0.06 | -0.18 |
| | cassava4.1_015051m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox 12 | 1.88 | 3.54 | 1.26 | 1.85 | 0.39 | 1.13 | 1.48 | 3.25 | 0.41 | 0.80 |
| | cassava4.1_009563m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox from Arabidopsis thaliana | 1.20 | 2.07 | 0.70 | 1.42 | 0.09 | 1.49 | 0.28 | 3.14 | 0.68 | 1.19 |
| | cassava4.1_010339m.g | RNA.regulation of transcription.MYB domain transcription factor family | MYB-like 102 | 1.89 | 3.41 | 1.09 | 2.51 | 0.28 | 2.22 | 0.52 | 3.88 | -0.22 | 0.54 |
| | cassava4.1_005470m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2 and C2HC zinc fingers superfamily protein | 1.00 | 1.61 | 0.91 | 1.28 | 0.18 | 1.65 | 0.65 | 2.01 | 0.33 | 0.93 |
| | cassava4.1_012335m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 62 | 2.38 | 4.45 | 1.50 | 3.31 | -0.18 | 3.75 | 1.91 | 5.55 | -0.27 | 2.18 |
| | cassava4.1_010945m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 73 | 2.06 | 1.80 | 1.31 | 1.60 | 0.23 | 0.49 | -0.14 | 1.97 | 0.36 | 0.41 |
| | cassava4.1_014990m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | DOF zinc finger protein 1 | 1.45 | 2.99 | 0.63 | 1.59 | -0.16 | 1.25 | 0.33 | 1.88 | 1.12 | 1.41 |
| | cassava4.1_032831m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 6 | 0.51 | 2.05 | 0.35 | 1.22 | -0.77 | 0.64 | -0.48 | 1.27 | -0.02 | 0.95 |
| | cassava4.1_034188m.g | RNA.regulation of transcription.TCP transcription factor family | TCP family transcription factor | 0.96 | 1.55 | 0.30 | 1.22 | 0.13 | 0.59 | -0.22 | 1.49 | 0.42 | 1.17 |
| | cassava4.1_019256m.g | RNA.regulation of transcription.bZIP transcription factor family | TGACG motif-binding factor 4 | 0.94 | 1.82 | 0.63 | 0.77 | 0.00 | 0.56 | -0.39 | 0.23 | 0.42 | 0.46 |
| | cassava4.1_004334m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor | Protein of unknown function | 0.62 | 1.42 | 0.07 | 0.54 | -0.10 | 0.57 | -0.18 | 0.36 | 0.22 | 0.38 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | family | (DUF1421) | | | | | | | | | | |
| | cassava4.1_000610m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 19 | 0.36 | 1.03 | 0.10 | 0.19 | -0.03 | 0.01 | 0.24 | 0.17 | 0.37 | 0.34 |
| | cassava4.1_000578m.g | RNA.regulation of transcription.MYB domain transcription factor family | DIRP ;Myb-like DNA-binding domain | 0.43 | 1.70 | 0.36 | 0.85 | -0.43 | -0.05 | 0.68 | 0.53 | 0.40 | 0.66 |
| | cassava4.1_004089m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Duplicated homeodomain-like superfamily protein | 1.07 | 2.83 | -0.60 | 0.73 | 0.12 | -0.79 | -0.37 | 0.06 | -0.29 | 0.41 |
| | cassava4.1_004015m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 2.66 | 3.26 | 0.61 | 1.06 | 0.14 | 1.05 | 0.37 | 1.60 | 1.03 | 2.29 |
| | cassava4.1_006968m.g | RNA.regulation of transcription.GRAS transcription factor family | scarecrow-like 3 | 2.37 | 2.84 | 0.43 | 0.34 | 0.32 | 0.88 | 0.72 | 2.84 | 0.91 | 2.15 |
| | cassava4.1_014027m.g | RNA.regulation of transcription.MYB-related transcription factor family | myb-like transcription factor family protein | 1.23 | 1.69 | 0.12 | 0.35 | 0.38 | 0.74 | -0.09 | 1.43 | 0.40 | 1.28 |
| | cassava4.1_032811m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | 1.13 | 1.49 | 0.07 | 0.04 | 0.07 | -0.36 | 0.42 | 0.79 | 0.21 | 0.93 |
| | cassava4.1_006275m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Duplicated homeodomain-like superfamily protein | 0.95 | 1.69 | 0.57 | 0.80 | 0.10 | 0.22 | 0.52 | 1.05 | 0.47 | 1.15 |
| C3 | cassava4.1_008554m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | CONSTANS-like 9 | -0.53 | -0.50 | -0.21 | -0.14 | -0.33 | -0.28 | 0.91 | 0.11 | 0.52 | 0.40 |
| | cassava4.1_000223m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | chromatin remodeling factor CHD3 (PICKLE) | -0.12 | 0.19 | 0.17 | 0.19 | -0.12 | -0.23 | 0.93 | -0.04 | 0.25 | 0.32 |
| | cassava4.1_011448m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-type zinc finger family protein | -2.19 | -1.42 | -0.78 | -2.07 | -0.03 | -2.63 | 0.02 | -0.31 | -0.90 | -1.25 |
| | cassava4.1_006018m.g | RNA.regulation of transcription.C2H2 zinc finger family | ZPR1 zinc-finger domain protein | -0.82 | -0.71 | -1.08 | -1.42 | -0.17 | -0.32 | 0.12 | 0.18 | -0.08 | -0.23 |
| | cassava4.1_015591m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -1.13 | -2.37 | -1.56 | -2.53 | -0.23 | -2.24 | 0.30 | 0.14 | 1.79 | -0.03 |
| | cassava4.1_007445m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 55 | -2.58 | -3.51 | -3.26 | -2.87 | -1.09 | -2.66 | -0.99 | -2.40 | -0.79 | -1.87 |
| | cassava4.1_002885m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 9 | -0.69 | -1.65 | -0.29 | -1.56 | -0.26 | -0.79 | 0.32 | -1.29 | 0.04 | -0.64 |
| | cassava4.1_011429m.g | RNA.regulation of transcription.MYB-related transcription factor family | myb-like transcription factor family protein | -0.98 | -1.98 | -0.87 | -2.41 | -0.08 | -1.72 | 0.48 | -1.18 | -0.14 | -0.95 |
| | cassava4.1_034105m.g | RNA.regulation of transcription.PWWP domain protein | ataxia-telangiectasia mutated | -0.42 | -0.58 | -0.51 | -1.02 | -0.20 | -0.53 | 0.21 | -0.51 | 0.26 | -0.28 |
| | cassava4.1_014358m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger protein 4 | -0.45 | -1.76 | -0.65 | -1.47 | 0.06 | -0.53 | -0.29 | -0.64 | -0.44 | -0.58 |
| | cassava4.1_015213m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2 and C2HC zinc fingers | -0.50 | -2.98 | -0.62 | -2.28 | 0.05 | -1.24 | -0.31 | -1.39 | -0.57 | -1.14 |

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| | | | superfamily protein | | | | | | | | | | |
| | cassava4.1_004886m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.28 | -0.92 | -0.07 | -0.34 | 0.16 | -0.21 | 0.27 | -0.18 | 0.15 | -0.26 |
| | cassava4.1_012303m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | heat shock transcription factor B2A | -0.26 | -1.23 | -0.43 | -0.73 | 0.08 | -0.50 | 0.32 | -0.36 | 0.02 | -0.43 |
| | cassava4.1_014521m.g | RNA.regulation of transcription.Alfin-like | alfin-like 5 | -0.25 | -0.85 | -0.29 | -0.84 | -0.13 | -0.04 | 0.04 | -0.04 | -0.13 | -0.21 |
| | cassava4.1_009182m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | ASH1-related protein 2 | -0.85 | -2.95 | -0.83 | -2.24 | 0.22 | -0.97 | 0.70 | -0.13 | -0.03 | -0.18 |
| | cassava4.1_002718m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | 0.07 | -0.34 | 0.29 | 0.29 | 0.34 | 0.93 | 0.54 | 0.36 | 1.11 | 0.81 |
| | cassava4.1_004194m.g | RNA.regulation of transcription.C2H2 zinc finger family | indeterminate(ID)-domain 5 | 0.41 | -0.36 | 0.25 | -0.29 | 0.23 | -0.12 | -0.11 | 0.08 | 1.26 | 1.54 |
| | cassava4.1_013453m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.66 | -2.11 | 0.06 | -0.47 | 0.31 | -0.08 | -0.13 | -0.43 | 1.37 | 1.49 |
| | cassava4.1_016167m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -1.59 | -3.12 | -0.61 | -2.97 | -0.46 | -2.00 | -1.47 | -0.57 | 0.65 | 0.52 |
| | cassava4.1_009138m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 106 | -1.56 | -2.53 | -0.55 | -1.96 | -0.09 | -1.25 | -1.02 | -0.92 | 0.02 | -0.51 |
| | cassava4.1_026975m.g | RNA.regulation of transcription.ARR | response regulator 3 | -3.37 | -4.11 | -0.21 | -1.41 | 0.20 | -0.01 | -0.31 | -0.61 | -1.32 | -1.85 |
| | cassava4.1_029813m.g | RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family | Lateral organ boundaries (LOB) domain family protein | -1.85 | -2.18 | -1.67 | -1.25 | -0.33 | -1.13 | -0.61 | -0.62 | -1.10 | -1.07 |
| | cassava4.1_017720m.g | RNA.regulation of transcription.bZIP transcription factor family | Basic-leucine zipper (bZIP) transcription factor family protein | -0.50 | -1.56 | -0.23 | -0.91 | 0.19 | 0.48 | -0.16 | 0.07 | -0.13 | -0.73 |
| | cassava4.1_011296m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | cytokinin-responsive gata factor 1 | -0.30 | -2.33 | -0.46 | -1.07 | 0.08 | -0.06 | -0.72 | -0.32 | -0.34 | -0.73 |
| | cassava4.1_013034m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein | -1.37 | -3.55 | -1.26 | -1.98 | 0.36 | 0.05 | -1.21 | -0.96 | -0.52 | -0.97 |
| | cassava4.1_015797m.g | RNA.regulation of transcription.ARR | response regulator 5 | -1.00 | -5.80 | -1.25 | -1.93 | -0.63 | -0.40 | -0.90 | -1.43 | -2.42 | -3.46 |
| | cassava4.1_018617m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 15 | -0.49 | -1.81 | 0.26 | -0.47 | 0.05 | 0.27 | -0.47 | -0.15 | -0.52 | -0.57 |
| | cassava4.1_012449m.g | RNA.regulation of transcription.MYB-related transcription factor family | myb-like transcription factor family protein | -0.25 | -2.26 | 0.42 | 0.24 | 0.08 | 0.57 | -0.20 | -0.41 | -0.07 | -0.69 |

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| | cassava4.1_030713m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | cycling DOF factor 2 | -0.47 | -1.65 | -0.20 | -0.18 | 0.10 | 1.15 | 0.12 | -0.71 | -0.32 | -0.74 |
| | cassava4.1_002464m.g | RNA.regulation of transcription.C3H zinc finger family | CCCH-type zinc finger protein with ARM repeat domain | -0.11 | -0.95 | -0.07 | -0.40 | -0.03 | 0.43 | 0.50 | -0.56 | -0.04 | -0.27 |
| | cassava4.1_012272m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 20 | -1.57 | -2.54 | -0.55 | -1.33 | 0.15 | 0.13 | 0.22 | -1.35 | -0.18 | -1.36 |
| | cassava4.1_016517m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.78 | -2.75 | -0.06 | -1.22 | 0.12 | -0.08 | -0.58 | -1.43 | -0.46 | -0.93 |
| | cassava4.1_015258m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box zinc finger family protein | -0.48 | -1.94 | -0.41 | -0.90 | 0.01 | -0.34 | -0.19 | -1.01 | -0.46 | -0.99 |
| | cassava4.1_006065m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | cycling DOF factor 2 | -0.23 | -1.34 | -0.18 | -0.59 | 0.13 | 0.23 | 0.01 | -0.56 | -0.18 | -0.68 |
| | cassava4.1_014772m.g | RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family | LOB domain-containing protein 37 | -1.11 | -4.49 | -0.55 | -0.46 | 0.01 | 0.42 | -1.14 | -2.56 | -0.80 | -1.52 |
| | cassava4.1_002279m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | -0.48 | -1.55 | -0.25 | -0.51 | 0.12 | 0.47 | -0.19 | -1.10 | -0.06 | -0.48 |
| | cassava4.1_006069m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | related to AP2.7 | -0.44 | -2.33 | 0.26 | 0.16 | 0.26 | 0.05 | -0.31 | -0.51 | -0.21 | -0.03 |
| | cassava4.1_016873m.g | RNA.regulation of transcription.Aux/IAA family | AUX/IAA transcriptional regulator family protein | -1.07 | -4.42 | -0.77 | -1.64 | -0.36 | -1.15 | -1.14 | -1.94 | -1.09 | -1.15 |
| | cassava4.1_009290m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | cryptochrome-interacting basic-helix-loop-helix 1 | -2.28 | -6.15 | -1.06 | -1.58 | -0.65 | -1.25 | -0.73 | -3.07 | -0.40 | -1.82 |
| | cassava4.1_014346m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger protein with CCT domain | -1.32 | -3.91 | -1.35 | -0.79 | -0.19 | -0.10 | -0.18 | -1.60 | -0.18 | -1.16 |
| | cassava4.1_031505m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 3 | -1.16 | -2.97 | -1.12 | -0.84 | -0.29 | -0.52 | -0.85 | -1.31 | -0.19 | -0.90 |
| | cassava4.1_001154m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 6 | 0.00 | 0.11 | 0.02 | -0.29 | -0.07 | -0.84 | -0.66 | -0.25 | -0.01 | -0.43 |
| | cassava4.1_025153m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-like zinc finger protein | -0.47 | -0.50 | -0.10 | -0.71 | -0.16 | -1.06 | -1.23 | -1.50 | -0.17 | -1.42 |
| | cassava4.1_005370m.g | RNA.regulation of transcription.C2H2 zinc finger family | indeterminate(ID)-domain 7 | 0.06 | -0.01 | -0.27 | -0.60 | -0.27 | -0.84 | -0.21 | -0.93 | -0.16 | -0.40 |
| | cassava4.1_030248m.g | RNA.regulation of transcription.AP2/EREBP, | AP2/B3 transcription factor family | 0.35 | 0.67 | -0.02 | -0.19 | -0.20 | -1.86 | 1.32 | -0.54 | 0.50 | -0.31 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | APETALA2/Ethylene-responsive element binding protein family | protein | | | | | | | | | | |
| | cassava4.1_014911m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 48 | -0.09 | 0.28 | -0.63 | -0.98 | -0.17 | -1.20 | 0.33 | -0.98 | -0.12 | -0.82 |
| | cassava4.1_011733m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | OBF binding protein 4 | 0.02 | -0.64 | -0.58 | -1.73 | -0.27 | -2.01 | -0.11 | 0.03 | 0.24 | 0.02 |
| | cassava4.1_029328m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | cooperatively regulated by ethylene and jasmonate 1 | 0.64 | 0.14 | 0.01 | -0.54 | -0.09 | -1.33 | 0.19 | 0.30 | 0.15 | -0.09 |
| | cassava4.1_004716m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 10 | 0.17 | -0.19 | -0.22 | -0.48 | -0.10 | -1.46 | -0.19 | 0.02 | -0.21 | -0.83 |
| | cassava4.1_013954m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper protein family | 0.15 | 0.31 | -0.67 | -1.10 | -0.62 | -1.84 | 0.02 | -0.25 | -0.33 | -1.15 |
| | cassava4.1_001312m.g | RNA.regulation of transcription.Argonaute | Argonaute family protein | -0.03 | -0.19 | -0.04 | -0.41 | -0.06 | -0.91 | 0.00 | -0.30 | -0.02 | -0.45 |
| | cassava4.1_005732m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | Rubisco methyltransferase family protein | 0.09 | 0.01 | -0.24 | -1.08 | -0.04 | -1.62 | -0.55 | -0.57 | -0.18 | -0.78 |
| | cassava4.1_013010m.g | RNA.regulation of transcription.MYB-related transcription factor family | Duplicated homeodomain-like superfamily protein | -0.23 | -0.83 | 0.08 | -0.19 | 0.12 | -0.88 | -0.61 | -0.15 | -0.50 | -0.93 |
| | cassava4.1_016343m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -0.45 | -2.42 | 1.38 | -0.45 | 0.43 | -1.26 | -2.63 | -0.26 | 0.65 | -1.69 |
| | cassava4.1_003646m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.52 | -1.44 | -0.01 | -0.57 | -0.08 | -1.24 | -0.99 | -0.86 | 0.15 | -0.63 |
| | cassava4.1_009755m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid inducible 9 | -0.83 | -1.91 | -0.42 | -1.24 | -0.29 | -0.88 | -1.34 | -1.69 | -0.13 | -1.23 |
| | cassava4.1_014818m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper protein family | -1.09 | -1.62 | -0.30 | -1.07 | -0.14 | -1.09 | -1.31 | -1.37 | -0.20 | -1.01 |
| | cassava4.1_032473m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | ethylene responsive element binding factor 6 | -1.31 | -3.51 | 0.88 | -2.74 | 0.21 | -2.16 | -2.02 | -0.50 | 0.20 | -3.31 |
| | cassava4.1_013214m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -0.89 | -3.46 | 1.03 | -1.42 | 0.38 | -1.65 | -0.30 | -0.07 | 0.90 | -2.24 |
| | cassava4.1_009548m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | 0.70 | -1.97 | 2.36 | 1.30 | 0.91 | -0.36 | 0.75 | 1.56 | 1.43 | -0.04 |
| | cassava4.1_004517m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 3 | -0.13 | -1.28 | -0.32 | -0.55 | -0.16 | -0.73 | -0.48 | -0.28 | -0.16 | -0.50 |
| | cassava4.1_008459m.g | RNA.regulation of transcription.bZIP transcription factor family | G-box binding factor 3 | -0.32 | -1.18 | -0.03 | -0.48 | -0.39 | -0.40 | 0.30 | 0.16 | -0.25 | -0.81 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_005881m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | phytochrome interacting factor 3-like 1 | -0.83 | -2.29 | -0.35 | -1.32 | -0.09 | -0.62 | 0.29 | -1.15 | -0.74 | -2.88 |
| | cassava4.1_001542m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 2 | -0.14 | -0.81 | -0.25 | -0.79 | -0.10 | -0.77 | 0.58 | -0.39 | -0.07 | -1.55 |
| | cassava4.1_007247m.g | RNA.regulation of transcription.E2F/DP transcription factor family | E2F transcription factor 1 | -0.65 | -1.20 | -0.16 | -1.04 | -0.32 | -0.89 | 0.81 | -1.08 | -0.41 | -1.52 |
| | cassava4.1_021075m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | unknow | 0.12 | -1.24 | -0.63 | -2.37 | 0.06 | -2.48 | 1.50 | -0.24 | -0.07 | -1.16 |
| | cassava4.1_010627m.g | RNA.regulation of transcription.CCAAT box binding factor family, HAP2 | nuclear factor Y, subunit A1 | 0.35 | -0.27 | -0.50 | -1.60 | 0.09 | -0.51 | 0.59 | 0.13 | -0.48 | -0.72 |
| | cassava4.1_024442m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.08 | -1.96 | -0.83 | -1.58 | -0.23 | -1.18 | 0.31 | -0.63 | -0.94 | -1.93 |
| | cassava4.1_011611m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | OBF binding protein 4 | -0.23 | -1.06 | -0.49 | -1.33 | -0.08 | -0.49 | -0.29 | -0.35 | -0.69 | -1.18 |
| | cassava4.1_010201m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | heat shock transcription factor C1 | -0.07 | -1.40 | -0.31 | -1.40 | 0.14 | -1.10 | 0.02 | 0.24 | -0.30 | -0.95 |
| | cassava4.1_015454m.g | RNA.regulation of transcription.MADS box transcription factor family | K-box region and MADS-box transcription factor family protein | 0.26 | 0.31 | 0.36 | 0.06 | -0.07 | 0.29 | 1.02 | 0.36 | -0.24 | -0.63 |
| | cassava4.1_008877m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.05 | -0.16 | 0.02 | -0.66 | 0.00 | -0.86 | 1.07 | -0.79 | -0.19 | -1.17 |
| | cassava4.1_009601m.g | RNA.regulation of transcription.General Transcription | RNA polymerase III RPC4 | -0.08 | 0.10 | -0.33 | -0.48 | 0.01 | -0.52 | 0.56 | -0.67 | -0.48 | -0.94 |
| | cassava4.1_013975m.g | RNA.regulation of transcription.MADS box transcription factor family | K-box region and MADS-box transcription factor family protein | -0.05 | 0.08 | -0.12 | -0.34 | -0.07 | -0.49 | 1.20 | -0.15 | -0.13 | -1.24 |
| | cassava4.1_002453m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeodomain GLABROUS 2 | -0.29 | -0.03 | -0.28 | -0.26 | 0.04 | -0.20 | 1.13 | -0.33 | 0.18 | -0.64 |
| | cassava4.1_001456m.g | RNA.regulation of transcription.PHD finger transcription factor | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain | -0.18 | -0.16 | -0.35 | -0.52 | -0.15 | -0.34 | 0.86 | -0.01 | 0.04 | -0.42 |
| | cassava4.1_015815m.g | RNA.regulation of transcription.ARR | response regulator 9 | -1.09 | -1.38 | -0.64 | -0.80 | 0.05 | -1.60 | -0.39 | -1.56 | -0.56 | -2.69 |
| | cassava4.1_017624m.g | RNA.regulation of transcription.Aux/IAA family | AUX/IAA transcriptional regulator family protein | -0.21 | -1.00 | -0.27 | -0.65 | -0.07 | -1.19 | 0.06 | -1.25 | -0.94 | -2.47 |
| | cassava4.1_003856m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.56 | 0.00 | 0.66 | 0.75 | 0.36 | -0.55 | -0.06 | -0.81 | 0.11 | -1.52 |
| | cassava4.1_010425m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | 0.16 | -0.57 | 0.20 | -0.58 | -0.09 | -1.55 | -0.25 | -1.13 | -0.46 | -1.52 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_015098m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 0.14 | -0.19 | -0.07 | -0.27 | -0.11 | -0.49 | -0.24 | -0.97 | -0.16 | -0.90 |
| | cassava4.1_022485m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | SWITCH/sucrose nonfermenting 3C | -0.09 | -0.08 | -0.09 | -0.14 | -0.05 | -0.19 | -0.35 | -1.47 | -0.17 | -0.83 |
| | cassava4.1_000922m.g | RNA.regulation of transcription.NIN-like bZIP-related family | NIN like protein 7 | 0.09 | 0.24 | -0.33 | -0.08 | 0.04 | -0.22 | -0.03 | -1.73 | -0.06 | -0.97 |
| | cassava4.1_008682m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.37 | -0.61 | -0.30 | -0.09 | -0.20 | -0.07 | -0.09 | -1.46 | -0.48 | -0.94 |
| | cassava4.1_012977m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | phosphate starvation response 1 | -0.52 | -1.26 | -0.32 | -0.47 | -0.05 | -0.34 | -0.60 | -2.53 | -0.28 | -1.35 |
| | cassava4.1_030151m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | -0.45 | -0.91 | -0.39 | -0.70 | -0.32 | -0.26 | -0.61 | -1.42 | -0.30 | -0.96 |
| | cassava4.1_010526m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | related to AP2 4 | -0.22 | -0.45 | -0.27 | -0.41 | 0.04 | 0.32 | -0.66 | -2.31 | -0.10 | -1.48 |
| | cassava4.1_001772m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | -0.10 | -0.45 | -0.23 | -0.27 | -0.19 | 0.17 | -0.11 | -1.36 | -0.12 | -0.70 |
| | cassava4.1_002969m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 1 | -0.26 | -0.38 | -0.10 | -0.45 | 0.11 | -0.20 | -0.05 | -0.90 | -0.36 | -0.59 |
| | cassava4.1_004983m.g | RNA.regulation of transcription.C2H2 zinc finger family | indeterminate(ID)-domain 7 | -0.17 | -0.44 | -0.08 | -0.55 | 0.06 | 0.01 | 0.11 | -0.93 | -0.19 | -0.83 |
| | cassava4.1_014024m.g | RNA.regulation of transcription.CCAAT box binding factor family, HAP5 | nuclear factor Y, subunit C2 | -0.33 | -0.94 | -0.32 | -0.76 | 0.00 | -0.23 | -0.13 | -1.73 | -0.38 | -1.64 |
| | cassava4.1_004443m.g | RNA.regulation of transcription.C2H2 zinc finger family | indeterminate(ID)-domain 5 | 0.22 | -0.63 | 0.08 | -0.62 | 0.04 | -0.10 | 0.02 | -1.49 | 0.21 | -0.55 |
| | cassava4.1_002166m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeodomain GLABROUS 2 | -0.12 | -0.41 | -0.40 | -0.48 | -0.17 | -0.28 | -0.14 | -0.90 | -0.21 | -0.66 |
| | cassava4.1_023381m.g | RNA.regulation of transcription.Nucleosome/chromatin assembly factor group | HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain | 0.11 | -0.40 | -0.23 | -0.57 | 0.02 | -0.11 | -0.28 | -1.80 | -0.03 | -0.99 |
| | cassava4.1_019292m.g | RNA.regulation of transcription.Aux/IAA family | unknow | -0.34 | -1.61 | -0.71 | -0.73 | -0.30 | -0.88 | -0.97 | -2.47 | -0.99 | -2.15 |
| | cassava4.1_005159m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.31 | -1.77 | 0.09 | -0.20 | 0.32 | -1.21 | -0.09 | -2.45 | 0.03 | -3.53 |
| | cassava4.1_006801m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | cycling DOF factor 3 | -0.50 | -1.54 | -0.46 | -0.89 | -0.31 | -1.03 | -0.89 | -2.04 | -0.52 | -2.23 |
| | cassava4.1_007759m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger protein 1 | -0.44 | -1.18 | -0.13 | -0.48 | -0.01 | -0.45 | -0.19 | -1.57 | -0.39 | -1.27 |
| | cassava4.1_007787m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger protein 1 | -0.38 | -1.30 | -0.26 | -0.45 | -0.12 | -0.69 | -0.09 | -1.75 | -0.28 | -1.63 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_013797m.g | RNA.regulation of transcription.bZIP transcription factor family | Basic-leucine zipper (bZIP) transcription factor family protein | -0.42 | -0.83 | -0.21 | -0.67 | -0.03 | -0.66 | -0.28 | -1.69 | -0.41 | -1.54 |
| | cassava4.1_006206m.g | RNA.regulation of transcription.C2H2 zinc finger family | indeterminate(ID)-domain 5 | -0.10 | -0.77 | 0.27 | -0.68 | -0.01 | -0.44 | -0.11 | -1.63 | -0.13 | -1.23 |
| | cassava4.1_011554m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.36 | -0.99 | 0.09 | -0.17 | 0.20 | 0.09 | -0.62 | -1.32 | -0.42 | -1.54 |
| | cassava4.1_009052m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | -0.16 | -1.60 | 0.30 | -0.89 | 0.01 | -0.34 | -0.85 | -2.04 | -0.79 | -2.26 |
| | cassava4.1_007443m.g | RNA.regulation of transcription.PHOR1 | ARM repeat superfamily protein | -0.73 | -0.99 | -0.15 | -0.35 | 0.02 | -0.47 | -1.11 | -2.06 | -0.32 | -2.11 |
| | cassava4.1_002303m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | -0.08 | -0.45 | -0.33 | -1.01 | -0.40 | -0.21 | 0.29 | -1.37 | -0.41 | -1.68 |
| | cassava4.1_034237m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20 | -0.81 | -0.77 | -0.85 | -0.74 | -0.05 | -0.48 | -0.04 | -1.93 | -0.71 | -2.47 |
| | cassava4.1_004904m.g | RNA.regulation of transcription.General Transcription | tetratricopeptide repeat (TPR)-containing protein | 0.18 | 0.47 | -0.38 | -0.74 | 0.39 | -0.23 | 0.25 | -0.68 | -0.44 | -1.38 |
| | cassava4.1_008876m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-like zinc finger protein | 0.17 | -0.07 | -0.22 | -0.86 | 0.18 | -0.45 | -0.85 | -1.19 | -0.52 | -1.73 |
| | cassava4.1_013986m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper protein family | -0.44 | 0.03 | -0.21 | -0.57 | 0.08 | -0.80 | -0.48 | -1.39 | -0.59 | -1.90 |
| | cassava4.1_011931m.g | RNA.regulation of transcription.MYB-related transcription factor family | Homeodomain-like superfamily protein | -0.06 | -0.15 | -0.16 | -0.79 | -0.02 | -0.50 | -0.17 | -1.25 | -0.65 | -1.45 |
| | cassava4.1_010816m.g | RNA.regulation of transcription.TCP transcription factor family | plastid transcription factor 1 | 0.14 | -0.19 | -0.02 | -0.31 | 0.17 | 0.00 | -0.08 | -0.69 | -0.68 | -0.99 |
| | cassava4.1_011084m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | -0.83 | -1.26 | -0.53 | -0.44 | 0.58 | -0.93 | 0.42 | -1.81 | -0.79 | -1.31 |
| | cassava4.1_009038m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | myb-like transcription factor family protein | -0.92 | -1.20 | 0.26 | 0.51 | -0.01 | 0.07 | 0.14 | -2.11 | -0.22 | -1.18 |
| | cassava4.1_013116m.g | RNA.regulation of transcription.MYB-related transcription factor family | Homeodomain-like/winged-helix DNA-binding family protein | -0.53 | -0.64 | 0.17 | 0.02 | 0.06 | -0.36 | 0.14 | -1.03 | -0.18 | -0.72 |
| | cassava4.1_012931m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 7 | -1.03 | -0.84 | -0.12 | -0.55 | -0.30 | -0.67 | 0.06 | -1.37 | -0.39 | -1.51 |
| | cassava4.1_006787m.g | RNA.regulation of transcription.Bromodomain proteins | bromodomain 4 | 0.04 | -0.31 | 0.31 | 0.06 | -0.07 | -0.30 | 0.35 | -1.42 | -0.25 | -1.50 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_031076m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | SET domain protein 14 | -0.30 | -0.50 | 0.05 | 0.04 | -0.01 | -0.27 | 0.47 | -1.24 | -0.16 | -1.05 |
| | cassava4.1_030224m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Duplicated homeodomain-like superfamily protein | -0.39 | -0.04 | -0.06 | -0.39 | 0.19 | -0.43 | 0.08 | -1.08 | -0.12 | -0.54 |
| | cassava4.1_031977m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | plant-specific transcription factor YABBY family protein | -0.69 | -0.86 | -0.04 | -0.25 | -0.10 | -1.33 | -0.06 | -1.56 | -0.41 | -1.23 |
| | cassava4.1_002216m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 2 | -0.50 | -0.39 | -0.26 | -0.77 | -0.24 | -1.28 | -0.21 | -1.29 | -0.22 | -0.96 |
| | cassava4.1_000076m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | DNA binding;ATP binding;nucleic acid binding;binding;helicases;ATP binding;DNA binding;helicases | 0.05 | 0.16 | 0.18 | 0.07 | -0.06 | -0.57 | 0.33 | -1.08 | 0.13 | -0.29 |
| | cassava4.1_025037m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Duplicated homeodomain-like superfamily protein | -0.30 | -0.19 | 0.06 | -0.33 | -0.18 | -0.93 | -0.03 | -1.16 | -0.26 | -0.68 |
| | cassava4.1_007837m.g | RNA.regulation of transcription.bZIP transcription factor family | bZIP transcription factor family protein | -0.24 | -1.30 | -0.23 | -0.31 | -0.33 | -0.97 | -0.08 | -2.39 | -0.36 | -1.23 |
| | cassava4.1_000316m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein | -0.18 | -0.72 | 0.29 | 0.12 | 0.19 | -0.41 | 0.24 | -1.41 | 0.11 | -0.41 |
| | cassava4.1_007149m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | -0.41 | -0.70 | -0.16 | -0.48 | -0.18 | -0.70 | -0.03 | -1.42 | -0.08 | -0.89 |
| | cassava4.1_023603m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | BEL1-like homeodomain 2 | -0.16 | -0.63 | 0.03 | -0.32 | -0.01 | -0.49 | 0.12 | -1.29 | -0.08 | -0.66 |
| | cassava4.1_000754m.g | RNA.regulation of transcription.C3H zinc finger family | zinc knuckle (CCHC-type) family protein | -0.48 | -0.88 | -0.30 | -0.54 | -0.22 | -1.17 | 0.33 | -1.70 | -0.15 | -1.33 |
| | cassava4.1_033475m.g | RNA.regulation of transcription.MADS box transcription factor family | unclear | -0.53 | -1.41 | -0.32 | -1.01 | -0.37 | -2.18 | 0.03 | -3.26 | -0.12 | -2.34 |
| | cassava4.1_001790m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | BEL1-like homeodomain 2 | 0.05 | -0.14 | -0.06 | -0.10 | 0.01 | -0.25 | 0.20 | -1.11 | -0.13 | -0.34 |
| | cassava4.1_001576m.g | RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family | high-level expression of sugar-inducible gene 2 | 0.11 | 0.06 | 0.19 | 0.40 | 0.09 | -0.27 | 0.37 | -1.16 | 0.13 | -0.57 |
| | cassava4.1_000609m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 19 | -0.99 | -1.31 | -0.39 | -0.59 | -0.35 | -0.97 | -0.20 | -3.01 | -0.27 | -1.50 |
| | cassava4.1_003781m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Duplicated homeodomain-like superfamily protein | -0.48 | -0.32 | -0.04 | -0.10 | -0.04 | -0.62 | 0.06 | -1.55 | 0.03 | -0.85 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_011813m.g | RNA.regulation of transcription.bZIP transcription factor family | bZIP transcription factor family protein | -0.35 | -0.46 | -0.41 | -1.96 | 0.24 | -0.99 | -0.14 | -1.83 | -0.46 | -1.23 |
| | cassava4.1_011886m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 5 | -0.20 | -0.81 | -0.41 | -1.29 | -0.04 | -1.50 | -0.58 | -1.84 | -0.62 | -1.35 |
| | cassava4.1_013480m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox 1 | -0.15 | -2.57 | -0.64 | -2.87 | 0.18 | -2.42 | -0.89 | -3.14 | -0.12 | -1.41 |
| | cassava4.1_013746m.g | RNA.regulation of transcription.MYB-related transcription factor family | myb-like transcription factor family protein | -0.34 | -2.43 | -1.31 | -3.13 | -0.08 | -3.04 | -1.15 | -3.96 | -0.20 | -2.33 |
| | cassava4.1_024212m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14 | 0.22 | -0.24 | -0.86 | -1.60 | -0.23 | -0.80 | -0.57 | -1.07 | -0.59 | -1.21 |
| | cassava4.1_017926m.g | RNA.regulation of transcription.Nucleosome/chromatin assembly factor group | high mobility group B3 | 0.06 | -0.77 | -0.54 | -1.18 | -0.02 | -1.04 | -0.45 | -0.55 | -0.73 | -1.90 |
| | cassava4.1_013973m.g | RNA.regulation of transcription.MYB-related transcription factor family | myb-like transcription factor family protein | 0.22 | -0.33 | -0.13 | -0.72 | -0.02 | -0.37 | -0.31 | -0.34 | -0.55 | -1.28 |
| | cassava4.1_018525m.g | RNA.regulation of transcription.Nucleosome/chromatin assembly factor group | high mobility group B3 | 0.06 | -0.38 | -0.41 | -0.76 | 0.02 | -0.46 | -0.33 | -0.24 | -0.82 | -1.68 |
| | cassava4.1_008584m.g | RNA.regulation of transcription.General Transcription | Transcription factor IIA, alpha/beta subunit | -0.07 | -0.43 | -0.40 | -0.65 | -0.01 | -0.67 | -0.07 | -0.53 | -0.28 | -1.11 |
| | cassava4.1_012505m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 31 | -0.12 | -1.01 | -0.13 | -1.27 | 0.23 | -1.24 | -0.33 | -0.97 | -0.58 | -1.86 |
| | cassava4.1_014431m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid inducible 11 | 0.11 | -0.47 | -0.70 | -1.74 | -0.29 | -1.21 | -0.21 | -1.20 | -0.79 | -1.89 |
| | cassava4.1_033803m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | cooperatively regulated by ethylene and jasmonate 1 | -0.08 | -0.13 | -0.26 | -0.92 | 0.08 | -0.95 | 0.17 | -0.77 | -0.31 | -1.40 |
| | cassava4.1_012485m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20 | -0.11 | -0.34 | -0.24 | -1.12 | -0.20 | -0.97 | -0.19 | -0.98 | -0.28 | -1.27 |
| | cassava4.1_015642m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.92 | -2.17 | -1.58 | -1.87 | -0.16 | -1.61 | -1.12 | -1.17 | 0.31 | -1.34 |
| | cassava4.1_006867m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.51 | -1.06 | -0.48 | -0.91 | 0.19 | -0.66 | -0.62 | -0.51 | -0.15 | -0.73 |
| | cassava4.1_008593m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc | chloroplast import apparatus 2 | -0.62 | -0.88 | -0.77 | -1.64 | -0.08 | -1.37 | -0.79 | -0.60 | 0.01 | -0.77 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | finger family | | | | | | | | | | | |
| | cassava4.1_013177m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox protein 2 | -0.61 | -1.53 | -0.29 | -1.93 | 0.04 | -1.28 | -0.54 | -0.64 | 0.11 | -1.03 |
| | cassava4.1_001995m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 4 | -0.21 | -0.65 | 0.17 | -0.97 | 0.21 | -1.49 | -0.50 | -1.29 | 0.44 | -0.45 |
| | cassava4.1_012160m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | -0.68 | -1.44 | -0.39 | -1.50 | 0.06 | -1.47 | -0.83 | -1.35 | 0.03 | -0.48 |
| | cassava4.1_016852m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger protein 7 | -0.74 | -1.87 | -0.54 | -2.09 | 0.05 | -2.80 | -0.81 | -1.08 | -0.38 | -1.61 |
| | cassava4.1_032952m.g | RNA.regulation of transcription.bZIP transcription factor family | TraB family protein | -0.83 | -1.60 | -0.23 | -1.02 | 0.02 | -2.72 | -0.25 | -1.86 | -0.15 | -1.63 |
| | cassava4.1_002286m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | Nucleic acid-binding, OB-fold-like protein | -0.61 | -0.97 | -0.12 | -1.12 | -0.05 | -1.71 | -0.33 | -1.08 | -0.22 | -0.76 |
| | cassava4.1_014928m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid inducible 14 | -0.29 | -1.29 | -0.49 | -1.09 | -0.30 | -1.28 | -1.02 | -1.13 | -0.68 | -1.48 |
| | cassava4.1_028782m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -0.27 | -2.16 | -0.92 | -1.97 | -0.01 | -0.60 | -1.01 | -1.84 | -0.64 | -2.53 |
| | cassava4.1_014217m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | Protein of unknown function (DUF688) | -0.01 | -1.88 | -0.02 | -1.42 | 0.20 | -0.63 | -0.67 | -1.18 | -0.42 | -1.34 |
| | cassava4.1_003741m.g | RNA.regulation of transcription.GRAS transcription factor family | RGA-like 2 | -0.47 | -1.75 | -0.53 | -1.19 | -0.12 | -0.90 | -0.73 | -1.27 | -0.62 | -0.96 |
| | cassava4.1_028288m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger protein with CCT domain | -1.81 | -5.01 | 0.08 | -2.08 | -0.21 | -3.08 | 0.00 | -2.48 | -0.42 | -2.39 |
| | cassava4.1_025708m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | phytochrome interacting factor 3-like 5 | -0.57 | -1.96 | -0.32 | -0.63 | -0.10 | -1.44 | 0.02 | -1.25 | -0.41 | -1.26 |
| | cassava4.1_010785m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-type zinc finger family protein | -1.38 | -3.58 | -0.94 | -1.36 | -0.67 | -2.99 | -1.19 | -2.19 | -1.19 | -2.26 |
| | cassava4.1_028748m.g | RNA.regulation of transcription.HSF,Heat-shock transcription factor family | heat shock transcription factor A3 | -0.38 | -1.50 | 0.03 | -0.45 | 0.10 | -0.99 | -0.19 | -0.71 | -0.30 | -1.35 |
| | cassava4.1_015068m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | salt tolerance homologue | -0.77 | -2.59 | -0.32 | -1.45 | 0.09 | -1.01 | 0.08 | -1.11 | -0.62 | -1.65 |
| | cassava4.1_010378m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | CONSTANS-like 5 | -0.21 | -1.53 | -0.24 | -1.26 | -0.10 | -0.91 | 0.02 | -0.95 | -0.38 | -1.00 |
| | cassava4.1_011192m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | CONSTANS-like 4 | 0.00 | -0.88 | -0.25 | -0.84 | 0.11 | -0.34 | -0.01 | -0.51 | -0.39 | -0.99 |
| | cassava4.1_013873m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger family protein | -0.52 | -2.47 | -0.20 | -1.85 | 0.02 | -1.30 | -0.45 | -1.45 | -0.94 | -2.55 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_011725m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | CONSTANS-like 4 | 0.10 | -1.16 | -0.20 | -1.16 | 0.10 | -0.78 | 0.07 | -0.98 | -0.49 | -1.40 |
| | cassava4.1_010032m.g | RNA.regulation of transcription.C3H zinc finger family | CCCH-type zinc finger family protein | -0.37 | -2.42 | -0.01 | -2.45 | 0.04 | -1.45 | 0.21 | -1.88 | -0.61 | -2.66 |
| | cassava4.1_014900m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid 7 | -0.91 | -2.87 | -1.64 | -2.60 | -0.59 | -2.93 | -0.96 | -2.40 | -1.16 | -2.32 |
| | cassava4.1_034451m.g | RNA.regulation of transcription.C2H2 zinc finger family | zinc finger (C2H2 type) family protein | -0.93 | -2.03 | -1.16 | -2.23 | -0.25 | -1.95 | -1.12 | -1.65 | -1.03 | -2.04 |
| | cassava4.1_013130m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | ZIM-like 1 | -0.45 | -1.74 | -0.50 | -1.19 | 0.00 | -1.20 | 0.11 | -1.70 | -0.42 | -1.75 |
| | cassava4.1_016451m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | Plant-specific transcription factor YABBY family protein | -0.63 | -1.73 | -0.57 | -1.48 | -0.09 | -1.03 | 0.09 | -1.53 | -0.65 | -2.16 |
| | cassava4.1_031586m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-type zinc finger family protein | -0.48 | -2.11 | -1.14 | -1.60 | -0.25 | -1.75 | -0.10 | -1.51 | -0.88 | -2.12 |
| | cassava4.1_015577m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid inducible 14 | -0.85 | -2.00 | -0.53 | -1.85 | -0.15 | -2.10 | -0.18 | -1.97 | -0.77 | -2.63 |
| | cassava4.1_027196m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 60 | -0.92 | -2.02 | -0.75 | -1.44 | -0.13 | -1.80 | -0.43 | -1.31 | -0.53 | -2.21 |
| | cassava4.1_013503m.g | RNA.regulation of transcription.MYB-related transcription factor family | Duplicated homeodomain-like superfamily protein | -0.19 | -0.71 | -0.33 | -0.85 | -0.06 | -1.06 | 0.08 | -0.60 | -0.29 | -0.97 |
| | cassava4.1_013487m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.94 | -1.24 | -0.23 | -1.14 | -0.04 | -0.88 | -0.33 | -0.95 | -0.10 | -0.95 |
| | cassava4.1_007846m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 61 | -1.82 | -2.61 | -0.91 | -3.13 | -0.08 | -2.22 | -1.43 | -2.74 | -0.71 | -2.38 |
| | cassava4.1_005852m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -0.92 | -1.59 | -0.55 | -1.11 | 0.10 | -1.60 | -0.22 | -2.35 | 0.06 | -1.20 |
| | cassava4.1_010095m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid inducible 9 | -1.00 | -1.45 | -0.74 | -1.34 | -0.21 | -1.75 | -0.47 | -1.66 | -0.36 | -0.98 |
| | cassava4.1_034383m.g | RNA.regulation of transcription.Bromodomain proteins | DNA-binding bromodomain-containing protein | -0.76 | -2.23 | -0.22 | -2.33 | -0.72 | -3.36 | 0.56 | -3.12 | -0.25 | -2.62 |
| | cassava4.1_028769m.g | RNA.regulation of transcription.FHA transcription factor | Forkhead-associated (FHA) domain-containing protein | -0.47 | -1.16 | -0.33 | -1.36 | -0.21 | -1.33 | 0.00 | -1.59 | -0.22 | -0.95 |
| | cassava4.1_002408m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 9 | -0.38 | -1.17 | -0.36 | -1.14 | -0.19 | -0.91 | -0.01 | -1.53 | 0.17 | -0.80 |
| | cassava4.1_001928m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox-7 | -0.39 | -1.21 | -0.18 | -1.13 | -0.20 | -0.99 | -0.05 | -1.33 | 0.01 | -0.77 |
| | cassava4.1_027046m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -1.47 | -4.61 | -0.78 | -2.63 | -0.04 | -3.48 | -0.24 | -4.02 | -0.10 | -2.56 |

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| | cassava4.1_025106m.g | RNA.regulation of transcription.C3H zinc finger family | zinc knuckle (CCHC-type) family protein | -0.91 | -3.15 | -0.35 | -2.06 | -0.16 | -2.83 | -0.59 | -2.43 | -0.40 | -1.82 |
| | cassava4.1_028677m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor family protein | -0.92 | -4.06 | -0.68 | -2.72 | -0.14 | -3.84 | 0.17 | -3.18 | -0.26 | -2.63 |
| | cassava4.1_025707m.g | RNA.regulation of transcription.MADS box transcription factor family | AGAMOUS-like 42 | -1.20 | -3.68 | -0.26 | -2.54 | -0.35 | -3.68 | -0.01 | -2.70 | -0.33 | -2.92 |
| | cassava4.1_031585m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | cytokinin-responsive gata factor 1 | -1.15 | -5.84 | -0.60 | -4.98 | -0.05 | -5.30 | -0.80 | -4.06 | -0.70 | -4.53 |
| | cassava4.1_007384m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | GBF's pro-rich region-interacting factor 1 | -0.26 | -2.08 | -0.20 | -1.61 | 0.03 | -1.65 | 0.03 | -1.60 | -0.30 | -1.27 |
| | cassava4.1_020375m.g | RNA.regulation of transcription.MYB-related transcription factor family | RAD-like 1 | -1.79 | -6.20 | -1.81 | -5.94 | -0.28 | -6.22 | -0.16 | -5.13 | -0.27 | -4.93 |
| | cassava4.1_000118m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox-1 | -0.72 | -2.63 | -0.45 | -2.33 | -0.11 | -2.89 | -0.33 | -2.62 | -0.63 | -2.43 |
| | cassava4.1_007418m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.89 | -2.52 | -0.66 | -2.38 | -0.10 | -2.56 | -0.15 | -3.00 | -0.46 | -2.65 |
| | cassava4.1_022856m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb-like HTH transcriptional regulator family protein | -1.15 | -5.04 | 0.01 | -3.57 | 0.06 | -4.15 | 0.11 | -4.96 | -0.52 | -4.66 |
| | cassava4.1_012587m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | cytokinin-responsive gata factor 1 | -0.59 | -2.05 | -0.26 | -1.70 | 0.02 | -1.43 | -0.37 | -1.74 | -0.40 | -1.55 |
| | cassava4.1_012217m.g | RNA.regulation of transcription.MYB-related transcription factor family | Homeodomain-like superfamily protein | -0.64 | -2.31 | -0.32 | -2.14 | -0.03 | -1.85 | -0.18 | -2.51 | -0.43 | -1.91 |
| | cassava4.1_001979m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 4 | -0.98 | -1.81 | -0.77 | -1.86 | -0.20 | -1.37 | -0.91 | -1.85 | -0.79 | -1.87 |
| | cassava4.1_012613m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -1.02 | -3.46 | -0.75 | -3.24 | 0.31 | -1.78 | -0.92 | -3.73 | -1.12 | -3.56 |
| | cassava4.1_017143m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | plant-specific transcription factor YABBY family protein | -0.99 | -1.71 | -0.67 | -1.18 | -0.06 | -1.08 | -0.56 | -1.73 | -0.60 | -1.41 |
| | cassava4.1_004019m.g | RNA.regulation of transcription.B3 transcription factor family | AP2/B3-like transcriptional factor family protein | -0.38 | -0.96 | 0.04 | -0.43 | 0.16 | -0.44 | 0.30 | -0.64 | -0.01 | -0.79 |
| | cassava4.1_017177m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | plant-specific transcription factor YABBY family protein | -0.80 | -1.78 | -0.29 | -1.04 | -0.20 | -1.03 | -0.27 | -1.42 | -0.41 | -1.65 |

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| | cassava4.1_010237m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-like zinc finger protein | -1.30 | -3.05 | -0.87 | -1.92 | 0.19 | -1.85 | -0.03 | -2.16 | -0.54 | -2.53 |
| | cassava4.1_011476m.g | RNA.regulation of transcription.MYB-related transcription factor family | Homeodomain-like superfamily protein | -0.59 | -2.06 | -0.32 | -0.89 | -0.11 | -1.24 | -0.18 | -1.77 | -0.35 | -1.65 |
| | cassava4.1_007456m.g | RNA.regulation of transcription.bZIP transcription factor family | bZIP transcription factor family protein | -1.61 | -2.68 | -0.62 | -2.51 | 0.05 | -1.60 | 0.25 | -3.64 | 0.06 | -2.80 |
| | cassava4.1_017602m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger family protein | -0.64 | -2.79 | -0.65 | -1.82 | -0.12 | -1.15 | 0.04 | -2.09 | -0.41 | -1.69 |
| | cassava4.1_031269m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2-type zinc finger family protein | -1.81 | -6.11 | -1.50 | -3.90 | -0.51 | -3.28 | -0.63 | -4.55 | -0.70 | -4.55 |
| | cassava4.1_020357m.g | RNA.regulation of transcription.MYB-related transcription factor family | RAD-like 6 | -1.70 | -3.91 | -1.17 | -2.80 | -0.11 | -2.10 | -0.03 | -2.91 | -0.51 | -2.43 |
| | cassava4.1_027289m.g | RNA.regulation of transcription.NIN-like bZIP-related family | Plant regulator RWP-RK family protein | -0.84 | -2.07 | -0.56 | -1.66 | -0.10 | -1.49 | 0.17 | -2.09 | -0.11 | -1.56 |
| | cassava4.1_030452m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | cycling DOF factor 2 | -1.54 | -3.97 | -1.72 | -2.83 | -0.41 | -4.02 | -1.36 | -5.65 | -0.77 | -4.45 |
| | cassava4.1_006216m.g | RNA.regulation of transcription.MYB-related transcription factor family | Homeodomain-like superfamily protein | -1.05 | -2.42 | -1.03 | -2.27 | -0.51 | -2.89 | -0.23 | -3.55 | -0.46 | -2.82 |
| | cassava4.1_002980m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 16 | -1.15 | -2.31 | -0.70 | -1.62 | 0.20 | -2.20 | -0.46 | -3.21 | -0.74 | -3.09 |
| | cassava4.1_034399m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.24 | -1.87 | -0.12 | -1.67 | 0.03 | -2.02 | -0.20 | -2.56 | -0.57 | -2.72 |
| | cassava4.1_009094m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14 | -0.65 | -2.69 | -0.77 | -2.23 | 0.03 | -2.21 | -0.77 | -3.23 | -0.58 | -3.32 |
| | cassava4.1_014849m.g | RNA.regulation of transcription.Aux/IAA family | indoleacetic acid-induced protein 16 | -0.66 | -1.99 | -0.46 | -1.76 | -0.13 | -1.65 | -0.79 | -2.01 | -0.72 | -3.23 |
| | cassava4.1_007172m.g | RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family | cycling DOF factor 3 | -0.46 | -3.27 | -1.12 | -3.09 | -0.11 | -2.50 | -0.66 | -3.22 | -0.54 | -4.11 |
| | cassava4.1_031883m.g | RNA.regulation of transcription.Nucleosome/chromatin assembly factor group | HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain | -1.58 | -5.82 | -2.26 | -6.28 | -0.86 | -4.21 | -0.87 | -5.83 | -0.98 | -8.71 |
| | cassava4.1_034343m.g | RNA.regulation of transcription.CCAAT box binding factor family, HAP5 | nuclear factor Y, subunit C4 | -0.26 | -1.94 | -0.12 | -2.18 | -0.25 | -1.36 | -0.19 | -3.18 | -0.68 | -3.80 |
| | cassava4.1_033968m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor family protein | -0.28 | -1.23 | -0.29 | -1.09 | -0.13 | -0.86 | -0.25 | -1.57 | -0.56 | -1.68 |
| | cassava4.1_024318m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14 | -0.38 | -1.41 | -0.52 | -1.95 | -0.02 | -1.40 | -0.77 | -2.26 | -0.86 | -2.27 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_014022m.g | RNA.regulation of transcription.bZIP transcription factor family | Basic-leucine zipper (bZIP) transcription factor family protein | -0.43 | -1.36 | 0.05 | -0.54 | -0.08 | -0.15 | -0.36 | -1.20 | -0.54 | -1.14 |
| | cassava4.1_012706m.g | RNA.regulation of transcription.Aux/IAA family | indole-3-acetic acid inducible 11 | -0.38 | -1.58 | -0.23 | -0.83 | -0.27 | -0.57 | -0.12 | -1.23 | -0.75 | -1.39 |
| | cassava4.1_006027m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.39 | -1.15 | -0.22 | -0.85 | -0.11 | -0.30 | -0.13 | -1.01 | -0.45 | -1.06 |
| | cassava4.1_012686m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | Plant-specific transcription factor YABBY family protein | -1.23 | -2.60 | -0.65 | -1.82 | -0.31 | -1.37 | -0.51 | -2.54 | -0.99 | -2.46 |
| | cassava4.1_013899m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.98 | -1.66 | -0.34 | -0.61 | -0.21 | -0.39 | -0.01 | -1.80 | -0.26 | -1.12 |
| | cassava4.1_014204m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 1 | -0.60 | -1.19 | -0.27 | -0.58 | 0.08 | -0.34 | -0.24 | -1.15 | -0.37 | -0.86 |
| | cassava4.1_007232m.g | RNA.regulation of transcription.Chromatin Remodeling Factors | switch subunit 3 | -0.86 | -1.43 | -0.02 | -0.70 | 0.06 | -0.08 | -0.30 | -1.28 | -0.21 | -1.02 |
| | cassava4.1_008380m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.69 | -2.29 | -0.13 | -1.41 | -0.31 | -0.87 | -0.01 | -2.53 | -0.09 | -1.45 |
| | cassava4.1_015296m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -0.31 | -1.26 | 0.24 | -0.64 | 0.03 | -0.26 | 0.06 | -1.63 | -0.16 | -1.16 |
| | cassava4.1_012965m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger family protein | -0.50 | -2.76 | -0.30 | -1.82 | -0.51 | -0.83 | -0.31 | -2.85 | -0.51 | -2.77 |
| | cassava4.1_009861m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.89 | -2.88 | -0.79 | -1.80 | 0.12 | -0.28 | -0.36 | -3.19 | -0.63 | -2.03 |
| | cassava4.1_009139m.g | RNA.regulation of transcription.E2F/DP transcription factor family | DP-E2F-like 1 | -0.63 | -1.37 | -0.35 | -1.03 | -0.01 | -0.54 | -0.40 | -1.66 | -0.35 | -1.06 |
| | cassava4.1_026662m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | GBF's pro-rich region-interacting factor 1 | -0.71 | -2.74 | -0.71 | -1.71 | -0.16 | -0.85 | -0.60 | -2.44 | -0.40 | -1.44 |
| | cassava4.1_015138m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.76 | -2.37 | -0.34 | -0.82 | -0.11 | -0.81 | -0.83 | -1.73 | -0.39 | -1.14 |
| | cassava4.1_007940m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger protein with CCT domain | -1.63 | -5.53 | -0.87 | -2.94 | 0.09 | -2.17 | -0.86 | -3.55 | -0.57 | -2.89 |
| | cassava4.1_010137m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc | CONSTANS-like 5 | -1.03 | -2.99 | -0.76 | -1.75 | -0.13 | -1.49 | -0.68 | -1.98 | -0.48 | -1.75 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | finger family | | | | | | | | | | | |
| | cassava4.1_016105m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | Plant-specific transcription factor YABBY family protein | -1.73 | -4.33 | -0.86 | -2.72 | -0.31 | -1.84 | -0.71 | -2.88 | -0.77 | -2.61 |
| | cassava4.1_016118m.g | RNA.regulation of transcription.C2C2(Zn) YABBY family | Plant-specific transcription factor YABBY family protein | -1.43 | -4.13 | -0.54 | -2.02 | -0.04 | -1.52 | -0.93 | -2.58 | -0.78 | -2.06 |
| | cassava4.1_007858m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | cryptochrome-interacting basic-helix-loop-helix 1 | -1.35 | -3.98 | -0.19 | -1.80 | -0.63 | -1.15 | -0.84 | -2.62 | -0.64 | -2.58 |
| | cassava4.1_007389m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox from Arabidopsis thaliana | -0.83 | -3.35 | 0.36 | -0.35 | 0.29 | -0.57 | 0.12 | -2.08 | -0.16 | -1.88 |
| | cassava4.1_005961m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -1.00 | -2.11 | -0.45 | -1.64 | -0.04 | -1.18 | -1.12 | -2.57 | -1.07 | -1.85 |
| | cassava4.1_016924m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | DREB and EAR motif protein 2 | -0.63 | -1.15 | -0.26 | -0.80 | 0.37 | -0.38 | -0.48 | -1.32 | -0.58 | -1.02 |
| | cassava4.1_006460m.g | RNA.regulation of transcription.SET-domain transcriptional regulator family | Arabinanase/levansucrase/invertase | -1.19 | -2.08 | -0.30 | -0.95 | 0.04 | -1.20 | -1.04 | -2.27 | -0.57 | -1.66 |
| | cassava4.1_016111m.g | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family | B-box type zinc finger family protein | -0.47 | -1.95 | -0.58 | -0.82 | -0.08 | -1.43 | -0.65 | -2.04 | -0.32 | -1.25 |
| | cassava4.1_006618m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 2 | -0.29 | -0.85 | -0.34 | -0.36 | 0.10 | -0.45 | -0.37 | -1.25 | -0.08 | -0.51 |
| | cassava4.1_034131m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | -1.37 | -2.71 | -1.33 | -2.11 | 0.16 | -0.14 | -0.72 | -2.30 | -0.33 | -1.66 |
| | cassava4.1_001764m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | -0.34 | -1.01 | -0.52 | -1.12 | 0.03 | -0.10 | -0.05 | -1.12 | 0.11 | -0.52 |
| | cassava4.1_004978m.g | RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family | Tesmin/TSO1-like CXC domain-containing protein | -0.52 | -1.16 | -0.25 | -0.53 | 0.08 | -0.37 | 0.48 | -0.99 | -0.05 | -0.53 |
| | cassava4.1_015543m.g | RNA.regulation of transcription.MADS box transcription factor family | K-box region and MADS-box transcription factor family protein | -0.55 | -0.87 | -0.48 | -0.59 | -0.23 | -0.35 | -0.03 | -1.05 | -0.14 | -0.52 |
| | cassava4.1_032318m.g | RNA.regulation of transcription.MYB-related transcription factor family | Homeodomain-like superfamily protein | -0.44 | -0.96 | -0.85 | -0.74 | -0.22 | 0.21 | -0.16 | -1.12 | 0.01 | -1.16 |

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| | cassava4.1_011576m.g | RNA.regulation of transcription.CCAAT box binding factor family, HAP2 | nuclear factor Y, subunit A3 | -0.69 | -0.87 | -1.14 | -1.94 | -0.05 | -0.48 | 0.11 | -1.40 | -0.58 | -1.51 |
| | cassava4.1_011567m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox 1 | -0.42 | -1.25 | -0.96 | -2.26 | 0.19 | -0.39 | 0.26 | -1.95 | -0.81 | -2.88 |
| | cassava4.1_032429m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.43 | -0.63 | -0.20 | -1.12 | -0.06 | -0.21 | 0.27 | -1.11 | -0.15 | -1.09 |
| | cassava4.1_024743m.g | RNA.regulation of transcription.TCP transcription factor family | TCP family transcription factor | -0.89 | -3.11 | -1.14 | -3.48 | -0.05 | -0.28 | -0.18 | -3.83 | -0.85 | -3.63 |
| | cassava4.1_006715m.g | RNA.regulation of transcription.GRAS transcription factor family | scarecrow-like 3 | -0.20 | -0.74 | -0.41 | -1.16 | 0.02 | -0.01 | 0.47 | -0.71 | 0.19 | -0.61 |
| | cassava4.1_013408m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | sequence-specific DNA binding transcription factors | -0.03 | -0.69 | -0.47 | -0.94 | 0.11 | -0.21 | 0.22 | -0.43 | -0.16 | -0.64 |
| C4 | cassava4.1_007151m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | 1.10 | 0.22 | 0.63 | 1.01 | -0.13 | 0.49 | -0.05 | -0.45 | 0.16 | 0.09 |
| | cassava4.1_004047m.g | RNA.regulation of transcription.bZIP transcription factor family | Basic-leucine zipper (bZIP) transcription factor family protein | 0.10 | 0.15 | 1.01 | 1.32 | 0.23 | 0.37 | -0.47 | -0.25 | 0.41 | 0.27 |
| | cassava4.1_000920m.g | RNA.regulation of transcription.Argonaute | Argonaute family protein | 0.43 | 0.67 | 0.68 | 1.48 | 0.29 | 0.71 | 0.19 | 0.46 | 0.32 | 0.50 |
| | cassava4.1_000998m.g | RNA.regulation of transcription.JUMONJI family | transferases, transferring glycosyl groups | 0.19 | -0.11 | 0.59 | 1.73 | 0.01 | 0.38 | 0.23 | -0.41 | 0.10 | 0.12 |
| | cassava4.1_001443m.g | RNA.regulation of transcription.JUMONJI family | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | -0.50 | -0.55 | 0.08 | 0.94 | -0.05 | -0.14 | -0.83 | -2.01 | -0.21 | -1.18 |
| | cassava4.1_015610m.g | RNA.regulation of transcription.MYB domain transcription factor family | myb domain protein 4 | 0.00 | 0.91 | -0.08 | 1.48 | 0.23 | 1.17 | -0.42 | -0.64 | 0.32 | -0.30 |
| | cassava4.1_021785m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | ARIA-interacting double AP2 domain protein | 0.26 | 1.35 | 0.00 | 0.78 | -0.08 | 0.20 | 0.08 | -0.47 | 0.23 | -0.14 |
| | cassava4.1_001357m.g | RNA.regulation of transcription.ARF, Auxin Response Factor family | auxin response factor 6 | 0.20 | 1.02 | -0.09 | -0.12 | -0.19 | -0.57 | -0.42 | -0.64 | -0.13 | -0.78 |
| | cassava4.1_032607m.g | RNA.regulation of transcription.bZIP transcription factor family | bZIP transcription factor family protein | 0.33 | 1.23 | -0.16 | -0.02 | 0.25 | -0.78 | -0.60 | -1.45 | -0.23 | -0.88 |
| | cassava4.1_012438m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | 0.87 | 1.83 | 0.12 | 0.06 | 0.08 | 0.36 | -1.88 | -1.92 | -0.52 | -1.42 |
| | cassava4.1_009136m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 26 | 0.27 | 0.49 | 0.10 | 0.11 | -0.17 | -0.18 | -0.18 | -0.95 | -0.27 | -0.53 |
| | cassava4.1_012777m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox 1 | 0.71 | 0.85 | -0.17 | 0.15 | 0.06 | 0.22 | -0.11 | -0.65 | -0.13 | -0.45 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_010485m.g | RNA.regulation of transcription.G2-like transcription factor family, GARP | Homeodomain-like superfamily protein | 0.57 | 1.24 | 0.43 | 0.69 | 0.21 | 1.14 | 0.06 | -0.42 | -0.19 | -0.65 |
| | cassava4.1_015664m.g | RNA.regulation of transcription.SNF7 | SNF7 family protein | 0.74 | 1.04 | 0.43 | 0.97 | 0.52 | 0.65 | 0.13 | 0.46 | -0.04 | 0.01 |
| | cassava4.1_002672m.g | RNA.regulation of transcription.C3H zinc finger family | zinc finger (CCCH-type) family protein | 1.27 | 0.89 | 0.58 | 0.65 | 0.27 | 0.81 | 0.44 | 1.07 | -0.34 | -0.46 |
| | cassava4.1_002724m.g | RNA.regulation of transcription.C3H zinc finger family | zinc finger (CCCH-type) family protein | 0.98 | 0.73 | 0.62 | 0.73 | 0.28 | 0.85 | 0.16 | 0.81 | -0.19 | -0.12 |
| | cassava4.1_016728m.g | RNA.regulation of transcription.Aux/IAA family | indoleacetic acid-induced protein 16 | 0.70 | 0.33 | 0.73 | 1.00 | 0.43 | 1.41 | 0.27 | 0.44 | -0.43 | -0.37 |
| | cassava4.1_012634m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | homeobox protein 6 | 1.26 | 1.10 | 0.64 | 1.20 | 0.25 | 2.19 | 0.78 | 1.53 | -0.19 | 0.51 |
| | cassava4.1_013436m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA-type zinc finger protein with TIFY domain | -0.14 | -0.60 | -0.23 | -0.26 | 0.06 | 0.39 | -0.73 | -0.79 | -0.50 | -1.51 |
| | cassava4.1_032088m.g | RNA.regulation of transcription.TCP transcription factor family | TCP family transcription factor | 0.06 | -0.32 | -0.45 | -0.11 | -0.04 | 1.66 | 0.12 | -0.70 | -0.58 | -1.39 |
| | cassava4.1_027174m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -1.54 | -1.72 | -0.27 | -0.27 | -1.59 | -0.82 | -1.38 | -2.53 | -0.13 | -0.39 |
| | cassava4.1_009849m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.55 | -1.03 | -0.34 | -0.16 | -0.09 | -0.20 | -0.10 | -1.36 | 0.13 | 0.12 |
| | cassava4.1_025309m.g | RNA.regulation of transcription.MADS box transcription factor family | AGAMOUS-like 30 | -1.49 | -1.66 | -0.52 | -0.30 | -0.33 | -1.25 | -0.74 | -2.71 | -0.45 | -0.90 |
| | cassava4.1_009158m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.87 | -0.74 | -0.11 | -0.16 | -0.17 | -0.14 | -0.93 | -2.68 | 0.33 | -0.22 |
| | cassava4.1_002081m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | GT-2-like 1 | -0.12 | -0.10 | -0.06 | 0.25 | -0.03 | -0.11 | -0.11 | -1.47 | 0.21 | 0.07 |
| | cassava4.1_010157m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | AP2/B3 transcription factor family protein | 0.79 | -1.70 | 1.67 | 1.62 | 0.38 | 1.59 | -0.26 | 0.59 | 1.53 | 1.00 |
| | cassava4.1_004685m.g | RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | -0.64 | -1.64 | 1.11 | 1.41 | 0.26 | 0.59 | -0.47 | -0.65 | 0.39 | 0.47 |
| | cassava4.1_002257m.g | RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family | TESMIN/TSO1-like CXC 2 | -2.50 | -3.77 | 0.01 | -0.72 | -0.38 | -1.39 | -1.16 | -2.58 | -0.27 | -0.56 |
| | cassava4.1_015402m.g | RNA.regulation of transcription.AP2/EREBP, | Integrase-type DNA-binding | 0.84 | -2.58 | 2.35 | 2.59 | 0.38 | 0.89 | -1.13 | -0.25 | 2.08 | -1.29 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | APETALA2/Ethylene-responsive element binding protein family | superfamily protein | | | | | | | | | | |
| | cassava4.1_003107m.g | RNA.regulation of transcription.C3H zinc finger family | zinc finger (CCCH-type) family protein | 0.22 | -1.28 | 1.84 | 0.87 | 0.69 | -0.08 | -0.21 | 0.11 | 0.84 | -0.83 |
| | cassava4.1_007562m.g | RNA.regulation of transcription.PHOR1 | ARM repeat superfamily protein | -0.04 | -1.34 | 2.03 | 1.52 | 0.87 | 0.27 | 0.28 | -0.21 | 2.07 | -1.14 |
| | cassava4.1_002125m.g | RNA.regulation of transcription.GRAS transcription factor family | SCARECROW-like 14 | 0.06 | -0.74 | 1.91 | 1.54 | 0.61 | 0.66 | -0.42 | -1.34 | 0.53 | -2.13 |
| | cassava4.1_034207m.g | RNA.regulation of transcription.PHOR1 | CYS, MET, PRO, and GLY protein 2 | -0.51 | -1.40 | 0.79 | 0.45 | 0.21 | 0.01 | -0.97 | -1.06 | -0.57 | -1.56 |
| | cassava4.1_005028m.g | RNA.regulation of transcription.GRAS transcription factor family | SCARECROW-like 13 | -0.05 | -0.99 | 0.49 | 0.02 | 0.26 | -0.29 | 0.06 | -0.56 | -0.22 | -0.63 |
| | cassava4.1_011430m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | GATA transcription factor 5 | -0.12 | -1.46 | 1.43 | 0.30 | 0.38 | -0.60 | -0.33 | -1.35 | -0.18 | -1.81 |
| | cassava4.1_002197m.g | RNA.regulation of transcription.GRAS transcription factor family | SCARECROW-like 14 | -0.09 | -0.81 | 0.64 | 0.29 | 0.19 | -0.19 | -0.24 | -0.59 | -0.03 | -1.19 |
| | cassava4.1_003039m.g | RNA.regulation of transcription.C3H zinc finger family | zinc finger (CCCH-type) family protein | -0.33 | -2.24 | 1.50 | 0.21 | 0.54 | -0.30 | -0.59 | -1.83 | 0.27 | -2.04 |
| | cassava4.1_005031m.g | RNA.regulation of transcription.GRAS transcription factor family | SCARECROW-like 13 | -0.21 | -1.30 | 0.73 | 0.06 | 0.41 | -0.19 | -0.06 | -1.12 | -0.14 | -1.22 |
| | cassava4.1_023451m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | Alcohol dehydrogenase transcription factor Myb/SANT-like family protein | -0.27 | -1.17 | 0.58 | -0.31 | 0.30 | -0.04 | -0.73 | -0.90 | -0.14 | -0.70 |
| | cassava4.1_028155m.g | RNA.regulation of transcription.GRAS transcription factor family | GRAS family transcription factor | -0.04 | -1.03 | -0.26 | -0.69 | -0.16 | -0.43 | -2.04 | -1.32 | -1.00 | -0.82 |
| | cassava4.1_022726m.g | RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family | Integrase-type DNA-binding superfamily protein | -0.31 | -0.50 | -0.62 | -0.66 | 0.58 | -0.08 | -1.30 | -1.45 | 0.01 | -0.42 |
| | cassava4.1_015251m.g | RNA.regulation of transcription.C2H2 zinc finger family | C2H2 and C2HC zinc fingers superfamily protein | -0.73 | -0.92 | -0.62 | -1.35 | -0.09 | -0.61 | -1.16 | -1.80 | -0.42 | -0.57 |
| | cassava4.1_025356m.g | RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family | Unknow | -0.72 | -1.38 | -0.62 | -0.78 | 0.18 | 0.97 | -1.88 | -2.88 | 0.21 | -0.65 |
| | cassava4.1_013285m.g | RNA.regulation of transcription.HB,Homeobox transcription factor family | Homeobox-leucine zipper protein family | -0.59 | -1.07 | -0.61 | -1.19 | -0.28 | -0.27 | -1.37 | -1.26 | -0.39 | -0.74 |
| | cassava4.1_027347m.g | RNA.regulation of transcription.TCP transcription factor family | TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14 | -1.69 | -1.82 | -0.69 | -1.10 | 0.12 | -0.47 | -1.71 | -1.81 | -1.13 | -1.62 |
| | cassava4.1_014770m.g | RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family | LOB domain-containing protein 37 | -1.12 | -1.94 | -0.62 | 0.33 | -0.19 | 1.33 | -0.96 | -2.03 | -0.72 | -0.60 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cassava4.1_011546m.g | RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family | sequence-specific DNA binding transcription factors | -0.12 | -0.40 | -0.12 | 0.36 | 0.18 | 0.71 | -0.48 | -1.06 | -0.46 | -0.05 |
| Signalling.light | cassava4.1_000531m.g | signalling.light | phytochrome B | 0.57 | 1.36 | 0.70 | 2.04 | 0.12 | 2.45 | -0.42 | 0.57 | 0.03 | 1.47 |
| | cassava4.1_000570m.g | signalling.light | phytochrome C | -0.16 | -0.13 | -0.25 | -0.36 | -0.03 | -0.32 | -0.01 | -0.90 | 0.02 | -0.34 |
| | cassava4.1_007276m.g | signalling.light | photolyase/blue-light receptor 2 | -0.02 | 0.66 | 0.91 | 2.56 | 0.06 | 3.38 | -0.62 | 1.67 | -0.02 | 2.32 |
| | cassava4.1_007222m.g | signalling.light | photolyase/blue-light receptor 2 | -0.58 | -1.23 | -0.37 | -0.17 | -0.22 | 0.62 | -0.36 | -0.48 | -0.24 | -0.15 |
| | cassava4.1_030861m.g | signalling.light | phytochrome kinase substrate 1 | -0.69 | -1.03 | -0.92 | -1.87 | 0.10 | -1.69 | -0.68 | -2.01 | -0.69 | -3.10 |
| | cassava4.1_003609m.g | signalling.light | Phototropic-responsive NPH3 family protein | -1.20 | -1.48 | -0.56 | -0.39 | 0.01 | -0.49 | -0.28 | -2.47 | 0.20 | -0.79 |
| | cassava4.1_003684m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.75 | -2.01 | -0.68 | -1.09 | 0.00 | -0.24 | -0.37 | -1.34 | -0.15 | -1.00 |
| | cassava4.1_032028m.g | signalling.light | Phototropic-responsive NPH3 family protein | -1.81 | -4.05 | -1.07 | -3.01 | -0.57 | -3.08 | -0.73 | -5.29 | -1.08 | -4.15 |
| | cassava4.1_004505m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.33 | -0.46 | -0.38 | -0.23 | -0.18 | -0.87 | 0.01 | -1.57 | -0.22 | -1.18 |
| | cassava4.1_016715m.g | signalling.light | Chlorophyll A-B binding family protein | -0.66 | -3.07 | 0.12 | -1.35 | -0.09 | -0.59 | 1.96 | 2.01 | 0.37 | 0.85 |
| | cassava4.1_003032m.g | signalling.light | cryptochrome 1 | -0.47 | -1.14 | -0.44 | -0.88 | -0.09 | -0.78 | -0.07 | -1.03 | -0.42 | -1.40 |
| | cassava4.1_002935m.g | signalling.light | cryptochrome 1 | -0.40 | -1.10 | -0.38 | -1.07 | -0.07 | -0.81 | -0.06 | -1.45 | -0.42 | -1.49 |
| | cassava4.1_023566m.g | signalling.light | PAS/LOV protein B | 0.16 | -0.26 | 0.25 | 0.01 | -0.18 | -0.47 | -0.44 | -1.18 | -0.29 | -0.93 |
| | cassava4.1_002824m.g | signalling.light | FAR1-related sequence 10 | -0.48 | -0.60 | -0.37 | -0.36 | 0.02 | -0.84 | -0.23 | -1.31 | -0.07 | -0.84 |
| | cassava4.1_027812m.g | signalling.light | Phototropic-responsive NPH3 family protein | -1.75 | -3.86 | -1.69 | -1.16 | -0.06 | -4.04 | -1.29 | -3.04 | -0.85 | -3.13 |
| | cassava4.1_008267m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.83 | -1.62 | -0.01 | -0.48 | 0.08 | -1.36 | -1.25 | 0.68 | -0.24 | 0.93 |
| | cassava4.1_004180m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.91 | 0.30 | -0.91 | -1.22 | -0.10 | -1.90 | -1.08 | -1.76 | -0.10 | -1.14 |
| | cassava4.1_005641m.g | signalling.light | Phototropic-responsive NPH3 family | -0.91 | -1.08 | -0.35 | -0.88 | -0.12 | -0.98 | -0.92 | -1.34 | -0.53 | -1.24 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | protein |  |  |  |  |  |  |  |  |  |  |
|  | cassava4.1_003719m.g | signalling.light | Phototropic-responsive NPH3 family protein | 0.17 | -0.19 | 0.36 | 1.33 | 0.27 | 2.16 | -0.61 | 0.68 | 0.59 | 2.44 |
|  | cassava4.1_025564m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.02 | -1.07 | 0.42 | -0.29 | -0.10 | -0.61 | -1.04 | -0.67 | -0.38 | -0.95 |
|  | cassava4.1_005067m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.22 | -1.03 | 0.32 | 0.41 | 0.41 | 0.82 | -0.38 | 0.84 | 0.08 | 1.19 |
|  | cassava4.1_004452m.g | signalling.light | Phototropic-responsive NPH3 family protein | -0.65 | -1.83 | -0.37 | -1.08 | -0.12 | -1.19 | -0.46 | -1.78 | -0.49 | -1.74 |
|  | cassava4.1_000918m.g | signalling.light | SPA (suppressor of phyA-105) protein family | -1.29 | -3.25 | -0.44 | -2.06 | -0.11 | -2.54 | -0.43 | -3.24 | -0.30 | -2.80 |
|  | cassava4.1_033918m.g | signalling.light | SPA1-related 3 | -0.76 | -2.26 | -0.40 | -1.87 | -0.07 | -2.19 | 0.14 | -2.55 | -0.16 | -1.88 |
|  | cassava4.1_001319m.g | signalling.light | SPA1-related 3 | -0.37 | -0.99 | -0.16 | -0.28 | -0.04 | -0.97 | 0.03 | -1.69 | -0.24 | -1.22 |
|  | cassava4.1_017713m.g | signalling.light | CCR-like | -0.22 | -2.80 | -0.02 | -5.12 | 0.08 | -5.10 | -0.04 | -2.66 | -0.28 | -3.40 |

## Supplemental Table S8. Genes annotated to redox pathway. The extent of differential expression is measured in terms of log2 fold change of treatment vs. control.

| Cassava ID | Mapman Category | Short Description | PG0 | FG0 | PG2 | FG2 | PG4 | FG4 | PG0 | FG0 | PG2 | FG2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | 120 day |  |  |  |  |  | 45 day |  |  |  |
| cassava4.1_024509m.g | redox.ascorbate and glutathione.ascorbate | ascorbate peroxidase 2 | -5.35 | -6.59 | -4.49 | -7.32 | -0.90 | -2.93 | 1.30 | -0.30 | -0.07 | -1.95 |
| cassava4.1_027646m.g | redox.ascorbate and glutathione.ascorbate | ascorbate peroxidase 4 | -1.36 | -2.69 | -0.52 | -3.09 | -0.10 | -4.20 | -0.48 | -2.85 | -0.61 | -2.03 |
| cassava4.1_006367m.g | redox.ascorbate and glutathione.ascorbate | monodehydroascorbate reductase 6 | -1.22 | -1.63 | -0.41 | -0.87 | -0.10 | -0.83 | -0.18 | -1.95 | -0.37 | -1.44 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cassava4.1_022665m.g | redox.ascorbate and glutathione.ascorbate | ascorbate peroxidase 4 | -1.16 | -2.91 | -0.18 | -2.38 | -0.01 | -3.35 | -0.78 | -3.22 | -0.72 | -2.18 |
| cassava4.1_016900m.g | redox.ascorbate and glutathione.ascorbate | thylakoidal ascorbate peroxidase | -1.04 | -2.89 | -0.74 | -2.35 | 0.03 | -2.11 | -0.46 | -2.44 | -0.73 | -2.45 |
| cassava4.1_015741m.g | redox.ascorbate and glutathione.ascorbate | stromal ascorbate peroxidase | -0.88 | -2.68 | -0.45 | -2.35 | -0.10 | -2.17 | -0.49 | -2.77 | -0.86 | -2.66 |
| cassava4.1_005802m.g | redox.ascorbate and glutathione.ascorbate | monodehydroascorbate reductase 4 | -0.54 | -1.66 | -0.33 | -1.38 | 0.07 | -1.15 | -0.15 | -1.69 | -0.41 | -1.80 |
| cassava4.1_013773m.g | redox.ascorbate and glutathione.ascorbate | dehydroascorbate reductase 1 | -0.41 | -1.13 | -0.25 | -1.02 | -0.06 | -0.84 | -0.47 | -1.07 | -0.54 | -1.34 |
| cassava4.1_013184m.g | redox.ascorbate and glutathione.ascorbate | ascorbate peroxidase 3 | -0.33 | -0.68 | -0.24 | -0.52 | 0.01 | -0.74 | -0.21 | -1.13 | -0.47 | -1.18 |
| cassava4.1_016102m.g | redox.ascorbate and glutathione.ascorbate | dehydroascorbate reductase 2 | -0.13 | -0.29 | -0.27 | -0.96 | 0.05 | -0.36 | 0.03 | -0.15 | -0.66 | -1.04 |
| cassava4.1_013461m.g | redox.ascorbate and glutathione.ascorbate | ascorbate peroxidase 1 | 0.95 | 0.72 | 0.59 | 0.96 | 0.18 | 1.28 | -0.06 | 0.69 | 0.00 | 0.84 |
| cassava4.1_014423m.g | redox.ascorbate and glutathione.ascorbate | ascorbate peroxidase 1 | 0.61 | 0.15 | 0.32 | 0.13 | 0.04 | 1.26 | 0.87 | 0.23 | -0.14 | -0.03 |
| cassava4.1_009867m.g | redox.ascorbate and glutathione.ascorbate | stromal ascorbate peroxidase | 1.59 | 1.68 | 0.86 | 1.55 | 0.10 | 1.59 | -0.18 | 1.55 | 0.46 | 1.94 |
| cassava4.1_006694m.g | redox.ascorbate and glutathione.ascorbate | monodehydroascorbate reductase 1 | 0.73 | 1.12 | 0.70 | 1.13 | 0.08 | 0.70 | -0.14 | 1.53 | 0.11 | 0.97 |
| cassava4.1_029735m.g | redox.ascorbate and glutathione.glutathione | glutamate-cysteine ligase | -0.93 | -1.50 | -0.67 | -0.52 | -0.67 | -2.36 | -0.58 | -2.78 | -0.08 | -1.17 |
| cassava4.1_006560m.g | redox.ascorbate and glutathione.glutathione | glutathione synthetase 2 | -0.78 | -0.59 | -0.70 | -0.69 | 0.12 | -0.21 | -0.45 | -2.31 | -0.39 | -1.18 |
| cassava4.1_015084m.g | redox.ascorbate and glutathione.glutathione | glutathione peroxidase 1 | -0.10 | -0.95 | -0.25 | -1.60 | 0.04 | -1.86 | 0.58 | -1.05 | -0.17 | -1.41 |

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| cassava4.1_012839m.g | redox.ascorbate and glutathione.glutathione | glutathione-disulfide reductase | 0.08 | 0.54 | -0.06 | 0.22 | -0.08 | 0.59 | -0.05 | 1.07 | 0.62 | 0.94 |
| cassava4.1_017755m.g | redox.ascorbate and glutathione.glutathione | glutathione peroxidase 6 | 1.14 | 1.53 | 0.50 | 0.49 | 0.22 | 1.14 | 0.55 | 1.50 | -0.12 | 0.43 |
| cassava4.1_030777m.g | redox.dismutases and catalases | catalase 2 | -0.56 | -2.94 | -0.09 | -1.99 | -0.15 | -2.45 | 0.02 | -1.67 | -0.74 | -3.05 |
| cassava4.1_018294m.g | redox.dismutases and catalases | copper/zinc superoxide dismutase 1 | 0.61 | 0.50 | 0.04 | 0.00 | 0.02 | -0.20 | 0.96 | 0.36 | 0.34 | 0.19 |
| cassava4.1_018049m.g | redox.dismutases and catalases | copper/zinc superoxide dismutase 3 | -0.68 | -1.32 | -0.55 | -0.96 | 0.14 | -0.52 | -0.11 | -0.52 | -0.43 | -0.67 |
| cassava4.1_006297m.g | redox.dismutases and catalases | catalase 2 | -0.39 | -2.44 | -0.40 | -2.08 | -0.04 | -1.87 | -0.16 | -1.66 | -0.82 | -2.61 |
| cassava4.1_024232m.g | redox.glutaredoxins | Thioredoxin superfamily protein | -1.19 | -2.99 | 0.03 | -3.20 | -0.97 | -2.34 | -0.15 | -5.26 | -1.16 | -2.78 |
| cassava4.1_008955m.g | redox.glutaredoxins | Glutaredoxin family protein | -0.82 | -1.35 | -0.13 | -0.70 | -0.33 | -0.62 | -0.43 | -1.35 | -0.43 | -0.70 |
| cassava4.1_033785m.g | redox.glutaredoxins | Thioredoxin superfamily protein | -0.69 | -0.30 | -0.37 | 0.27 | -0.54 | -0.59 | 1.40 | -0.86 | -0.59 | 0.06 |
| cassava4.1_014034m.g | redox.glutaredoxins | Glutaredoxin family protein | -0.62 | -0.85 | -0.55 | -0.88 | -0.07 | -0.16 | 0.03 | -0.66 | -0.16 | -0.57 |
| cassava4.1_034311m.g | redox.glutaredoxins | Glutaredoxin family protein | -0.62 | -2.36 | -0.29 | -1.46 | 0.02 | -0.67 | -0.07 | -1.32 | -0.49 | -1.80 |
| cassava4.1_024311m.g | redox.glutaredoxins | Glutaredoxin family protein | -0.51 | -1.64 | -0.51 | -0.74 | 0.07 | -0.44 | -0.48 | -1.33 | 0.01 | 0.00 |
| cassava4.1_018918m.g | redox.glutaredoxins | Thioredoxin superfamily protein | -0.43 | -0.96 | -1.38 | -1.65 | -0.02 | -1.11 | -1.14 | -2.36 | -0.61 | -2.08 |
| cassava4.1_019956m.g | redox.glutaredoxins | Thioredoxin superfamily protein | -0.11 | -1.65 | -0.50 | -1.87 | 0.04 | -1.84 | -0.33 | -1.08 | -0.46 | -1.58 |
| cassava4.1_019954m.g | redox.glutaredoxins | Thioredoxin superfamily protein | 0.59 | 0.35 | -0.26 | -1.05 | 0.00 | -1.60 | -0.38 | -0.84 | -1.02 | -2.56 |
| cassava4.1_002749m.g | redox.glutaredoxins | glutaredoxin-related | 0.01 | 1.09 | 0.23 | 0.99 | 0.13 | 0.58 | -0.23 | -0.01 | -0.53 | -0.64 |
| cassava4.1_018797m.g | redox.glutaredoxins | Glutaredoxin family protein | 0.03 | -0.06 | 0.39 | 0.77 | -0.06 | 1.04 | -0.26 | -0.02 | -0.25 | 0.44 |
| cassava4.1_019777m.g | redox.glutaredoxins | Glutaredoxin family protein | 0.58 | 1.35 | 0.58 | 0.68 | 0.18 | 0.19 | 0.18 | 1.36 | -0.01 | 0.84 |
| cassava4.1_018177m.g | redox.glutaredoxins | Thioredoxin superfamily protein | 1.07 | -0.59 | 1.52 | 1.73 | 0.36 | 0.47 | -0.85 | 0.17 | 0.79 | -0.26 |
| cassava4.1_016021m.g | redox.peroxiredoxin | Thioredoxin superfamily protein | -1.44 | -2.73 | -0.72 | -2.58 | -0.23 | -2.89 | -1.03 | -2.49 | -1.05 | -2.52 |
| cassava4.1_016588m.g | redox.peroxiredoxin | peroxiredoxin IIF | -0.08 | -0.12 | -0.14 | 0.04 | 0.07 | 1.03 | 0.11 | 1.12 | -0.18 | 0.91 |
| cassava4.1_015438m.g | redox.peroxiredoxin | Thioredoxin superfamily protein | -0.98 | -2.91 | -0.38 | -1.40 | -0.04 | -0.69 | -0.74 | -1.94 | -0.98 | -1.98 |
| cassava4.1_013279m.g | redox.thioredoxin | atypical CYS HIS rich thioredoxin 4 | -1.27 | -2.10 | -0.69 | -2.64 | -0.30 | -3.70 | -0.03 | -4.18 | -0.67 | -3.58 |
| cassava4.1_005499m.g | redox.thioredoxin | NADPH-dependent thioredoxin reductase C | -0.98 | -1.69 | -0.24 | -1.13 | -0.10 | -1.05 | -0.61 | -2.13 | -0.45 | -1.51 |
| cassava4.1_027763m.g | redox.thioredoxin | ferredoxin/thioredoxin reductase subunit A (variable subunit) 2 | -0.93 | -2.14 | -1.24 | -3.01 | 0.22 | -1.31 | -0.04 | -2.04 | -0.80 | -2.16 |

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| cassava4.1_017096m.g | redox.thioredoxin | Thioredoxin superfamily protein | -0.92 | -3.73 | -0.64 | -4.13 | -0.01 | -4.36 | -0.11 | -2.53 | -0.98 | -3.80 |
| cassava4.1_015744m.g | redox.thioredoxin | ferredoxin/thioredoxin reductase subunit A (variable subunit) 2 | -0.69 | -1.82 | -0.60 | -1.49 | -0.10 | -1.03 | -0.17 | -1.53 | -0.53 | -1.19 |
| cassava4.1_021142m.g | redox.thioredoxin | ferredoxin thioredoxin reductase catalytic beta chain family protein | -0.67 | -1.89 | -0.18 | -1.98 | 0.10 | -1.70 | -0.36 | -1.49 | -0.93 | -2.37 |
| cassava4.1_018403m.g | redox.thioredoxin | ferredoxin thioredoxin reductase catalytic beta chain family protein | -0.63 | -1.37 | -0.41 | -1.25 | -0.06 | -0.69 | -0.43 | -1.10 | -0.51 | -0.95 |
| cassava4.1_015817m.g | redox.thioredoxin | Thioredoxin superfamily protein | -0.62 | -2.30 | -0.56 | -1.61 | -0.17 | -1.09 | -0.28 | -1.79 | -0.60 | -1.49 |
| cassava4.1_012905m.g | redox.thioredoxin | atypical CYS HIS rich thioredoxin 4 | -0.56 | -1.55 | -0.37 | -2.49 | -0.14 | -2.88 | 0.38 | -2.78 | -0.73 | -3.14 |
| cassava4.1_017711m.g | redox.thioredoxin | Rubredoxin-like superfamily protein | -0.49 | -1.69 | -0.31 | -1.04 | -0.03 | -0.80 | -0.22 | -0.71 | -0.42 | -0.95 |
| cassava4.1_011786m.g | redox.thioredoxin | APR-like 4 | -0.48 | -1.04 | 0.18 | 0.11 | 0.15 | 0.07 | -0.29 | -0.57 | -0.53 | -0.78 |
| cassava4.1_016798m.g | redox.thioredoxin | WCRKC thioredoxin 1 | -0.46 | -1.05 | -0.30 | -2.42 | 0.06 | -2.89 | 0.01 | -1.13 | -0.43 | -1.90 |
| cassava4.1_012801m.g | redox.thioredoxin | chloroplastic drought-induced stress protein of 32 kD | -0.42 | -2.36 | -0.27 | -2.49 | 0.13 | -1.85 | -0.57 | -1.02 | -0.76 | -1.95 |
| cassava4.1_017734m.g | redox.thioredoxin | thioredoxin Y2 | -0.33 | -0.32 | -0.31 | -0.74 | 0.08 | -0.88 | -0.43 | -0.84 | -0.77 | -1.44 |
| cassava4.1_015481m.g | redox.thioredoxin | atypical CYS HIS rich thioredoxin 2 | -0.32 | -0.86 | -0.32 | -0.60 | -0.10 | -0.42 | -0.21 | -0.06 | -0.32 | -0.30 |
| cassava4.1_016825m.g | redox.thioredoxin | thioredoxin F2 | -0.23 | -1.12 | -0.13 | -1.26 | 0.02 | -1.36 | -0.31 | -1.31 | -0.61 | -1.82 |
| cassava4.1_008355m.g | redox.thioredoxin | PDI-like 1-1 | 0.07 | 0.32 | 0.80 | 1.01 | 0.01 | 0.85 | -0.25 | 0.58 | 0.13 | 1.33 |
| cassava4.1_006109m.g | redox.thioredoxin | PDI-like 1-1 | 0.18 | 0.49 | 0.64 | 1.24 | 0.40 | 1.27 | 0.65 | 1.76 | 0.85 | 2.54 |
| cassava4.1_019244m.g | redox.thioredoxin | C-terminal cysteine residue is changed to a serine 1 | 0.23 | -0.34 | -0.69 | -1.66 | -0.19 | -1.74 | 0.15 | 0.21 | -0.56 | -0.85 |
| cassava4.1_007986m.g | redox.thioredoxin | PDI-like 2-2 | 0.30 | 0.54 | 0.62 | 1.01 | -0.10 | 1.06 | -0.51 | 0.39 | 0.31 | 1.58 |
| cassava4.1_016073m.g | redox.thioredoxin | thioredoxin domain-containing protein 9 homolog | 0.39 | 0.97 | 0.45 | 0.83 | -0.07 | -0.09 | -0.60 | 1.29 | 0.06 | 0.83 |
| cassava4.1_015299m.g | redox.thioredoxin | atypical CYS HIS rich thioredoxin 2 | 0.46 | -0.66 | 0.63 | 0.51 | -0.01 | 0.48 | 0.24 | 1.15 | -0.20 | 0.82 |
| cassava4.1_010463m.g | redox.thioredoxin | thioredoxin family protein | 0.51 | 1.22 | 1.43 | 1.78 | -0.11 | 1.57 | -0.30 | 1.09 | 0.75 | 2.78 |
| cassava4.1_018507m.g | redox.thioredoxin | thioredoxin H-type 1 | 0.97 | 1.28 | 0.35 | 0.77 | 0.11 | 0.95 | 0.74 | 1.30 | -0.85 | -0.09 |
| cassava4.1_017131m.g | redox.thioredoxin | thioredoxin M-type 4 | 1.05 | 1.27 | 0.23 | 0.14 | 0.11 | 0.30 | 0.20 | 0.55 | -0.11 | 0.29 |
| cassava4.1_018594m.g | redox.thioredoxin | thioredoxin H-type 7 | 1.05 | 1.83 | 2.31 | 3.90 | -0.03 | 3.12 | -2.60 | 2.04 | 0.43 | 3.38 |
| cassava4.1_016044m.g | misc.glutathione S transferases | glutathione S-transferase F11 | -6.30 | -2.95 | -1.90 | -5.44 | -0.70 | -3.41 | -3.37 | -4.08 | -1.25 | -4.67 |

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| cassava4.1_015784m.g | misc.glutathione S transferases | glutathione S-transferase TAU 25 | -1.37 | -4.34 | -0.92 | -5.09 | 0.01 | -4.70 | -0.37 | -2.78 | -0.82 | -3.50 |
| cassava4.1_014463m.g | misc.glutathione S transferases | glutathione S-transferase F11 | -1.09 | -2.73 | -1.11 | -2.87 | -0.10 | -1.62 | -1.16 | -1.59 | -0.60 | -1.72 |
| cassava4.1_012409m.g | misc.glutathione S transferases | Glutathione S-transferase family protein | -0.69 | -1.22 | -0.09 | -0.88 | -0.16 | -1.09 | -0.72 | -1.60 | -0.86 | -1.42 |
| cassava4.1_015854m.g | misc.glutathione S transferases | glutathione S-transferase TAU 19 | -0.66 | -1.50 | -1.58 | -2.29 | -0.49 | 0.04 | 0.37 | 1.00 | 0.11 | 0.84 |
| cassava4.1_015612m.g | misc.glutathione S transferases | glutathione S-transferase tau 7 | -0.46 | -2.78 | -0.04 | -2.85 | 0.17 | -2.70 | -0.86 | -2.27 | -0.60 | -2.63 |
| cassava4.1_014626m.g | misc.glutathione S transferases | glutathione S-transferase THETA 2 | -0.43 | -0.49 | -0.23 | -0.49 | 0.00 | -0.93 | 0.08 | -0.04 | 0.00 | -0.33 |
| cassava4.1_015872m.g | misc.glutathione S transferases | glutathione S-transferase TAU 19 | -0.23 | -1.57 | -0.14 | -0.95 | -0.07 | -0.40 | -0.29 | -0.66 | -0.72 | -1.37 |
| cassava4.1_015406m.g | misc.glutathione S transferases | Glutathione S-transferase family protein | -0.11 | 0.68 | -0.12 | 0.38 | -0.21 | 2.00 | -0.06 | 1.38 | 0.64 | 2.35 |
| cassava4.1_018515m.g | misc.glutathione S transferases | microsomal glutathione s-transferase, putative | -0.08 | 0.19 | -0.59 | -0.62 | 0.16 | 0.39 | 0.05 | 1.35 | 0.09 | 0.74 |
| cassava4.1_015709m.g | misc.glutathione S transferases | glutathione S-transferase tau 7 | 0.13 | -0.60 | 0.17 | -0.62 | -0.18 | -0.97 | 0.29 | -1.07 | -0.44 | -1.61 |
| cassava4.1_008745m.g | misc.glutathione S transferases | Glutathione S-transferase family protein | 0.81 | 1.09 | 0.07 | 0.20 | -0.05 | 0.14 | -0.17 | 1.21 | 0.40 | 0.79 |
| cassava4.1_015861m.g | misc.glutathione S transferases | glutathione S-transferase TAU 8 | 1.00 | 1.69 | 1.13 | 1.53 | -0.04 | 0.50 | 1.29 | 1.23 | -2.08 | -0.47 |
| cassava4.1_015761m.g | misc.glutathione S transferases | glutathione S-transferase TAU 25 | 1.85 | 0.12 | 0.73 | 0.16 | 0.24 | -0.54 | 0.90 | 0.03 | -1.26 | -2.41 |
| cassava4.1_016175m.g | misc.glutathione S transferases | glutathione S-transferase PHI 9 | 0.83 | 1.16 | 0.70 | 1.10 | 0.16 | 1.81 | 0.84 | 2.28 | 0.49 | 1.97 |
| cassava4.1_007092m.g | misc.glutathione S transferases | glutathione S-transferase tau 7 | 1.32 | 2.15 | 0.30 | 0.09 | -0.68 | 1.25 | 0.02 | 1.89 | 0.96 | 2.51 |