

Table S2. Differentially regulated genes response to stimuli (Fold change > 2.0, *p*-value < 0.01).

| Gene symbol | Fold change | <i>p</i> -value | Product |
|-------------|-------------|-----------------|--|
| 2G05060 | 42.734 | 0.001 | alternative oxidase AlxA, putative |
| 6G04670 | 10.830 | 0.000 | ER-associated proteolytic system protein Der1, putative |
| 4G11310 | 9.925 | 0.004 | fructose-1,6-bisphosphatase Fbp1, putative |
| 3G12270 | 9.780 | 0.000 | glutathione peroxidase Hyr1, putative |
| 2G11070 | 9.087 | 0.000 | tyrosyl-DNA phosphodiesterase, putative |
| 5G05640 | 8.266 | 0.006 | RTA1 domain protein, putative |
| 3G07940 | 7.516 | 0.000 | phosphoinositide-specific phospholipase C, putative |
| 5G02300 | 7.228 | 0.008 | peroxidase, putative |
| 3G10770 | 5.965 | 0.003 | RTA1 domain protein, putative |
| 4G03460 | 5.116 | 0.000 | HLH DNA binding domain protein, putative |
| 6G13340 | 5.045 | 0.004 | mismatch-specific thymine-DNA glycosylase, putative |
| 2G02090 | 4.879 | 0.000 | methylated-DNA-protein-cysteine methyltransferase |
| 4G10210 | 4.514 | 0.001 | phospholipid-transporting ATPase (DRS2), putative |
| 4G11140 | 4.389 | 0.001 | DNA polymerase iota, putative |
| 2G16520 | 4.184 | 0.002 | phospholipase D (PLD), putative |
| 2G15130 | 3.633 | 0.000 | ABC multidrug transporter, putative |
| 1G14330 | 3.627 | 0.003 | ABC transporter, putative |
| 1G01720 | 3.615 | 0.002 | protein kinase and ribonuclease Ire1, putative |
| 6G07700 | 3.582 | 0.005 | chromosomal organization and DNA repair protein Mms21, putative |
| 5G08660 | 2.997 | 0.002 | nuclear protein Qri2/Nse4, putative |
| 5G11430 | 2.892 | 0.002 | quinone oxidoreductase, putative |
| 6G14140 | 2.612 | 0.003 | RTA1 domain protein, putative |
| 3G04070 | 2.579 | 0.001 | bZIP transcription factor HacA |
| 3G14230 | 2.572 | 0.009 | BAR adaptor protein RVS167, putative |
| 2G03070 | 2.239 | 0.002 | conserved hypothetical protein |
| 1G14950 | 2.201 | 0.002 | sugar 1,4-lactone oxidase, putative |
| 7G01970 | 2.171 | 0.002 | RTA1 domain protein, putative |
| 6G03760 | 2.169 | 0.003 | HhH-GPD family base excision DNA repair protein |
| 5G01800 | 2.137 | 0.001 | DNA repair protein Rad14, putative |
| 6G02070 | 2.130 | 0.009 | phospholipid-translocating P-type ATPase domain-containing protein |
| 2G09560 | 2.089 | 0.002 | mitochondrial genome maintenance protein Mgm101, putative |
| 5G08950 | 0.477 | 0.002 | RAS small monomeric GTPase (Rsr1), putative |
| 8G07130 | 0.475 | 0.002 | AhpC/TSA family thioredoxin peroxidase, putative |
| 2G11180 | 0.452 | 0.001 | developmental regulator FlbA |
| 6G11590 | 0.451 | 0.007 | 4-carboxymuconolactone decarboxylase family protein |
| 3G05770 | 0.450 | 0.008 | RAS small monomeric GTPase, putative |
| 5G04333 | 0.442 | 0.004 | RNA polymerase TFIIH complex subunit Ssl1, putative |
| 1G05800 | 0.410 | 0.001 | MAP kinase kinase (Mkk2), putative |
| 5G07860 | 0.392 | 0.002 | phosphatase family protein |
| 6G09930 | 0.379 | 0.002 | bZIP transcription factor AP-1/Yap1, putative |
| 3G12530 | 0.377 | 0.005 | sensor histidine kinase/response regulator, putative |
| 1G13250 | 0.374 | 0.004 | 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase Plc1, putative |
| 2G10730 | 0.372 | 0.003 | DNA polymerase alpha catalytic subunit, putative |

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|---------|-------|-------|---|
| 1G15270 | 0.367 | 0.004 | heat shock protein Hsp98/Hsp104/ClpA, putative |
| 1G14680 | 0.362 | 0.003 | DNA-dependent RNA polymerase II largest subunit, putative |
| 3G06780 | 0.357 | 0.010 | DNA polymerase zeta catalytic subunit, putative |
| 3G05650 | 0.356 | 0.000 | alpha,alpha-trehalose-phosphate synthase subunit Tps2, putative |
| 6G07500 | 0.348 | 0.008 | DNA excision repair protein Rad2 |
| 1G05040 | 0.343 | 0.001 | protein mitochondrial targeting protein (Mas1), putative |
| 4G08300 | 0.337 | 0.000 | DNA mismatch repair protein Msh6, putative |
| 5G13220 | 0.333 | 0.004 | conserved hypothetical protein |
| 6G12570 | 0.328 | 0.000 | EH domain binding protein epsin 2 |
| 5G07880 | 0.309 | 0.003 | a-pheromone receptor PreA |
| 1G05240 | 0.283 | 0.007 | PHD finger and BAH domain protein (Snt2), putative |
| 1G16970 | 0.281 | 0.003 | ADP-ribosylation factor family protein |
| 4G10860 | 0.277 | 0.003 | conserved hypothetical protein |
| 4G06970 | 0.277 | 0.009 | RAD52 DNA repair protein RADC |
| 4G08900 | 0.266 | 0.006 | CDK-activating kinase assembly factor MAT1 |
| 4G09150 | 0.264 | 0.003 | ABC multidrug transporter, putative |
| 1G10940 | 0.248 | 0.000 | MAP kinase kinase kinase SskB, putative |
| 6G12290 | 0.246 | 0.006 | PH domain protein |
| 2G04960 | 0.238 | 0.002 | RecQ family helicase MusN |
| 2G17170 | 0.230 | 0.004 | Na ⁺ /H ⁺ antiporter Nha1 |
| 2G11840 | 0.211 | 0.000 | transcriptional corepressor Cyc8, putative |
| 4G00660 | 0.201 | 0.001 | sensor histidine kinase/response regulator, putative |
| 4G06570 | 0.188 | 0.004 | Ras guanine-nucleotide exchange protein, putative |
| 5G11280 | 0.183 | 0.003 | conserved hypothetical protein |
| 3G01750 | 0.178 | 0.001 | G protein coupled receptor family protein |
| 3G10830 | 0.177 | 0.000 | glutathione S-transferase GstA |
| 7G06890 | 0.170 | 0.000 | Dyp-type peroxidase family protein |
| 8G00710 | 0.156 | 0.003 | secreted antimicrobial peptide, putative |
| 2G00200 | 0.131 | 0.001 | catalase, putative |
| 5G02430 | 0.118 | 0.004 | ATP dependent DNA ligase domain protein |
| 6G12820 | 0.093 | 0.006 | MAP kinase MpkB |
| 7G02200 | 0.076 | 0.009 | meiotic recombination protein (Dmc1), putative |
| 6G10900 | 0.071 | 0.000 | UV-endonuclease UVE-1 |
| 1G05850 | 0.059 | 0.000 | erythromycin esterase, putative |
| 1G01550 | 0.033 | 0.006 | high affinity zinc ion transporter, putative |
| 4G00180 | 0.009 | 0.000 | fatty acid oxygenase, putative |
