

Supplemental Table 1. Differentially expressed *Aspergillus fumigatus* genes after incubation with platelets for the times indicated expressed as Log 2 relative fold change.

| Locus | Protein name | 15 min | 30 min | 1 h | 3 h |
|------------|--|--------------|--------------|--------------|--------------|
| Afu1g01410 | hypothetical protein | -0.99 | -0.95 | -1.18 | -0.67 |
| Afu1g01530 | GrpB domain protein | 0.44 | 1.23 | 0.75 | -0.09 |
| Afu1g01640 | kinesin family protein | | 1.18 | 0.67 | 2.22 |
| Afu1g01680 | branched-chain amino acid aminotransferase | 0.68 | 1.57 | 1.61 | -0.58 |
| Afu1g01940 | hypothetical protein | 0.35 | -0.02 | -0.11 | 1.03 |
| Afu1g01950 | hypothetical protein | -0.37 | -0.22 | 1.17 | -0.48 |
| Afu1g02070 | cytochrome C1/Cyt1 | -0.16 | -1.03 | -1.11 | -0.10 |
| Afu1g02110 | Phe-inhibited DAHP synthase AroG | -0.38 | 0.05 | 0.53 | -1.09 |
| Afu1g02610 | rRNA processing protein | -0.66 | -1.10 | -0.19 | -0.02 |
| Afu1g02630 | rRNA processing protein Pwp1 | -0.72 | -1.07 | 0.10 | -1.12 |
| Afu1g02985 | hypothetical protein | -0.21 | 1.14 | 1.24 | -0.13 |
| Afu1g03500 | topoisomerase I | 0.70 | 1.01 | 1.32 | 0.31 |
| Afu1g03800 | C6 transcription factor | -0.62 | -0.81 | -0.91 | -1.15 |
| Afu1g03950 | cytochrome P450 sterol C-22 desaturase, putative | -0.61 | -1.44 | -1.56 | -0.45 |
| Afu1g04430 | hypothetical protein | 2.18 | 0.26 | -0.35 | 2.66 |
| Afu1g04540 | NADH-cytochrome b5 reductase | 0.69 | -0.88 | -1.13 | 0.48 |
| Afu1g04860 | rhodopsin family protein | 0.43 | 1.05 | 1.72 | 0.26 |
| Afu1g05130 | PH domain protein | -0.16 | 1.13 | 1.29 | -0.76 |
| Afu1g05210 | G-protein complex gamma subunit GpgA | -0.15 | -1.58 | -1.63 | 0.54 |
| Afu1g05310 | nucleolar ATPase Kre33 | -0.90 | -1.20 | -0.30 | -0.43 |
| Afu1g05370 | hypothetical protein | -0.30 | 1.38 | 0.55 | -0.35 |
| Afu1g05460 | hypothetical protein | 0.78 | 0.70 | 1.46 | 0.93 |
| Afu1g05600 | hypothetical protein | 0.96 | 1.26 | 0.49 | 0.69 |
| Afu1g05690 | hypothetical protein | 0.89 | 0.27 | -0.29 | 1.07 |
| Afu1g06100 | glutaredoxin Grx1 | 0.01 | 0.44 | 1.26 | -0.03 |
| Afu1g06280 | short-chain dehydrogenase/reductase family protein, putative | 1.39 | 0.85 | 0.84 | 1.79 |
| Afu1g06350 | pathogenesis associated protein Cap20 | 1.26 | 3.52 | 2.92 | 0.19 |
| Afu1g06600 | 60S ribosome biogenesis protein Rrp14 | -0.88 | -0.83 | 0.11 | -1.03 |
| Afu1g07750 | SWIRM domain protein Fun19 | -0.48 | 1.05 | 1.02 | -0.96 |
| Afu1g08930 | WD repeat protein | 0.28 | 0.59 | 1.03 | 0.50 |
| Afu1g09270 | transmembrane glycoprotein | -1.46 | -0.21 | -0.33 | -0.40 |
| Afu1g09380 | hypothetical protein | 0.37 | 0.28 | 1.15 | 0.20 |
| Afu1g09510 | GPI anchored serine-threonine rich protein | 0.38 | -1.14 | -1.67 | 1.61 |
| Afu1g09530 | hypothetical protein | 0.51 | 1.10 | 0.70 | 0.74 |
| Afu1g09540 | vacuolar transporter chaperon Vtc1 | 0.43 | 0.73 | 0.42 | 1.03 |
| Afu1g09550 | dynein light chain (Tctex1) | 0.30 | -0.47 | -1.12 | 0.81 |
| Afu1g09570 | hypothetical protein | -0.11 | 0.68 | 1.23 | 0.10 |
| Afu1g09590 | hypothetical protein | 1.10 | 0.94 | 2.45 | 0.41 |
| Afu1g09660 | mitochondrial 2-oxodicarboxylate carrier protein, putative | 0.00 | -0.98 | -1.12 | -0.01 |
| Afu1g09670 | HLH transcription factor (GlcD gamma) | -0.01 | 1.41 | 1.49 | -0.77 |
| Afu1g09690 | tRNA ligase | 0.00 | 1.60 | 1.96 | -1.25 |
| Afu1g09700 | ankyrin repeat protein | -0.70 | 1.95 | 2.60 | -1.01 |

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|------------|--|--------------|--------------|--------------|--------------|
| Afu1g09710 | hypothetical protein | 0.43 | 0.78 | 1.58 | -0.42 |
| Afu1g09770 | La domain family | -1.28 | -1.15 | -0.11 | -0.94 |
| Afu1g10190 | pre-mRNA splicing factor (Prp31) | -0.02 | 1.15 | 1.92 | -0.03 |
| Afu1g10200 | cell cycle control protein (Cwf4) | 0.14 | 1.07 | 1.34 | -0.40 |
| Afu1g10340 | integral membrane protein, Mpv17/PMP22 family | 0.83 | 1.46 | 1.69 | 0.73 |
| Afu1g10410 | DNA repair protein RAD51 | 0.40 | 0.46 | 1.12 | 0.51 |
| Afu1g10470 | hypothetical protein | -0.16 | 0.35 | 1.01 | -0.37 |
| Afu1g10560 | GTP binding protein | -0.53 | -0.96 | 0.53 | -1.23 |
| Afu1g10710 | mRNA splicing protein (Prp5) | 0.44 | 1.77 | 1.72 | 0.48 |
| Afu1g10850 | ubiquitin-like modifier SUMO | 0.67 | 0.75 | 1.53 | 1.36 |
| Afu1g10860 | nuclear pore complex protein Nup107 | -1.11 | -0.59 | -0.04 | -0.40 |
| Afu1g10990 | ribosomal RNA processing protein | 0.44 | 0.35 | 1.00 | 0.21 |
| Afu1g11000 | C6 transcription factor | 0.08 | 1.21 | 1.02 | -0.52 |
| Afu1g11030 | xylitol dehydrogenase | -0.40 | -1.21 | -0.28 | -0.66 |
| Afu1g11120 | hypothetical protein | 0.78 | 0.78 | 1.34 | 0.65 |
| Afu1g11200 | hypothetical protein | 0.47 | 0.67 | 1.34 | -0.11 |
| Afu1g11715 | hypothetical protein | -1.22 | -0.73 | -0.41 | -0.45 |
| Afu1g11900 | PQ loop repeat protein | 0.05 | 2.43 | 2.07 | -0.43 |
| Afu1g12030 | hypothetical protein | 0.88 | 1.45 | 1.48 | 0.38 |
| Afu1g12170 | translation elongation factor EF-Tu | -0.44 | -1.37 | -1.36 | 0.16 |
| Afu1g12290 | NADH-ubiquinone oxidoreductase 19 kDa subunit | -0.20 | -1.50 | -1.70 | -0.39 |
| Afu1g12800 | isocitrate dehydrogenase, NAD-dependent | -0.10 | -1.39 | -1.68 | -0.29 |
| Afu1g13040 | possible dual specificity protein phosphatase 3 | -0.30 | 2.04 | 1.81 | -0.70 |
| Afu1g13060 | regulator of nonsense transcripts | 0.18 | 0.13 | 1.03 | -0.68 |
| Afu1g13090 | anthranilate synthase multifunctional protein TrpC, putative | -0.48 | -0.14 | 0.01 | -1.13 |
| Afu1g13200 | hypothetical protein | -1.16 | -0.57 | -0.38 | -0.56 |
| Afu1g13220 | cytochrome P450 pisatin demethylase | 0.90 | -0.19 | 0.01 | 1.84 |
| Afu1g13230 | hypothetical protein | 0.47 | 2.22 | 2.81 | -1.57 |
| Afu1g13300 | GTP cyclohydrolase II | 0.06 | 1.34 | 0.72 | -0.15 |
| Afu1g13310 | bZIP transcription factor | 0.19 | 1.98 | 2.13 | -0.14 |
| Afu1g13370 | aflatoxin B1-aldehyde reductase GliO-like | 0.71 | 1.35 | 0.45 | 0.84 |
| Afu1g13430 | hypothetical protein | -0.73 | -0.37 | -1.40 | -0.28 |
| Afu1g13460 | hypothetical protein | -0.39 | 0.56 | 1.22 | -0.58 |
| Afu1g13490 | spermidine synthase | -0.36 | -1.56 | -1.30 | -0.40 |
| Afu1g13570 | small nuclear ribonucleoprotein complex protein Nhp2, putative | -0.26 | -1.22 | -0.24 | -0.44 |
| Afu1g13870 | alpha-1,2-mannosyltransferase (Alg9) | -1.30 | -0.26 | -0.49 | -0.10 |
| Afu1g13900 | DNA-directed RNA polymerase I subunit (Rpa190), putative | -0.33 | -1.06 | -0.07 | -1.01 |
| Afu1g14060 | C2H2 finger domain protein | 0.32 | 1.66 | 2.20 | 0.04 |
| Afu1g14120 | nuclear segregation protein (Bfr1) | -0.31 | -1.57 | -0.93 | 0.09 |
| Afu1g14550 | Mn superoxide dismutase MnSOD | -0.41 | -0.97 | -1.96 | -0.31 |
| Afu1g14570 | phosphoribosyl-AMP cyclohydrolase | -0.48 | -1.16 | -1.14 | -0.57 |
| Afu1g14750 | C2H2 transcription factor (Sfp1) | 0.31 | 0.42 | 1.02 | 0.40 |
| Afu1g15030 | SDA1 domain protein | -0.58 | -1.07 | -0.01 | -0.85 |
| Afu1g15160 | hypothetical protein | 0.62 | 1.10 | 0.88 | 0.83 |
| Afu1g15220 | hypothetical protein | -0.07 | -0.79 | -1.20 | -0.17 |

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|------------|--|--------------|--------------|--------------|--------------|
| Afu1g15300 | choline transport protein | -0.84 | -0.88 | -0.55 | -1.07 |
| Afu1g15830 | hypothetical protein | 1.12 | 1.22 | 1.52 | 1.25 |
| Afu1g16280 | mitochondrial F1F0-ATP synthase g subunit | 0.16 | -0.99 | -1.40 | 0.32 |
| Afu1g16450 | hypothetical protein | -0.71 | -0.65 | -0.19 | -1.66 |
| Afu1g16550 | dihydrouridine synthase family protein | -0.99 | -0.30 | 0.56 | -1.59 |
| Afu1g16564 | DUF455 domain protein | -0.10 | 0.97 | 2.78 | 0.33 |
| Afu1g16570 | MIND kinetochore complex component Mtw1 | -0.02 | 2.07 | 2.40 | -0.18 |
| Afu1g16750 | mitochondrial cation transporter | -0.15 | -0.27 | -1.02 | -0.50 |
| Afu1g16840 | TCTP family protein | 0.58 | 0.17 | 2.09 | 0.72 |
| Afu1g16940 | DEAD/DEAH box helicase | -0.60 | 0.51 | 1.11 | -0.56 |
| Afu1g17270 | FRE family ferric-chelate reductase | -1.00 | -0.94 | -0.48 | -0.08 |
| Afu1g17400 | peptidase S41 family protein | 0.27 | -0.36 | -1.17 | 1.57 |
| Afu1g17460 | C6 transcription factor | 0.41 | 1.25 | 1.12 | 0.11 |
| Afu1g17670 | salicylate hydroxylase | 0.19 | -1.07 | -0.25 | -0.74 |
| Afu2g00570 | GNAT family acetyltransferase | 0.53 | 0.74 | 1.02 | -2.35 |
| Afu2g00580 | hypothetical protein | 0.56 | 2.97 | 2.97 | 0.23 |
| Afu2g00790 | hypothetical protein | 1.14 | 2.11 | 1.51 | 0.78 |
| Afu2g00930 | xylosidase/glycosyl hydrolase | 0.65 | 1.34 | 0.94 | 0.26 |
| Afu2g00940 | hypothetical protein | 0.35 | 2.92 | 3.15 | -0.13 |
| Afu2g00980 | hypothetical protein | 0.12 | 1.13 | 2.20 | -0.84 |
| Afu2g01110 | hypothetical protein | -0.49 | 1.63 | 1.79 | -0.43 |
| Afu2g01120 | DNA repair protein Ntg1 | -0.65 | 0.93 | 1.56 | -0.62 |
| Afu2g01730 | hypothetical protein | 0.33 | 0.55 | 1.16 | 0.20 |
| Afu2g01920 | glutaminyl-tRNA synthetase | 0.10 | 0.40 | 0.57 | -1.03 |
| Afu2g01980 | nuclear protein (Sgd1) | -0.33 | -1.08 | 0.19 | -0.23 |
| Afu2g02080 | C2H2 finger domain protein | 0.49 | 0.69 | 1.13 | 0.23 |
| Afu2g02290 | 37S ribosomal protein Rsm22 | 0.07 | 0.84 | 1.05 | 0.10 |
| Afu2g02310 | actin cortical patch protein Sur7 | -0.42 | -0.27 | -2.24 | 0.58 |
| Afu2g02490 | hypothetical protein | -0.39 | 0.46 | 0.44 | -1.99 |
| Afu2g02530 | casein kinase I | -1.82 | -0.05 | -0.27 | -1.63 |
| Afu2g02590 | aspartyl-tRNA synthetase Dps1 | -0.28 | 1.05 | 1.13 | -0.53 |
| Afu2g02600 | hypothetical protein | -0.06 | 1.23 | 1.59 | 0.15 |
| Afu2g02890 | tRNA splicing 2' phosphotransferase 1 | 0.80 | 2.39 | 3.18 | -0.31 |
| Afu2g03120 | cell wall glucanase (Utr2) | -0.47 | -1.18 | -0.05 | -0.69 |
| Afu2g03260 | RNA binding protein (Rbm8A) | -0.98 | 0.17 | -0.11 | -1.32 |
| Afu2g04470 | hypothetical protein | 1.30 | 0.75 | 0.62 | 2.31 |
| Afu2g04550 | MFS sugar transporter | 0.52 | 0.70 | 1.05 | 0.24 |
| Afu2g04600 | C6 transcription factor | -1.10 | -0.39 | -0.61 | -0.20 |
| Afu2g04700 | RNA binding effector protein Scp160 | -0.39 | -1.28 | -1.31 | -0.10 |
| Afu2g05115 | hypothetical protein | 0.93 | 1.19 | 0.90 | 0.44 |
| Afu2g05180 | NF-X1 finger and helicase domain protein | 0.49 | 1.68 | 1.50 | -1.35 |
| Afu2g05480 | DNA-directed RNA polymerase I 13.1 kDa polypeptide, putative | -0.66 | -0.01 | -0.38 | -1.29 |
| Afu2g06110 | chromatin remodeling and histone acetyltransferase complexes subunit (Arp4) putative | 0.17 | 0.88 | 1.04 | 0.01 |
| Afu2g06150 | protein disulfide isomerase Pdi1 | 0.30 | 0.53 | 2.49 | 1.36 |

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|------------|---|--------------|--------------|--------------|--------------|
| Afu2g06200 | hypothetical protein | 0.72 | 0.61 | 1.38 | 0.28 |
| Afu2g06290 | nuclear division Rft1 protein | 0.24 | 1.06 | 1.13 | 0.11 |
| Afu2g06310 | ATP-dependent RNA helicase | 0.03 | 0.89 | 2.32 | 1.00 |
| Afu2g06320 | replication protein A 70 kDa DNA-binding subunit | 0.71 | 1.35 | 3.21 | 1.35 |
| Afu2g07340 | COP9 subunit 3 | -0.20 | 0.24 | 1.00 | -0.15 |
| Afu2g07420 | actin-bundling protein Sac6 | 0.21 | 0.54 | 2.28 | 0.88 |
| Afu2g07500 | prolidase pepP | -0.62 | -1.53 | -1.10 | 0.38 |
| Afu2g07700 | hypothetical protein | 0.56 | 0.62 | 1.21 | -0.24 |
| Afu2g08300 | DnaJ domain protein | -1.20 | -0.38 | 0.56 | -1.09 |
| Afu2g08430 | acetyltransferase, CysE/LacA/LpxA/NodL family | -0.15 | -1.07 | -1.18 | -0.06 |
| Afu2g08550 | peptidyl-prolyl cis/trans isomerase | 0.25 | 1.79 | 1.83 | 0.55 |
| Afu2g08590 | 4'-phosphopantetheinyl transferase NpgA/CfwA | -0.55 | -1.18 | -0.35 | -0.17 |
| Afu2g08750 | mitochondrial inner membrane nuclease Nuc1 | 0.25 | 0.74 | 1.17 | -0.21 |
| Afu2g08820 | hypothetical protein | 1.30 | 0.31 | 0.11 | 1.09 |
| Afu2g09030 | secreted dipeptidyl peptidase DppV | 1.13 | -0.43 | -1.06 | 1.88 |
| Afu2g09430 | hypothetical protein | 2.01 | 0.26 | -0.65 | 2.04 |
| Afu2g09480 | hypothetical protein | 0.84 | 0.56 | 1.11 | 0.74 |
| Afu2g09510 | hypothetical protein | -0.67 | 0.20 | 0.34 | -1.53 |
| Afu2g09710 | protein kinase (NpkA) | 0.83 | 0.57 | 1.29 | 0.23 |
| Afu2g09940 | hypothetical protein | -0.34 | -1.10 | -0.17 | -0.04 |
| Afu2g10070 | carbamoyl-phosphate synthase, large subunit | -0.76 | -1.32 | -1.46 | -0.44 |
| Afu2g10310 | DUF408 domain protein | 0.49 | 1.21 | 1.48 | -0.36 |
| Afu2g10330 | hypothetical protein | -0.30 | 2.42 | 2.80 | -0.15 |
| Afu2g10420 | branched-chain amino acid aminotransferase, cytosolic | -0.47 | -0.65 | -1.47 | -1.53 |
| Afu2g10640 | SAGA complex subunit (Ada2) | 0.28 | 0.45 | 1.15 | 0.42 |
| Afu2g10830 | hypothetical protein | 0.36 | 0.40 | 0.82 | 1.00 |
| Afu2g11020 | triosephosphate isomerase | 1.16 | -0.56 | -0.26 | 1.51 |
| Afu2g11040 | U-box domain protein | -1.14 | 0.61 | -0.01 | -1.94 |
| Afu2g11270 | alpha-1,3-glucan synthase Ags2 | -1.04 | -0.47 | -0.40 | -0.50 |
| Afu2g11450 | rRNA processing protein Rrp8 | -0.02 | 0.06 | 1.22 | 0.05 |
| Afu2g11510 | nucleolar GTP-binding protein (Nog1) | -1.23 | -1.29 | 0.14 | -1.41 |
| Afu2g11730 | Protein kinase domain-containing protein | -1.30 | -1.33 | -0.10 | -0.60 |
| Afu2g12470 | acetylmornithine aminotransferase | -0.34 | 1.13 | 1.10 | -0.63 |
| Afu2g12540 | hypothetical protein | 0.86 | 0.70 | 0.54 | 1.14 |
| Afu2g12590 | Lectin C-type domain protein | 0.04 | 1.26 | 1.08 | 0.12 |
| Afu2g12630 | allergenic cerato-platinin Asp F13 | 1.51 | 1.45 | 1.88 | 0.50 |
| Afu2g12680 | hypothetical protein | 1.01 | 0.45 | 1.03 | 0.02 |
| Afu2g12770 | alpha-L-arabinofuranosidase | -0.59 | -1.09 | -0.21 | -0.52 |
| Afu2g13320 | mitochondrial membrane fission protein (Fis1) | 0.70 | 0.42 | 1.07 | 1.21 |
| Afu2g13400 | membrane protein TMS1 | -0.34 | 1.43 | 1.21 | -0.88 |
| Afu2g13420 | hypothetical protein | -0.63 | -0.51 | -1.01 | -0.35 |
| Afu2g13470 | pyrimidine 5'-nucleotidase | 0.98 | 2.00 | 2.47 | 1.11 |
| Afu2g13710 | NADH-ubiquinone oxidoreductase 49 kDa subunit | -0.96 | -0.61 | 0.01 | -1.20 |
| Afu2g13830 | hypothetical protein | -0.28 | 1.57 | 0.32 | 0.20 |
| Afu2g13870 | mitochondrial carrier protein | -0.08 | 1.09 | 1.29 | -0.30 |
| Afu2g13890 | annexin ANXC3.2 | 0.21 | -0.06 | 1.13 | 0.52 |

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|------------|--|--------------|--------------|--------------|--------------|
| Afu2g13930 | hypothetical protein | 0.16 | 1.96 | 2.24 | -0.72 |
| Afu2g13940 | hypothetical protein | -0.23 | 2.01 | 1.93 | 0.00 |
| Afu2g13970 | hypothetical protein | 0.65 | 2.23 | 2.19 | -0.27 |
| Afu2g14090 | extragenic suppressor of the bimD6 mutation | 0.14 | 1.87 | 2.33 | -0.28 |
| Afu2g14370 | hypothetical protein | -1.09 | -0.52 | -0.61 | -0.68 |
| Afu2g14760 | BCS1-like ATPase | -1.07 | 1.67 | 2.22 | -1.93 |
| Afu2g15110 | C2H2 finger domain protein | 0.67 | 3.75 | 4.56 | 0.38 |
| Afu2g15165 | hypothetical protein | 0.20 | 0.32 | 1.10 | 0.68 |
| Afu2g15200 | hypothetical protein | 2.07 | 0.44 | -0.12 | 1.86 |
| Afu2g15220 | DNA repair protein Pso2/Snm1 | -0.44 | 1.06 | 1.53 | -0.81 |
| Afu2g15690 | hypothetical protein | 0.26 | 0.35 | 1.15 | 0.55 |
| Afu2g15700 | hexokinase family protein XprF | 1.19 | 0.62 | 0.67 | 0.72 |
| Afu2g15830 | TRAF-like signal transducer | -0.09 | 1.07 | 1.60 | -0.14 |
| Afu2g15960 | nucleotide binding protein Nbp35 | 0.05 | 0.64 | 1.23 | 0.07 |
| Afu2g16060 | hypothetical protein | -1.21 | -0.92 | -0.26 | -0.15 |
| Afu2g16080 | nuclear cohesin complex subunit (Psc3) | -1.09 | -0.56 | -0.99 | -0.87 |
| Afu2g16360 | DRAP deaminase (Rib2) | 0.21 | 2.43 | 2.44 | -0.27 |
| Afu2g16370 | 60S ribosomal protein L32 | 1.11 | 1.07 | 2.71 | 0.92 |
| Afu2g16390 | hypothetical protein | 1.18 | 1.03 | 0.69 | 1.06 |
| Afu2g16750 | nonsense-mediated mRNA decay protein 3 | -0.58 | 0.56 | 1.63 | -0.87 |
| Afu2g16985 | integral membrane protein | 0.23 | 0.59 | 1.11 | 0.11 |
| Afu2g16990 | hypothetical protein | 1.17 | 2.68 | 2.54 | 1.12 |
| Afu2g17240 | C2H2 finger domain protein | 0.50 | 2.18 | 3.30 | -0.03 |
| Afu2g17390 | hypothetical protein | -0.22 | 0.51 | 1.38 | -0.14 |
| Afu2g17610 | sulfatase domain protein | 0.54 | 1.20 | 1.55 | 1.20 |
| Afu2g17840 | MFS transporter | -0.24 | -1.95 | -2.27 | -0.23 |
| Afu3g00560 | hypothetical protein | -0.24 | 1.11 | 0.54 | 0.05 |
| Afu3g00720 | DUF500 and UBA/TS-N domain protein | 0.28 | -0.10 | 2.18 | 0.38 |
| Afu3g00730 | hypothetical protein | 0.50 | 0.06 | 1.56 | 0.41 |
| Afu3g00810 | cholestenol delta-isomerase | -1.10 | -0.75 | -0.46 | -0.48 |
| Afu3g00850 | hypothetical protein | -0.75 | -1.13 | -0.98 | -0.71 |
| Afu3g01070 | tyrosinase | -0.76 | -1.57 | -2.46 | -0.96 |
| Afu3g01130 | cell wall protein | -0.58 | -1.04 | -0.89 | -1.48 |
| Afu3g01150 | GPI anchored cell wall protein | 1.29 | -0.19 | -0.17 | 1.17 |
| Afu3g01196 | hypothetical protein | 0.25 | 0.90 | 1.43 | -0.23 |
| Afu3g01260 | acetyltransferase, GNAT family family | 0.00 | 1.26 | 1.20 | -0.62 |
| Afu3g01440 | DUF1212 domain membrane protein | 0.56 | 1.71 | 1.99 | 0.51 |
| Afu3g01530 | phosphatidylglycerol specific phospholipase | 1.12 | 0.36 | 0.68 | 1.02 |
| Afu3g01580 | GMC oxidoreductase | -0.09 | 3.90 | 3.30 | 0.03 |
| Afu3g02120 | short-chain dehydrogenase/reductase family protein, putative | 1.33 | 0.79 | 1.37 | 1.12 |
| Afu3g02270 | mycelial catalase Cat1 | 3.41 | 0.17 | -0.31 | 3.41 |
| Afu3g03280 | FAD binding monooxygenase | 0.86 | 1.25 | 0.40 | -0.06 |
| Afu3g03610 | hypothetical protein | 0.78 | 1.00 | 2.31 | 2.65 |
| Afu3g03750 | hypothetical protein | 1.13 | 1.13 | 1.08 | 1.13 |
| Afu3g04200 | N2,N2-dimethylguanosine tRNA methyltransferase | -1.17 | -0.25 | 0.01 | -0.84 |
| Afu3g05420 | mitochondrial tricarboxylate transporter (Ctp), putative | 0.44 | 0.47 | 1.17 | 1.03 |

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|------------|---|--------------|--------------|--------------|--------------|
| Afu3g05830 | hypothetical protein | 0.82 | 1.75 | 1.82 | 0.80 |
| Afu3g05860 | exosome complex exonuclease Rrp4 | -1.04 | 0.02 | -0.22 | -1.16 |
| Afu3g05940 | transcription factor Rba50 | 0.45 | 1.99 | 1.61 | 0.06 |
| Afu3g06000 | sister chromatid cohesion acetyltransferase Eco1, putative | -0.05 | 0.83 | 1.07 | -0.21 |
| Afu3g06070 | histone H1 | -0.48 | -1.65 | -1.45 | 0.08 |
| Afu3g06260 | translation initiation factor SUI1 | 0.18 | 1.93 | 1.76 | -0.36 |
| Afu3g06290 | C6 transcription factor | -1.32 | -0.26 | -0.26 | -0.40 |
| Afu3g06510 | hypothetical protein | -0.11 | -0.67 | -1.27 | 0.63 |
| Afu3g06770 | mRNA splicing protein | -0.08 | 2.02 | 2.18 | -0.01 |
| Afu3g07330 | essential protein Yae1 | -1.12 | -0.41 | 0.17 | -0.81 |
| Afu3g07600 | hypothetical protein | 0.00 | 0.89 | 1.86 | 0.16 |
| Afu3g07610 | hypothetical protein | 0.67 | 0.03 | 1.06 | 0.16 |
| Afu3g07820 | proteasome regulatory particle subunit Rpt1 | 0.61 | 0.49 | 1.04 | 0.96 |
| Afu3g07850 | pheromone maturation dipeptidyl aminopeptidase DapB | -1.28 | -0.69 | -1.33 | -0.62 |
| Afu3g07870 | extracellular serine-rich protein | 1.72 | -0.04 | -1.21 | 1.18 |
| Afu3g07910 | UDP-glucose 4-epimerase | 0.76 | 0.49 | 0.21 | 1.11 |
| Afu3g08040 | polymerase (RNA) II (DNA directed) polypeptide D | 0.43 | 1.19 | 1.49 | 0.64 |
| Afu3g08090 | 60S ribosomal protein Nsa2 | -0.85 | -0.67 | 0.58 | -1.11 |
| Afu3g08110 | cell wall protein | -0.32 | -0.84 | -1.63 | -0.07 |
| Afu3g08350 | protein transport membrane glycoprotein Sec20 | 0.18 | 0.98 | 1.45 | 0.12 |
| Afu3g08380 | inorganic diphosphatase | 0.52 | 0.43 | 2.19 | 2.12 |
| Afu3g08390 | tRNA dihydrouridine synthase (Smm1) | -0.53 | 1.04 | 1.46 | -0.79 |
| Afu3g09020 | DNA primase subunit Pri1 | 0.45 | 0.17 | 1.34 | -0.01 |
| Afu3g09580 | hypothetical protein | -0.15 | -1.13 | -0.58 | -0.71 |
| Afu3g09770 | RNA-binding protein (Nab3) | -1.39 | -0.40 | -0.13 | -0.59 |
| Afu3g09840 | hypothetical protein | 0.89 | 0.75 | 1.02 | 0.35 |
| Afu3g09920 | hypothetical protein | 1.24 | 1.14 | 1.00 | 0.49 |
| Afu3g10110 | electron transfer flavoprotein-ubiquinone oxidoreductase | 0.03 | 0.65 | 1.05 | -0.06 |
| Afu3g10320 | RING finger domain protein | 0.12 | 1.21 | 1.30 | -0.66 |
| Afu3g10440 | hypothetical protein | 0.51 | 1.58 | 0.79 | 0.28 |
| Afu3g10770 | RTA1 domain protein | 0.14 | 1.68 | 1.86 | -1.03 |
| Afu3g10800 | eukaryotic translation initiation factor 3 subunit CLU1/TIF31 | -0.69 | -2.00 | -1.58 | -0.21 |
| Afu3g10890 | ATP dependent RNA helicase (Dbp8) | -0.94 | -0.75 | 0.79 | -1.22 |
| Afu3g11080 | MAP kinase kinase kinase (Bck1) | -1.43 | -1.03 | -0.49 | -0.91 |
| Afu3g11220 | ribonuclease T2 family | -1.37 | 1.63 | 0.51 | -1.07 |
| Afu3g11310 | hypothetical protein | -0.32 | -0.46 | 0.72 | -1.31 |
| Afu3g11360 | eukaryotic translation initiation factor 3 subunit EifCe | 0.36 | 0.22 | 1.11 | 0.47 |
| Afu3g11630 | hypothetical protein | 0.25 | 1.43 | 0.60 | -0.01 |
| Afu3g12050 | F-box domain protein | 0.03 | 1.30 | 0.87 | -0.06 |
| Afu3g12060 | Methionine synthase, vitamin-B12 independent | 1.02 | 1.12 | 0.31 | 0.45 |
| Afu3g12320 | lipase/serine esterase | 0.19 | 1.77 | 1.75 | 0.09 |
| Afu3g12460 | hypothetical protein | 1.04 | 0.22 | 0.38 | 0.40 |
| Afu3g12490 | protein arginine methyltransferase RmtB | -0.55 | -1.36 | -0.18 | -0.63 |
| Afu3g12680 | hypothetical protein | -0.10 | -0.75 | -0.57 | -1.20 |
| Afu3g12710 | hypothetical protein | -1.13 | -1.24 | -0.44 | -0.71 |
| Afu3g12840 | Signal peptidase I | -0.53 | 0.85 | 1.31 | -1.08 |

| | | | | | |
|------------|---|--------------|--------------|--------------|--------------|
| Afu3g12900 | MFS transporter | 1.38 | 0.17 | 0.00 | 2.25 |
| Afu3g13110 | extracellular serine-threonine rich protein | 1.04 | -1.18 | -1.02 | 1.65 |
| Afu3g13180 | hypothetical protein | 0.10 | 1.48 | 1.99 | -0.27 |
| Afu3g13280 | DEAD/DEAH box helicase (Sbp4) | -0.83 | -1.54 | -0.45 | -1.09 |
| Afu3g13510 | flavin containing amine oxidase | 0.21 | 1.81 | 1.26 | 0.49 |
| Afu3g13700 | transferase family protein | 0.40 | -1.05 | -1.17 | 1.02 |
| Afu3g14120 | hypothetical protein | 1.00 | 1.06 | 0.73 | 1.14 |
| Afu3g14150 | F-box domain protein | 0.85 | 2.47 | 2.58 | -0.21 |
| Afu3g14590 | copper amine oxidase | 0.14 | -0.99 | -1.44 | -0.22 |
| Afu3g15080 | hypothetical protein | -0.38 | 2.39 | 3.36 | -0.53 |
| Afu4g00160 | short-chain dehydrogenase | -1.55 | -0.70 | -1.10 | -0.64 |
| Afu4g00200 | F-box domain protein | -0.24 | 1.68 | 1.80 | -1.12 |
| Afu4g00870 | antigenic cell wall galactomannoprotein | -0.80 | -0.35 | -0.46 | -1.02 |
| Afu4g00970 | IMP-specific 5'-nucleotidase (Isn1) | -0.11 | -0.22 | 2.18 | -0.10 |
| Afu4g00980 | hypothetical protein | -1.20 | 0.86 | 1.36 | -1.72 |
| Afu4g01140 | MFS multidrug transporter | 2.16 | 2.23 | 1.12 | 1.49 |
| Afu4g01210 | hypothetical protein | 0.67 | 0.79 | 1.61 | -0.09 |
| Afu4g01420 | spore wall assembly protein Dit1 | 1.20 | -0.28 | -0.65 | 1.46 |
| Afu4g01440 | glutathione S-transferase family protein | 1.09 | 0.34 | 0.66 | 0.43 |
| Afu4g02900 | sensor histidine kinase/response regulator | -0.74 | -0.68 | -1.03 | -0.25 |
| Afu4g02990 | vesicle-mediated transport protein (Imh1) | 0.51 | 0.94 | 1.23 | 0.24 |
| Afu4g03120 | mitochondrial cytochrome b2 | 0.73 | -0.68 | -1.19 | 1.63 |
| Afu4g03170 | hypothetical protein | -0.89 | 3.24 | 2.95 | -0.52 |
| Afu4g03240 | cell wall serine-threonine-rich galactomannoprotein Mp1 | 1.76 | 1.09 | 0.03 | 1.55 |
| Afu4g03320 | membrane bound cation transporter | 0.25 | 0.24 | 1.45 | 0.91 |
| Afu4g03400 | hypothetical protein | 0.92 | -0.30 | 0.09 | 2.19 |
| Afu4g03490 | tripeptidyl-peptidase (TppA) | -0.57 | -2.01 | -1.78 | -0.03 |
| Afu4g03650 | ribosome associated DnaJ chaperone Zuo1n | -0.13 | 0.48 | 1.06 | -0.46 |
| Afu4g03770 | chlorohydrolase family protein | -0.78 | 1.57 | 1.64 | -1.39 |
| Afu4g03820 | hypothetical protein | 0.52 | 0.99 | 1.09 | 0.71 |
| Afu4g03880 | 60S ribosomal protein L7 | -0.89 | -1.17 | -1.33 | 0.09 |
| Afu4g03940 | ferric-chelate reductase | -0.66 | -0.92 | -1.32 | -0.18 |
| Afu4g04480 | hypothetical protein | -1.48 | -0.77 | -0.60 | -0.74 |
| Afu4g05870 | oxidoreductase, short-chain dehydrogenase/reductase family | 0.86 | 2.14 | 0.99 | 0.87 |
| Afu4g05900 | hypothetical protein | -0.36 | 0.42 | 1.14 | -0.64 |
| Afu4g06010 | peptide alpha-N-acetyltransferase Nat2 | -0.22 | -1.15 | -1.21 | -0.28 |
| Afu4g06020 | cyclin dependent kinase inhibitor Pho81 | -0.07 | -1.14 | -0.40 | -0.21 |
| Afu4g06100 | hypothetical protein | 0.60 | 1.29 | 1.28 | 0.72 |
| Afu4g06410 | hypothetical protein | 1.15 | 0.64 | 0.75 | 1.21 |
| Afu4g06910 | outer mitochondrial membrane protein porin | -0.23 | -0.63 | -1.26 | 0.02 |
| Afu4g06930 | methionine aminopeptidase, type II | 0.30 | 0.28 | 1.86 | 0.64 |
| Afu4g06950 | integral ER membrane protein Scs2 | -0.21 | 0.59 | 1.66 | 0.91 |
| Afu4g07070 | hypothetical protein | 1.01 | 0.08 | 0.41 | -0.09 |
| Afu4g07430 | UBX domain protein | -0.01 | 1.95 | 1.63 | -0.08 |
| Afu4g07490 | hypothetical protein | -0.38 | -0.22 | 0.22 | -1.46 |
| Afu4g07500 | small nucleolar ribonucleoprotein complex subunit, putative | -1.09 | -1.04 | -0.67 | -0.95 |

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|------------|--|-------------|--------------|--------------|--------------|
| Afu4g07670 | INO80 chromatin remodeling complex (les1) | -0.06 | 0.62 | 1.27 | -0.19 |
| Afu4g07680 | hypothetical protein | 0.20 | 1.17 | 1.07 | 0.23 |
| Afu4g07710 | pyruvate carboxylase | -0.53 | -0.95 | -1.36 | -0.53 |
| Afu4g08380 | hypothetical protein | 1.29 | 0.67 | -0.50 | 1.44 |
| Afu4g08420 | hypothetical protein | 1.94 | -0.33 | 0.31 | 2.14 |
| Afu4g08720 | lysophospholipase Plb1 | -0.06 | -0.46 | -1.57 | -0.46 |
| Afu4g08910 | hypothetical protein | 0.28 | 1.71 | 1.58 | -0.26 |
| Afu4g08990 | molybdenum cofactor sulfurase protein (HxB) | -0.26 | 1.58 | 1.10 | -1.03 |
| Afu4g09100 | DnaJ domain protein | 0.14 | 2.09 | 2.69 | 0.08 |
| Afu4g09260 | hypothetical protein | 2.84 | 0.15 | -0.13 | 3.03 |
| Afu4g09330 | hypothetical protein | -0.05 | 0.87 | 2.04 | 0.48 |
| Afu4g09470 | cytochrome P450 monooxygenase | -0.24 | -0.77 | -1.03 | -0.64 |
| Afu4g09760 | hypothetical protein | 0.58 | 1.95 | 2.24 | 0.74 |
| Afu4g09870 | hypothetical protein | 0.93 | 0.72 | 1.27 | 0.57 |
| Afu4g09930 | hypothetical protein | 1.12 | 1.24 | 1.31 | 1.03 |
| Afu4g10260 | hypothetical protein | -0.02 | 0.51 | 1.35 | -0.35 |
| Afu4g10410 | aspartate aminotransferase | 0.38 | -0.12 | -0.17 | 1.14 |
| Afu4g10430 | mitochondrial peptidyl-tRNA hydrolase Pth2 | 1.15 | 1.01 | 2.21 | 1.66 |
| Afu4g10520 | CSL family zinc finger-containing protein | 0.42 | 2.75 | 3.24 | 0.17 |
| Afu4g10850 | hypothetical protein | -0.94 | -1.01 | -0.57 | -1.21 |
| Afu4g11130 | hypothetical protein | 1.35 | 1.31 | 0.67 | 2.04 |
| Afu4g11320 | hypothetical protein | 3.13 | 1.19 | 1.73 | 3.04 |
| Afu4g11390 | ubiquinol-cytochrome c reductase complex 17 kd protein | -0.07 | -1.13 | -2.00 | 0.17 |
| Afu4g11460 | aminotransferase, classes I and II | 0.03 | -0.57 | -1.19 | -0.38 |
| Afu4g11490 | hypothetical protein | 1.05 | 0.70 | 0.20 | 1.15 |
| Afu4g11750 | hypothetical protein | 0.76 | 0.55 | 2.35 | 0.88 |
| Afu4g11880 | splicing factor 3a subunit 2 | -0.02 | 1.47 | 1.49 | -0.05 |
| Afu4g11930 | formamidopyrimidine-DNA glycosylase | -0.11 | -0.48 | 0.08 | -1.11 |
| Afu4g11960 | iron-sulfur cluster assembly associated protein Nar1, putative | -0.12 | 2.43 | 2.21 | -0.58 |
| Afu4g11980 | anthranilate phosphoribosyltransferase | 0.83 | 1.28 | 0.98 | 0.41 |
| Afu4g12030 | hypothetical protein | -0.55 | -1.04 | 0.24 | -0.78 |
| Afu4g12110 | TPR domain protein | -0.69 | -1.27 | -0.40 | -0.81 |
| Afu4g12170 | 50S ribosomal protein L2 | -0.26 | -1.33 | -0.83 | -0.08 |
| Afu4g12350 | hypothetical protein | 0.19 | 0.94 | 2.21 | 0.97 |
| Afu4g12500 | hypothetical protein | -0.36 | 0.58 | 1.24 | -0.39 |
| Afu4g12550 | hypothetical protein | -0.22 | 0.02 | 1.87 | 0.27 |
| Afu4g12720 | phosphoesterase | 1.15 | 0.74 | 1.02 | 0.44 |
| Afu4g12940 | hypothetical protein | 0.94 | 0.71 | 1.42 | 0.69 |
| Afu4g13000 | lysine-specific histone demethylase Aof2 | -0.61 | -0.44 | -1.61 | -0.32 |
| Afu4g13360 | endo-1,3(4)-beta-glucanase | 1.37 | 0.86 | 0.82 | 0.55 |
| Afu4g13490 | AP-3 adaptor complex subunit mu | 0.38 | 1.26 | 0.55 | 0.57 |
| Afu4g13860 | extracellular salicylate hydroxylase/monooxygenase, putative | 0.53 | 2.27 | 1.76 | 0.26 |
| Afu4g13872 | hypothetical protein | -0.50 | -0.52 | -1.12 | -0.61 |
| Afu4g14010 | short chain dehydrogenase/reductase family protein | -0.29 | -0.63 | 0.10 | -1.07 |
| Afu4g14030 | hypothetical protein | 0.81 | 1.02 | 1.67 | 0.10 |
| Afu4g14060 | hypothetical protein | 0.86 | 0.24 | -0.04 | 1.00 |

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|------------|---|--------------|--------------|--------------|--------------|
| Afu4g14175 | hypothetical protein | 1.26 | 1.94 | 2.65 | 1.86 |
| Afu4g14250 | hypothetical protein | 1.10 | -0.08 | 0.30 | 2.29 |
| Afu4g14500 | hypothetical protein | 1.07 | 0.67 | -0.50 | 1.11 |
| Afu5g00790 | ABC multidrug transporter | 0.20 | 0.69 | 1.57 | 0.24 |
| Afu5g00800 | hypothetical protein | 0.35 | 2.49 | 2.20 | -0.48 |
| Afu5g00890 | integral membrane protein | 0.30 | 0.31 | 1.23 | 0.27 |
| Afu5g01005 | hypothetical protein | 1.28 | 0.05 | -0.51 | 1.71 |
| Afu5g01010 | hypothetical protein | 1.41 | 0.07 | 0.05 | 1.57 |
| Afu5g01242 | hypothetical protein | -0.85 | -1.20 | -1.02 | -1.42 |
| Afu5g01300 | integral membrane protein | 0.91 | 1.41 | 1.44 | 0.15 |
| Afu5g01740 | deoxyhypusine synthase | -0.42 | -0.48 | -1.49 | -0.30 |
| Afu5g01770 | hypothetical protein | -0.14 | 1.08 | 1.23 | -0.62 |
| Afu5g01870 | DNA replication factor C subunit Rfc3 | -0.58 | -1.06 | -0.57 | -0.73 |
| Afu5g01920 | GPI anchored protein | 1.15 | 1.98 | 2.69 | 0.82 |
| Afu5g02120 | F-box domain protein | 1.03 | 0.62 | 0.44 | 1.29 |
| Afu5g02330 | major allergen and cytotoxin AspF1 | -0.36 | -1.34 | -1.46 | -0.34 |
| Afu5g02400 | catabolite degradation protein | 0.73 | 1.25 | 1.45 | 0.71 |
| Afu5g02720 | phosphoribosylformylglycinamide synthase | -0.65 | -1.56 | -0.72 | -1.37 |
| Afu5g02760 | fatty acid elongase (Gns1) | -0.75 | -1.66 | -1.65 | 0.06 |
| Afu5g03050 | transcriptional regulator Cwf13/SkiP | -0.31 | 1.14 | 1.24 | -0.85 |
| Afu5g03470 | tRNA-guanine transglycosylase family protein | -0.74 | -1.38 | -0.38 | -0.87 |
| Afu5g03510 | PQ loop repeat protein | -0.47 | -0.65 | -1.31 | -0.33 |
| Afu5g03560 | glutamyl-tRNA synthetase | 0.36 | 0.58 | 1.33 | 0.75 |
| Afu5g03700 | hypothetical protein | 1.17 | 0.59 | 0.57 | 0.50 |
| Afu5g03790 | ferrooxidoreductase Fet3 | 0.59 | 0.43 | 0.17 | 1.11 |
| Afu5g04040 | hypothetical protein | -0.35 | 0.96 | 1.54 | -0.39 |
| Afu5g04050 | scramblase family protein | 0.30 | 1.78 | 1.88 | -0.16 |
| Afu5g04150 | hypothetical protein | -0.08 | 0.93 | 1.66 | -0.23 |
| Afu5g04210 | ubiquinol-cytochrome C reductase complex core protein 2 | -0.31 | -1.52 | -1.59 | -0.31 |
| Afu5g04370 | NADH-ubiquinone oxidoreductase, subunit G | -0.09 | -1.13 | -1.40 | -0.03 |
| Afu5g04410 | hypothetical protein | 0.50 | 1.24 | 2.08 | -0.80 |
| Afu5g05500 | D-3-phosphoglycerate dehydrogenase | 0.03 | 0.24 | -0.15 | -1.47 |
| Afu5g05630 | 60S ribosomal protein L23 | -0.13 | -0.13 | 1.41 | 0.88 |
| Afu5g05730 | hypothetical protein | 0.59 | 1.01 | 0.74 | 0.96 |
| Afu5g05830 | CorA family metal ion transporter | -0.83 | -0.65 | -1.20 | -0.70 |
| Afu5g05850 | hypothetical protein | -0.10 | 1.64 | 1.81 | -0.29 |
| Afu5g05930 | RNA processing factor 1 | -1.30 | 0.10 | 0.62 | -1.10 |
| Afu5g05940 | peptidyl-tRNA hydrolase | -0.56 | -1.50 | -1.02 | 0.04 |
| Afu5g06060 | sulfur metabolism regulator SkpA | 0.52 | 0.89 | 1.95 | 0.05 |
| Afu5g06070 | ABC multidrug transporter Mdr1 | 0.31 | 2.03 | 1.81 | -1.61 |
| Afu5g06140 | histone acetyltransferase | 0.66 | 2.09 | 1.99 | 0.48 |
| Afu5g06170 | hypothetical protein | -1.49 | 0.02 | 0.51 | -1.63 |
| Afu5g06400 | hypothetical protein | -1.50 | -0.98 | -0.70 | -1.34 |
| Afu5g06540 | NADH-ubiquinone oxidoreductase subunit B17.2 | -0.59 | -0.85 | -1.16 | -0.17 |
| Afu5g06560 | hypothetical protein | -0.40 | -1.01 | -0.63 | -0.54 |
| Afu5g06780 | carbamoyl-phosphate synthase, small subunit | -0.70 | -0.39 | -0.41 | -1.03 |

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|------------|---|--------------|--------------|--------------|--------------|
| Afu5g06915 | hypothetical protein | 1.01 | 0.87 | 0.99 | 0.54 |
| Afu5g07230 | carboxyphosphonoenolpyruvate phosphonomutase-like protein | -0.62 | -0.63 | -0.19 | -1.04 |
| Afu5g07640 | RNA 3'-terminal phosphate cyclase | -0.41 | 3.81 | 4.04 | -0.81 |
| Afu5g07850 | decapping enzyme Dcp1 | 0.77 | 1.47 | 0.65 | -0.06 |
| Afu5g07902 | hypothetical protein | -1.05 | -0.84 | -0.75 | -0.72 |
| Afu5g07960 | C2H2 finger and ankyrin domain protein | 0.61 | 1.52 | 2.90 | 0.01 |
| Afu5g08110 | origin recognition complex subunit 2 | -0.09 | 2.93 | 2.89 | -0.63 |
| Afu5g08390 | response regulator | 1.21 | 1.17 | 0.64 | 0.76 |
| Afu5g08540 | septin AspA | -0.68 | -1.72 | -1.73 | 0.06 |
| Afu5g08650 | hypothetical protein | 1.52 | 0.62 | 1.81 | 1.60 |
| Afu5g08730 | hypothetical protein | 0.71 | 2.87 | 2.91 | -0.28 |
| Afu5g08750 | hypothetical protein | 0.17 | 1.70 | 1.57 | 0.12 |
| Afu5g08800 | hypothetical protein | 2.59 | -0.71 | -0.80 | 2.89 |
| Afu5g08870 | hypothetical protein | 0.70 | 0.52 | -0.10 | 1.22 |
| Afu5g08890 | homoaconitase LysF | -1.32 | -0.94 | -1.10 | -0.36 |
| Afu5g08970 | oligosaccharyl transferase subunit (beta) | 0.42 | 0.20 | 0.82 | 1.15 |
| Afu5g09200 | ubiquitin conjugating enzyme (UbcC) | 0.28 | 1.77 | 1.74 | 0.04 |
| Afu5g09620 | tRNA methyltransferase subunit GCD14 | 0.10 | 0.38 | 1.04 | 0.37 |
| Afu5g10120 | NRPS-like enzyme | 0.43 | 1.47 | 1.78 | 0.48 |
| Afu5g10240 | hypothetical protein | 1.11 | 1.52 | 1.41 | 1.08 |
| Afu5g10250 | hypothetical protein | 0.46 | 0.68 | 1.57 | 0.52 |
| Afu5g10290 | fructose-bisphosphate aldolase | -0.11 | -0.46 | -1.09 | -0.41 |
| Afu5g10470 | riboflavin aldehyde-forming enzyme | -1.21 | -0.51 | -0.45 | -0.54 |
| Afu5g10510 | ABC transporter | -0.24 | -0.05 | -0.11 | -2.01 |
| Afu5g10800 | G-patch domain protein | -0.45 | 1.22 | 1.66 | -0.17 |
| Afu5g11040 | pantoate--beta-alanine ligase | -0.36 | -0.56 | -1.09 | 0.51 |
| Afu5g11630 | hypothetical protein | 0.88 | -0.47 | -1.07 | 0.69 |
| Afu5g11670 | Leucine carboxyl methyltransferase family | -0.96 | -1.08 | -0.37 | -0.77 |
| Afu5g11990 | alpha-1,3-mannosyltransferase (Alg3) | -0.80 | -1.25 | -0.10 | -0.62 |
| Afu5g12010 | serine/threonine protein phosphatase | -0.25 | 0.98 | 1.05 | -0.14 |
| Afu5g12090 | hypothetical protein | 0.40 | 0.49 | 2.22 | 1.03 |
| Afu5g12550 | N-acetylglucosaminyl-phosphatidylinositol deacetylase, putative | -0.40 | -0.62 | -1.23 | -0.33 |
| Afu5g12580 | GTP binding protein (GTPBP1) | 0.54 | 1.93 | 1.97 | 0.36 |
| Afu5g12600 | DNA excision repair protein (Rad5) | 0.63 | 0.89 | 1.21 | 0.00 |
| Afu5g12800 | 50S ribosomal protein L4 | -0.96 | -0.87 | -1.17 | 0.25 |
| Afu5g12890 | microfibrillar-associated protein MfaP1 | -0.06 | 0.97 | 1.24 | -0.78 |
| Afu5g12895 | ssDNA binding protein Ssb3 | 0.01 | 1.19 | 1.08 | -0.10 |
| Afu5g13060 | DUF1275 domain protein | -1.12 | 1.24 | 0.34 | -1.23 |
| Afu5g13220 | hypothetical protein | -0.04 | 1.56 | 1.36 | 0.23 |
| Afu5g13300 | aspartic endopeptidase Pep1/aspergillopepsin F | 0.30 | 0.24 | -0.24 | 1.06 |
| Afu5g13370 | mitochondrial DNA helicase (Pif1) | 0.56 | 0.53 | 1.53 | 0.17 |
| Afu5g13392 | transmembrane GTPase Fzo1 | -1.20 | -0.98 | -0.47 | -0.84 |
| Afu5g13750 | calcium binding protein Caleosin | 0.92 | 0.83 | 0.48 | 1.74 |
| Afu5g13840 | NUDIX domain | -0.26 | 0.24 | 1.20 | -0.14 |

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|------------|---|--------------|--------------|--------------|--------------|
| Afu5g13920 | Hsp90 binding co-chaperone (Sba1) | 0.31 | 1.01 | 1.58 | -0.02 |
| Afu5g14510 | beta-lactamase | 0.73 | 0.05 | 0.00 | 1.16 |
| Afu6g00280 | NmrA-like family protein | -0.03 | 2.61 | 2.04 | -0.52 |
| Afu6g00310 | serine carboxypeptidase (CpdS) | -1.05 | -2.93 | -3.21 | -0.22 |
| Afu6g00520 | hypothetical protein | 1.62 | 1.96 | 2.03 | 2.02 |
| Afu6g00555 | hypothetical protein | -0.38 | 0.60 | 1.46 | 0.11 |
| Afu6g01900 | flavin-binding monooxygenase-like protein | 0.96 | -0.61 | -0.37 | 1.06 |
| Afu6g02200 | C2HC5 finger protein | 1.21 | 1.85 | 3.41 | 0.53 |
| Afu6g02380 | ubiquitin C-terminal hydrolase | -0.86 | 0.71 | 1.17 | -1.63 |
| | structural maintenance of chromosome complex subunit | | | | |
| Afu6g02700 | SmcA | 0.34 | 0.29 | 1.30 | -0.04 |
| Afu6g02820 | metalloreductase | -1.71 | -1.27 | -2.32 | -0.52 |
| Afu6g02830 | hypothetical protein | 0.03 | 0.81 | 1.38 | -0.29 |
| Afu6g03350 | GNAT family N-acetyltransferase | -0.04 | 0.60 | 1.35 | -2.14 |
| Afu6g03460 | hypothetical protein | 1.18 | -1.00 | -0.63 | 1.53 |
| Afu6g03660 | onanonoxo-7-onima-8-eninoihemlysoneda | 0.43 | -0.47 | -1.15 | 0.69 |
| Afu6g03680 | hypothetical protein | 1.50 | 0.69 | 0.20 | 3.68 |
| Afu6g04100 | Mis6 domain protein | 1.04 | 1.04 | 0.37 | 0.89 |
| Afu6g04180 | hypothetical protein | -0.27 | 1.76 | 1.31 | -0.67 |
| Afu6g04320 | RNA binding protein | 0.00 | 1.05 | 1.36 | -0.33 |
| Afu6g04750 | Hsp70 nucleotide exchange factor (Fes1) | -1.06 | 0.68 | 0.01 | -1.32 |
| Afu6g04800 | lysine decarboxylase-like protein | 1.08 | 1.65 | 2.78 | 1.06 |
| Afu6g04970 | phosphoserine aminotransferase | 0.55 | 0.86 | 1.37 | -1.02 |
| Afu6g05040 | DNA replication factor C subunit Rfc4 | -0.84 | -1.15 | 0.44 | -0.54 |
| | adoMet-dependent tRNA methyltransferase (MTase) complex | | | | |
| Afu6g06330 | subunit Trm112 | 0.22 | 0.55 | 1.06 | -0.11 |
| Afu6g06750 | 14-3-3 family protein | 0.19 | -1.10 | -0.19 | -0.49 |
| Afu6g06990 | von Willebrand and RING finger domain protein | 0.72 | 0.76 | 0.08 | 1.00 |
| Afu6g07000 | hypothetical protein | 2.13 | 2.51 | 1.25 | 3.59 |
| Afu6g07020 | SAM and PH domain protein (Boi1) | 1.78 | -0.54 | 0.01 | 1.74 |
| Afu6g07100 | diphthamide biosynthesis protein Dph2 | -0.19 | 0.71 | 1.15 | -0.37 |
| Afu6g07120 | nuclear movement protein NudC | 0.44 | 1.34 | 1.45 | 0.11 |
| Afu6g07200 | hypothetical protein | 1.70 | 0.06 | -0.30 | 2.71 |
| Afu6g07370 | hypothetical protein | 2.55 | 0.15 | -0.51 | 2.79 |
| Afu6g07390 | isocitrate dehydrogenase LysB | 0.02 | -1.67 | -1.24 | 0.23 |
| Afu6g07410 | hypothetical protein | -1.22 | -0.51 | -0.46 | -1.04 |
| Afu6g07430 | pyruvate kinase | -1.65 | -1.48 | -1.20 | -0.98 |
| Afu6g07590 | hypothetical protein | -0.80 | 0.86 | 1.26 | -1.01 |
| | chromosomal organization and DNA repair protein Mms21, | | | | |
| Afu6g07700 | putative | 0.57 | 1.34 | 1.98 | 0.26 |
| Afu6g07970 | calpain-like protein | 0.54 | 0.58 | 1.46 | 0.67 |
| Afu6g08560 | NRPS-like enzyme | -0.26 | -0.44 | -1.04 | -0.62 |
| Afu6g08570 | DNA damage repair protein Mus42 | 0.69 | 1.02 | 1.05 | 0.28 |
| Afu6g08790 | C6 transcription factor (PrnA) | -1.16 | -0.51 | -0.55 | -0.62 |
| Afu6g08860 | sugar isomerase, KpsF/GutQ | 0.60 | 1.13 | 1.31 | -0.41 |
| Afu6g09315 | hypothetical protein | 0.57 | 0.56 | -1.22 | 0.32 |

| Afu6g10280 | hypothetical protein | 0.43 | 1.83 | 2.13 | 0.76 | |
|------------|---|--------------|--------------|--------------|--------------|--|
| Afu6g10530 | transcriptional elongation regulator Elc1/Elongin C, putative | 0.45 | 1.92 | 1.78 | -0.62 | |
| Afu6g10790 | MFS amine transporter | -0.10 | 0.91 | 0.69 | -1.06 | |
| Afu6g10840 | hypothetical protein | -0.09 | 1.28 | 1.29 | -0.25 | |
| Afu6g10890 | actin cytoskeleton organization protein App1 | 0.76 | 1.21 | 1.76 | 0.44 | |
| Afu6g10940 | hypothetical protein | -0.18 | 0.37 | 1.06 | -0.14 | |
| Afu6g11070 | DEAD box RNA helicase (Hca4) | -0.30 | -0.69 | 0.11 | -1.43 | |
| Afu6g11130 | possible replication factor-a protein | 0.37 | 0.69 | 1.08 | 0.20 | |
| Afu6g11160 | isopentenyl-diphosphate delta-isomerase | -0.06 | 0.14 | 2.41 | 0.43 | |
| Afu6g11170 | C2H2 finger domain protein (Ezf) | 0.35 | 1.09 | 1.31 | 0.53 | |
| Afu6g11560 | integral membrane protein | -0.01 | 2.23 | 1.98 | -0.43 | |
| Afu6g11720 | hypothetical protein | -0.58 | -1.21 | -0.14 | -1.28 | |
| Afu6g12145 | hypothetical protein | -1.14 | -0.17 | -0.51 | -0.76 | |
| Afu6g12320 | hypothetical protein | -0.76 | 0.38 | 0.83 | -1.39 | |
| Afu6g12330 | WD domain protein | -0.09 | 1.09 | 1.81 | -0.23 | |
| Afu6g12540 | RING finger protein | 0.18 | 1.70 | 2.19 | 0.05 | |
| Afu6g12650 | hypothetical protein | 0.51 | 2.02 | 2.39 | 0.16 | |
| Afu6g12790 | NADH-ubiquinone oxidoreductase 39 kDa subunit | -0.25 | -1.98 | -2.43 | -0.22 | |
| Afu6g12900 | mitochondrial carrier protein | 0.25 | 1.36 | 1.00 | -0.54 | |
| Afu6g13100 | magnesium dependent phosphatase | 0.18 | 0.92 | 1.25 | 0.07 | |
| Afu6g13150 | hypothetical protein | 0.84 | 1.32 | 0.22 | 0.85 | |
| Afu6g13210 | oxidoreductase, short-chain dehydrogenase/reductase family | 0.72 | 0.35 | -0.46 | 1.07 | |
| Afu6g13310 | 26S proteasome non-ATPase regulatory subunit Nas2, putative | -0.22 | 0.97 | 1.46 | 0.19 | |
| Afu6g13346 | hypothetical protein | 0.34 | 0.31 | -0.17 | 1.20 | |
| Afu6g13640 | hypothetical protein | 0.20 | 2.61 | 1.94 | 0.00 | |
| Afu6g13750 | ferric-chelate reductase | -0.66 | -0.63 | -1.06 | 0.33 | |
| Afu6g14090 | CFEM domain protein | -0.32 | -2.33 | -2.85 | -0.01 | |
| Afu6g14270 | hypothetical protein | 0.45 | 1.58 | 0.84 | 0.26 | |
| Afu6g14360 | cytochrome P450 monooxygenase | 0.89 | 0.36 | -0.10 | 1.37 | |
| Afu6g14490 | beta-glucosidase | -1.29 | -0.50 | -0.70 | -0.52 | |
| Afu7g00180 | NAD dependent epimerase/dehydratase | 0.20 | 0.59 | 2.04 | 0.29 | |
| Afu7g00310 | hypothetical protein | -0.66 | -1.04 | -0.91 | -1.46 | |
| Afu7g00440 | GABA permease | 0.89 | -0.03 | -0.26 | 1.04 | |
| Afu7g00580 | hypothetical protein | 1.54 | -0.31 | 0.90 | 2.10 | |
| Afu7g00820 | hypothetical protein | 1.43 | 1.12 | 0.83 | 1.54 | |
| Afu7g01240 | phytase | 0.48 | -0.79 | -1.23 | 1.19 | |
| Afu7g01620 | hypothetical protein | -0.09 | 1.32 | 1.37 | 0.20 | |
| Afu7g01720 | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase | 0.74 | 1.10 | 0.71 | 0.74 | |
| Afu7g01920 | DNA-dependent RNA polymerase II RPB140 | 0.37 | 0.99 | 1.40 | 0.30 | |
| Afu7g01930 | GTP-binding protein EsdC | 1.83 | -0.51 | -0.28 | 2.37 | |
| Afu7g01940 | nuclear pore complex subunit Nup85 | -0.03 | 0.40 | 1.24 | 0.23 | |
| Afu7g02050 | arrestin (or S-antigen), N-terminal domain protein | 1.00 | 1.25 | 1.27 | 1.80 | |
| Afu7g02070 | AIF-like mitochondrial oxidoreductase (Nfrl) | 0.37 | -2.23 | -2.20 | 0.26 | |
| Afu7g02080 | RNA polymerase I subunit Rpa43 | -1.07 | -1.65 | -0.39 | -1.14 | |
| Afu7g02230 | mRNA binding post-transcriptional regulator (Csx1), putative | -0.73 | -1.28 | -0.44 | -1.30 | |

| | | | | | |
|------------|---|--------------|--------------|--------------|--------------|
| Afu7g03830 | DNA repair protein Rad7, protein | 0.52 | 1.99 | 2.31 | 0.53 |
| Afu7g03970 | hypothetical protein | -0.46 | -1.31 | -1.38 | 0.17 |
| Afu7g03980 | PCI domain protein | -0.60 | -0.43 | -0.16 | -1.03 |
| Afu7g04040 | hexokinase | 0.29 | 0.14 | -0.08 | 1.00 |
| Afu7g04140 | L-galactose dehydrogenase (L-GalDH) | 0.66 | 1.15 | 1.04 | 0.51 |
| Afu7g04290 | amino acid permease (Gap1) | 1.44 | 0.60 | -0.39 | 1.57 |
| Afu7g04500 | ATP phosphoribosyltransferase His1 | -0.65 | -1.69 | -1.61 | -0.69 |
| Afu7g04530 | alcohol dehydrogenase, zinc-containing | 2.19 | 1.01 | 0.83 | 0.29 |
| Afu7g04560 | hypothetical protein | -0.21 | -0.55 | -1.07 | 0.16 |
| Afu7g04870 | glutamine-serine-proline rich protein | 0.35 | 0.90 | 1.74 | 0.21 |
| Afu7g05370 | septin AspB | -0.27 | -0.61 | -1.32 | 0.13 |
| Afu7g05420 | mitochondrial intermembrane space protein Mia40 | -0.08 | -1.03 | -1.58 | 0.12 |
| Afu7g05730 | hypothetical protein | 0.43 | 1.05 | 0.78 | -0.02 |
| Afu7g06080 | ubiE/COQ5 methyltransferase | 1.49 | -0.13 | 0.07 | 1.16 |
| Afu7g06270 | cyanamide hydratase | 0.76 | -0.22 | 0.00 | 1.04 |
| Afu7g06440 | F-box domain protein | 0.01 | -0.36 | -0.27 | 1.00 |
| Afu7g06630 | cytochrome P450 monooxygenase | 1.18 | 0.43 | 0.40 | 1.08 |
| Afu7g06675 | COG3602 family protein | 0.30 | 1.15 | 1.19 | 0.15 |
| Afu7g06680 | AAA family ATPase | 2.28 | 4.11 | 4.40 | 0.07 |
| Afu7g06690 | flavin-containing monooxygenase | -0.42 | 3.96 | 3.72 | -0.49 |
| Afu8g01310 | ferric-chelate reductase (Fre2) | 1.09 | 0.67 | 0.28 | 0.17 |
| Afu8g01370 | CmcJ-like methyltransferase | 0.68 | 0.41 | 0.49 | 1.07 |
| Afu8g01390 | glycosyl hydrolase | 0.89 | -1.43 | -2.07 | 0.82 |
| Afu8g01820 | hypothetical protein | -1.26 | -0.74 | -0.60 | -0.51 |
| Afu8g02060 | glycan biosynthesis protein (PigL) | -0.28 | -0.75 | -1.04 | -0.50 |
| Afu8g02250 | hypothetical protein | -0.26 | 0.89 | 1.35 | -0.25 |
| Afu8g02490 | hypothetical protein | -0.30 | 1.96 | 2.29 | -0.85 |
| Afu8g02810 | ELMO/CED-12 family protein | 0.47 | 1.02 | 1.09 | 0.56 |
| Afu8g02830 | UPD-GlcNAc transporter (Mnn2-2) | 0.24 | -0.73 | -1.43 | -0.01 |
| Afu8g02870 | hypothetical protein | 0.93 | 1.87 | 1.37 | 0.34 |
| Afu8g03930 | Hsp70 chaperone (HscA) | -0.23 | -1.13 | -0.68 | -0.16 |
| Afu8g04030 | LMBR1 domain protein | 0.19 | 1.04 | 0.76 | 0.38 |
| Afu8g04250 | pentatricopeptide repeat protein | 0.05 | 1.02 | 1.51 | -0.52 |
| Afu8g04260 | translocation protein (Sec66) | 0.41 | 0.42 | 1.99 | 0.88 |
| Afu8g04540 | C6 transcription factor | -0.43 | -0.12 | -1.18 | -0.38 |
| Afu8g05140 | oxidoreductin | 1.07 | 1.91 | 1.16 | 1.10 |
| Afu8g05170 | autophagy protein Apg6 | 0.58 | 1.48 | 1.18 | 0.56 |
| Afu8g05330 | methylenetetrahydrofolate dehydrogenase | -0.59 | -1.38 | -0.91 | -0.82 |
| Afu8g05650 | hypothetical protein | 1.11 | 0.47 | 1.67 | 1.17 |
| Afu8g05710 | MFS sugar transporter Stl1 | 1.35 | 3.73 | 3.25 | -0.09 |
| Afu8g05720 | DUF567 domain protein | 0.34 | 0.23 | 1.44 | 0.29 |
| Afu8g06070 | hypothetical protein | 0.10 | -1.18 | -0.09 | 1.51 |
| Afu8g06405 | isoflavone reductase family protein | 1.17 | 0.83 | 0.29 | 1.15 |
| Afu8g07090 | extracellular proline-serine rich protein | 0.64 | -0.76 | -1.10 | 0.90 |
| Afu8g07130 | AhpC/TSA family thioredoxin peroxidase | 0.16 | -2.02 | -2.59 | 0.27 |