**Table S4** Differentially expressed *Triticum aestivum*-ESTs

| **Sequence ID** | **Fold Change**[a] | ***p-value*** | **Sequence description** |
|---|---|---|---|
| Ta_S58847638 | (+)ND | 0.003693 | Hypothetical protein osi_06374 [Oryza sativa Indica Group] |
| Ta_S58840665 | (+)ND | 0.044869 | Hypothetical protein osj_33218 [Oryza sativa Japonica Group] |
| Ta_S58861971 | (+)ND | 0.030767 | Protein |
| contig_119 | (+)ND | 2.56E-07 | Not found |
| Ta_S58868582 | (+)ND | 0.000289 | Not found |
| Ta_S37855427 | (+)ND | 0.002587 | Not found |
| Ta_S32661173 | (+)ND | 0.037164 | Not found |
| Ta_S58882496 | 951.2 | 9.05E-23 | Not found |
| contig_160 | 765.2 | 6.84E-21 | Not found |
| contig_3469 | 645.0 | 2.00E-32 | Transcriptional regulator |
| Ta_S58859374 | 571.2 | 0.004452 | Not found |
| Ta_S37940839 | 505.1 | 0.005203 | Pre-mrna processing protein expressed |
| contig_4627 | 389.5 | 2.60E-16 | Not found |
| Ta_S58863092 | 340.5 | 0.003014 | Alpha-l-fucosidase 2 precursor |
| contig_2198 | 123.6 | 0.015971 | Not found |
| Ta_S52544833 | 80.0 | 0.037528 | Small heat shock protein |
| Ta_S16236735 | 76.4 | 0.019596 | Heat-shock protein |
| Ta_S58854607 | 59.8 | 0.001188 | Replication factor c subunit |
| Ta_S16229254 | 48.9 | 0.04891 | Kda class iv heat shock protein |
| Ta_S52547097 | 46.7 | 0.028523 | Probable serine threonine-protein kinase at1g54610-like |
| Ta_S58853475 | 39.9 | 4.51E-05 | Not found |
| contig_5353 | 34.0 | 5.87E-10 | Not found |
| Ta_S52541981 | 29.4 | 0.019756 | Kda class iii heat shock |
| Ta_S58886208 | 23.3 | 0.010146 | Not found |
| contig_2820 | 22.2 | 0.038959 | Not found |
| Ta_S58858619 | 19.9 | 0.029221 | Low molecular weight heat shock protein |
| Ta_S12923094 | 19.5 | 0.025603 | Not found |
| Ta_S58850802 | 18.8 | 9.18E-05 | Not found |
| Ta_S52541158 | 18.5 | 0.020768 | PREDICTED: uncharacterized protein LOC100846009 [Brachypodium distachyon] |

|  |  |  |  |
|---|---|---|---|
| contig_2853 | 16.8 | 0.0424 | Not found |
| Ta_S58884106 | 14.9 | 0.000358 | Af114171_11disease resistance protein rpm1 homolog |
| Ta_S58859323 | 14.8 | 0.041305 | Not found |
| Ta_S22373503 | 14.5 | 0.035288 | Hsf-type dna-binding domain containing expressed |
| Ta_S58884158 | 14.0 | 5.29E-09 | Cytochrome p450 liketbp |
| contig_4027 | 13.8 | 0.012235 | Hsf-type dna-binding domain containing expressed |
| Ta_S58887920 | 12.5 | 0.018728 | Pentatricopeptide repeat-containing protein mitochondrial-like |
| Ta_S37815739 | 12.4 | 5.25E-05 | Caffeic acid 3-o- |
| Ta_S58844263 | 12.1 | 0.015089 | Not found |
| Ta_S17982440 | 12.1 | 3.85E-11 | Serine acetyltransferase |
| Ta_S58846190 | 11.9 | 0.006763 | La domain family |
| Ta_S37845209 | 10.5 | 0.01791 | Not found |
| Ta_S32681735 | 10.3 | 0.000194 | Not found |
| Ta_S32654208 | 9.9 | 0.005766 | Not found |
| contig_565 | 9.7 | 0.013784 | Not found |
| Ta_S58857445 | 9.4 | 0.009264 | Serine threonine-protein kinase |
| Ta_S58895571 | 8.9 | 0.002269 | Not found |
| Ta_S16248940 | 8.5 | 0.017956 | Not found |
| contig_312 | 8.5 | 1.58E-05 | Not found |
| Ta_S58889424 | 8.0 | 0.001986 | Not found |
| Ta_S58891564 | 7.9 | 6.03E-05 | Cytochrome p450 liketbp |
| Ta_S58856591 | 7.6 | 0.033515 | Not found |
| Ta_S59490000 | 6.9 | 0.046498 | Myb transcription factor |
| Ta_S13230809 | 6.6 | 0.015398 | Not found |
| Ta_S32507710 | 6.2 | 4.26E-06 | Heat shock cognate 70 kda expressed |
| Ta_S58842184 | 5.7 | 0.028196 | Serine threonine-protein kinase rio1-like |
| Ta_S12902351 | 5.7 | 0.040947 | Endo-beta- -glucanase |
| contig_4604 | 5.6 | 0.044513 | Aberrant pollen transmission |
| Ta_S58859081 | 5.5 | 0.002069 | Protein |
| Ta_S13177111 | 5.4 | 0.023428 | Not found |
| Ta_S58839733 | 5.3 | 0.009311 | Rna pseudourine synthase 7 |
| Ta_S13203445 | 5.3 | 0.007348 | Not found |
| Ta_S13130963 | 5.3 | 0.003439 | Not found |

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|---|---|---|---|
| Ta_S13128615 | 5.0 | 0.005439 | Not found |
| contig_5105 | 5.0 | 0.002405 | Calcium-transporting atpase plasma membrane-type-like |
| contig_5384 | 4.9 | 6.71E-05 | Not found |
| contig_3896 | 4.9 | 0.023133 | Atp synthase f0 subunit 6 |
| contig_2359 | 4.8 | 0.0422 | Not found |
| Ta_S58906848 | 4.8 | 0.035364 | Not found |
| contig_3292 | 4.7 | 0.001588 | Ribonucleotide reductase |
| Ta_S58850217 | 4.7 | 0.035126 | Pentatricopeptide repeat-containing protein |
| Ta_S58851704 | 4.6 | 0.019086 | Dna helicase |
| Ta_S52543987 | 4.5 | 0.021261 | F-box protein at5g07610-like |
| contig_2239 | 4.5 | 0.000884 | Abc transporter b family member 20-like |
| Ta_S12999712 | 4.5 | 0.004115 | Retrotransposon unclassified |
| Ta_S16246863 | 4.4 | 0.048563 | F-box protein at5g52880-like |
| Ta_S50388141 | 4.4 | 0.000164 | Not found |
| contig_5480 | 4.3 | 0.001514 | Dna repair protein rad50 |
| Ta_S13165985 | 4.3 | 0.027464 | Auxin-induced protein 15a |
| Ta_S58862793 | 4.3 | 0.049535 | Not found |
| contig_3750 | 4.3 | 0.006817 | Transformation transcription domain-associated protein |
| Ta_S13177057 | 4.2 | 0.009059 | Protein (low-affinity nitrate transporter) |
| contig_2223 | 4.2 | 0.012425 | Not found |
| contig_4749 | 4.2 | 0.012448 | Not found |
| Ta_S13243932 | 4.2 | 0.010607 | Protein |
| Ta_S13167109 | 4.2 | 0.016915 | Not found |
| Ta_S13227407 | 4.1 | 0.0135 | Not found |
| Ta_S58857760 | 4.1 | 0.015583 | Not found |
| Ta_S22371585 | 4.1 | 0.020454 | Not found |
| Ta_S58842370 | 4.0 | 0.015452 | Gdp-mannose transporter |
| contig_6225 | 3.9 | 0.001586 | Terminal uridylyltransferase 7-like |
| contig_4425 | 3.9 | 0.003578 | Not found |
| Ta_S37759224 | 3.9 | 0.006323 | Bowman-birk trypsin inhibitor-like protein |
| Ta_S19223311 | 3.8 | 0.000329 | Snf2 super family |
| contig_4264 | 3.8 | 0.000279 | Not found |
| Ta_S58862912 | 3.8 | 0.023386 | Not found |

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|---|---|---|---|
| Ta_S16192587 | 3.8 | 0.01741 | Not found |
| contig_4719 | 3.7 | 0.028446 | Hypothetical protein RAZWK3B_00585 [Roseobacter sp. Azwk-3b] |
| contig_2770 | 3.7 | 0.0001 | Beta-amyrin synthase |
| Ta_S13166085 | 3.7 | 0.022504 | Not found |
| Ta_S17888799 | 3.7 | 0.004178 | PREDICTED: uncharacterized protein LOC100839923 [Brachypodium distachyon] |
| contig_3741 | 3.7 | 0.00033 | Beta-expansin 2 precursor |
| Ta_S58853302 | 3.7 | 0.017175 | Not found |
| contig_1173 | 3.7 | 0.008315 | Not found |
| Ta_S58853221 | 3.7 | 0.019972 | PREDICTED: uncharacterized protein LOC100835027 [Brachypodium distachyon] |
| Ta_S12888461 | 3.7 | 0.043034 | Not found |
| Ta_S21611732 | 3.6 | 0.038114 | Not found |
| contig_6844 | 3.6 | 0.047101 | Not found |
| contig_5883 | 3.6 | 0.007309 | Amino acid permease family expressed |
| contig_5199 | 3.6 | 0.002266 | Disease resistance protein rpm1-like |
| Ta_S58868812 | 3.6 | 0.034298 | Epstein-barr virus ebna-1-like protein |
| Ta_S13144009 | 3.6 | 0.045792 | 60s ribosomal protein l34 |
| Ta_S32530535 | 3.5 | 0.002146 | Not found |
| contig_896 | 3.5 | 0.000232 | Not found |
| Ta_S32510701 | 3.5 | 0.023986 | Mitogen-activated protein kinase kinase 6-like (MAPK) |
| contig_1850 | 3.5 | 0.002 | Casein kinase i isoform delta-like |
| Ta_S58861829 | 3.4 | 0.011656 | Beta-glucosidase 5-like isoform 2 |
| Ta_S22370985 | 3.4 | 0.022688 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_4443 | 3.4 | 0.045306 | Not found |
| contig_6114 | 3.4 | 0.031475 | Mac perforin domain containing protein |
| contig_2182 | 3.4 | 0.007848 | Protein |
| Ta_S32501583 | 3.4 | 0.016771 | Protein |
| Ta_S58848661 | 3.3 | 0.025071 | Not found |
| Ta_S58846759 | 3.3 | 0.031009 | Not found |
| contig_3927 | 3.3 | 0.042921 | Not found |
| contig_1285 | 3.3 | 0.048853 | Microtubule organization protein |
| Ta_S13146836 | 3.3 | 0.015823 | 60s ribosomal protein l7-1 |

| | | | |
|---|---|---|---|
| Ta_S58884395 | 3.2 | 9.90E-05 | Pg1 protein |
| Ta_S17981880 | 3.2 | 0.006262 | Not found |
| contig_3422 | 3.2 | 0.043532 | Hth dna-binding expressed |
| Ta_S58846451 | 3.2 | 0.022381 | Not found |
| Ta_S58894107 | 3.2 | 0.024519 | Amino acid permease |
| Ta_S13172731 | 3.2 | 0.046943 | Cytochrome c oxidase polypeptide vib |
| Ta_S32667864 | 3.2 | 0.016896 | Protein |
| contig_6563 | 3.2 | 0.035511 | Cytochrome p450 71e1 |
| Ta_S22381097 | 3.2 | 0.005502 | Otu-like cysteine protease family protein |
| Ta_S58899343 | 3.1 | 0.003699 | Metal transporter nramp6-like |
| contig_6095 | 3.1 | 0.00717 | Not found |
| contig_1160 | 3.1 | 0.013055 | Brefeldin a-inhibited guanine nucleotide-exchange protein 1-like |
| contig_2296 | 3.1 | 0.006482 | Hypothetical protein osi_11910 [Oryza sativa Indica Group] |
| Ta_S17976596 | 3.1 | 0.008875 | Sulphate transporter |
| Ta_S58857404 | 3.1 | 0.036759 | PREDICTED: uncharacterized protein LOC100842944 [Brachypodium distachyon] |
| Ta_S58841493 | 3.1 | 0.022736 | Retrotransposon unclassified |
| Ta_S17890893 | 3.1 | 0.039251 | Glutamine synthetase |
| contig_4775 | 3.1 | 0.000578 | 2-aminoethanethiol dioxygenase-like |
| contig_3720 | 3.0 | 0.014501 | Not found |
| Ta_S58851753 | 3.0 | 0.026695 | Tesmin tso1-like cxc domain containing expressed |
| Ta_S13048497 | 3.0 | 0.039859 | Reticulon |
| contig_4741 | 3.0 | 0.007305 | Embryogenesis-associated protein emb8-like |
| contig_1001 | 3.0 | 0.00441 | Not found |
| contig_2667 | 3.0 | 0.045329 | Not found |
| Ta_S17897607 | 2.9 | 0.018235 | Major facilitator protein |
| Ta_S43485972 | 2.9 | 0.010123 | Protein phosphatase 2c |
| contig_2113 | 2.9 | 0.013425 | Speckle-type poz protein |
| contig_6873 | 2.9 | 0.018253 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_4732 | 2.9 | 0.024764 | Mrna-capping enzyme |
| contig_5266 | 2.9 | 0.012367 | Erect panicle 2 partial |
| contig_3994 | 2.9 | 0.026436 | Nodulin-like protein |
| Ta_S37772528 | 2.9 | 0.049742 | Minor histocompatibility antigen h13 |

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|---|---|---|---|
| Ta_S58851000 | 2.9 | 0.017112 | Probable lrr receptor-like serine threonine-protein kinase at3g47570-like |
| Ta_S14911635 | 2.9 | 0.047019 | Not found |
| Ta_S13138899 | 2.9 | 0.002761 | Not found |
| contig_237 | 2.9 | 0.008549 | 32 kda protein |
| Ta_S13165765 | 2.9 | 0.009439 | Not found |
| contig_4540 | 2.9 | 0.028159 | Os02g0159200 [Oryza sativa Japonica Group] |
| contig_4292 | 2.9 | 0.006344 | Nb-arc domain containing expressed |
| contig_3393 | 2.9 | 0.034167 | Not found |
| Ta_S58860687 | 2.9 | 0.006996 | Ulp1 protease |
| contig_3183 | 2.9 | 0.04096 | Phosphatidylinositol -kinase-like |
| contig_2394 | 2.9 | 0.024308 | Nbs-lrr partial |
| contig_3573 | 2.9 | 0.0236 | Transposon expressed |
| Ta_S16199319 | 2.9 | 0.023912 | Not found |
| contig_1438 | 2.9 | 0.037843 | Not found |
| contig_1600 | 2.9 | 0.04453 | Rna recognition motif family expressed |
| Ta_S32526552 | 2.8 | 0.04364 | Not found |
| Ta_S32659341 | 2.8 | 0.030422 | Ribosomal protein s12 |
| contig_614 | 2.8 | 0.010706 | Not found |
| contig_3699 | 2.8 | 0.02532 | Histidine kinase- dna gyrase b- and hsp90-like atpase family protein |
| Ta_S26021394 | 2.8 | 0.040444 | Not found |
| contig_4303 | 2.8 | 0.029942 | Not found |
| contig_814 | 2.8 | 0.009313 | Not found |
| Ta_S58840365 | 2.7 | 0.036137 | Not found |
| Ta_S13046163 | 2.7 | 0.018747 | Pppde peptidase domain-containing protein 2-like |
| Ta_S58894413 | 2.7 | 0.035843 | 6-phosphofructokinase 4 |
| contig_3852 | 2.7 | 0.020831 | Calpain-like protein |
| contig_2943 | 2.7 | 0.017313 | Nadh-ubiquinone oxidoreductase subunit |
| Ta_S58851084 | 2.7 | 0.026077 | Not found |
| contig_2700 | 2.7 | 0.015973 | Kinase-interacting protein 1 |
| Ta_S58864379 | 2.7 | 0.02852 | Poly polymerase-like |
| Ta_S26022473 | 2.7 | 0.017016 | Zinc-finger protein |

|  |  |  |  |
|---|---|---|---|
| Ta_S13140457 | 2.7 | 0.026444 | Not found |
| Ta_S13124877 | 2.7 | 0.001877 | Initiation factor |
| contig_3450 | 2.7 | 0.004636 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_6410 | 2.7 | 0.006995 | Aldose reductase |
| contig_31 | 2.6 | 0.036198 | Vacuolar protein sorting 13c |
| Ta_S58885340 | 2.6 | 0.006231 | Dynamin-related protein 1e |
| Ta_S58858194 | 2.6 | 0.028588 | Leukocyte receptor cluster |
| contig_1142 | 2.6 | 0.04773 | Blight resistance protein |
| Ta_S32626973 | 2.6 | 0.029205 | Peptide transporter ptr2-like |
| contig_3362 | 2.6 | 0.002923 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S58890953 | 2.6 | 0.04389 | Not found |
| Ta_S58847478 | 2.6 | 0.028481 | Nuclear factor related to kappa-b-binding protein |
| contig_708 | 2.6 | 0.041728 | Secondary cell wall-related glycosyltransferase family 47 |
| contig_6208 | 2.6 | 0.034429 | Not found |
| Ta_S58839330 | 2.6 | 0.023975 | Hypothetical protein osi_07633 [Oryza sativa Indica Group] |
| contig_5714 | 2.6 | 0.039284 | Actin depolymerizing factor 4 |
| contig_1361 | 2.6 | 0.040104 | Not found |
| contig_7159 | 2.6 | 0.023099 | Serine carboxypeptidase |
| Ta_S32526666 | 2.6 | 0.017006 | Dehydration stress-induced protein |
| Ta_S17979451 | 2.6 | 0.023471 | Magnesium transporter nipa2 |
| Ta_S58861380 | 2.5 | 0.045323 | G-type lectin s-receptor-like serine threonine-protein kinase rks1-like |
| Ta_S16212763 | 2.5 | 0.019474 | Galactose-1-phosphate uridylyltransferase |
| Ta_S32667278 | 2.5 | 0.019801 | Not found |
| Ta_S17889461 | 2.5 | 0.027488 | Sphingoid long-chain bases kinase 1 |
| contig_2612 | 2.5 | 0.031927 | Cytochrome c oxidase assembly protein |
| contig_3696 | 2.5 | 0.005704 | U5 small nuclear ribonucleoprotein 200 kda helicase |
| Ta_S13141197 | 2.5 | 0.035223 | O-methyltransferase zrp4 |
| Ta_S12998046 | 2.5 | 0.023305 | Nadh-plastoquinone oxidoreductase subunit k |
| Ta_S13146753 | 2.5 | 0.025228 | 60s ribosomal protein l34 |
| Ta_S22378208 | 2.5 | 0.031434 | Beta-amyrin synthase |
| Ta_S58850705 | 2.5 | 0.041082 | Dna-directed rna polymerase e subunit 1-like |
| Ta_S58882670 | 2.5 | 0.039607 | Serine protease-like protein |

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|---|---|---|---|
| Ta_S12906375 | 2.5 | 0.034624 | Mitochondrial substrate carrier family protein |
| contig_2456 | 2.5 | 0.021233 | Leaf senescence related |
| Ta_S12977114 | 2.4 | 0.000897 | Rrna intron-encoded homing endonuclease |
| Ta_S17893420 | 2.4 | 0.008429 | Beta-expansin 1a expressed |
| Ta_S26028788 | 2.4 | 0.03883 | Somatic embryogenesis receptor kinase |
| Ta_S16267847 | 2.4 | 0.040243 | Hsf-type dna-binding domain containing expressed |
| contig_2743 | 2.4 | 0.037249 | Tbc domain containing protein |
| contig_2382 | 2.4 | 0.045883 | Transcription factor bhlh128 |
| Ta_S24512908 | 2.4 | 0.039708 | Not found |
| contig_2923 | 2.4 | 0.032901 | Callose synthase |
| contig_2142 | 2.4 | 0.037606 | Hypothetical protein osi_15330 [Oryza sativa Indica Group] |
| Ta_S58895262 | 2.4 | 0.041213 | Protein |
| contig_3502 | 2.4 | 0.030821 | Vacuolar protein sorting 13c |
| Ta_S58846204 | 2.4 | 0.047479 | Not found |
| Ta_S37811862 | 2.4 | 0.021538 | Dna binding protein |
| Ta_S58853267 | 2.4 | 0.012625 | Lipid-binding serum glyco protein |
| contig_2635 | 2.4 | 0.020216 | Abc transporter c family member 9-like |
| Ta_S50381169 | 2.4 | 0.049165 | Btb poz domain-containing protein at1g04390-like |
| Ta_S17977835 | 2.4 | 0.03057 | Cytochrome b561 |
| contig_3132 | 2.4 | 0.027554 | Sister chromatid cohesion protein pds5 |
| contig_56 | 2.4 | 0.014155 | Atp-dependent clp protease atp-binding subunit |
| Ta_S20999571 | 2.3 | 0.030328 | Probable xyloglucan endotransglucosylase hydrolase protein 8-like |
| Ta_S32516159 | 2.3 | 0.032981 | Not found |
| contig_7109 | 2.3 | 0.008957 | Glutamine expressed |
| contig_2242 | 2.3 | 0.035709 | Premnaspirodiene oxygenase-like |
| Ta_S17880905 | 2.3 | 0.048284 | 50s ribosomal protein l33 |
| Ta_S13148233 | 2.3 | 0.015525 | 60s ribosomal protein l34 |
| Ta_S26028472 | 2.3 | 0.043489 | Nbs-lrr disease resistance protein homologue |
| contig_2730 | 2.3 | 0.026903 | Chd3-type chromatin-remodeling factor pickle-like |
| contig_6511 | 2.3 | 0.049041 | Wd repeat-containing protein |
| Ta_S12983024 | 2.3 | 0.04741 | Golgin candidate 5-like |
| contig_619 | 2.3 | 0.032178 | Protein |
| contig_5981 | 2.3 | 0.019981 | Serine threonine-protein kinase sapk3-like |

| | | | |
|---|---|---|---|
| Ta_S32590426 | 2.3 | 0.003332 | Nadh-ubiquinone oxidoreductase chain |
| Ta_S37852405 | 2.3 | 0.00411 | Protein kinase xa21 |
| Ta_S32655890 | 2.3 | 0.02744 | Protein |
| Ta_S32683311 | 2.2 | 0.031013 | Ternary complex factor mip1-like |
| Ta_S58886404 | 2.2 | 0.035635 | Tbc domain containing protein |
| contig_5002 | 2.2 | 0.013931 | Not found |
| Ta_S17512385 | 2.2 | 0.047833 | Not found |
| Ta_S37937220 | 2.2 | 0.027311 | Hypothetical protein SORBIDRAFT_04g028380 [Sorghum bicolor] |
| Ta_S58860293 | 2.2 | 0.03301 | Ubx domain-containing protein |
| contig_791 | 2.2 | 0.00475 | Regulator of nonsense transcripts 1 homolog |
| contig_6109 | 2.2 | 0.039413 | Probable importin subunit beta-4-like |
| contig_6922 | 2.2 | 0.030893 | Poly polymerase catalytic domain containing expressed |
| Ta_S58895865 | 2.2 | 0.04609 | Not found |
| Ta_S52542495 | 2.2 | 0.023677 | Cs 5 |
| contig_2968 | 2.2 | 0.036214 | Eukaryotic translation initiation factor 3 subunit c-like |
| Ta_S17890867 | 2.2 | 0.015013 | Os08g0110800 [Oryza sativa Japonica Group] |
| contig_4114 | 2.2 | 0.048739 | PREDICTED: uncharacterized protein LOC100827929 [Brachypodium distachyon] |
| Ta_S13012043 | 2.2 | 0.030101 | Diphosphonucleotide phosphatase expressed |
| contig_2240 | 2.2 | 0.048342 | Fkbp12-rapamycin complex-associated protein |
| Ta_S58855127 | 2.2 | 0.023961 | Protein far1-related sequence 12-like |
| Ta_S47005448 | 2.2 | 0.004909 | Sterol c-14 reductase |
| contig_2914 | 2.2 | 0.035397 | Protease do-like 7-like |
| contig_7023 | 2.2 | 0.034854 | Acc oxidase |
| contig_5777 | 2.2 | 0.034466 | Beach domain-containing protein lvsa-like |
| contig_2895 | 2.2 | 0.027153 | Serine threonine-protein kinase sapk2 |
| Ta_S13043514 | 2.1 | 0.024076 | PREDICTED: uncharacterized protein LOC100841045 [Brachypodium distachyon] |
| contig_2509 | 2.1 | 0.024492 | Not found |
| contig_6340 | 2.1 | 0.016588 | Protein |
| Ta_S22387577 | 2.1 | 0.010013 | Thioredoxin-like 4a |
| contig_4225 | 2.1 | 0.035959 | Calcium-transporting atpase endoplasmic reticulum-type-like |
| contig_4592 | 2.1 | 0.029819 | Not found |

| | | | |
|---|---|---|---|
| contig_354 | 2.1 | 0.040756 | Cytochrome b5 reductase 4-like |
| contig_691 | 2.1 | 0.027289 | U3 small nucleolar rna-associated protein 10 and nuc211 domain-containing protein |
| Ta_S32635933 | 2.1 | 0.039078 | Nodulin-related partial |
| contig_4052 | 2.1 | 0.045423 | Arp2 3 complex 34 kda subunit |
| Ta_S22378449 | 2.1 | 0.018241 | Protein |
| Ta_S32565776 | 2.1 | 0.010922 | Duf246 domain-containing protein at1g04910-like |
| contig_3678 | 2.1 | 0.03295 | Not found |
| Ta_S58881778 | 2.1 | 0.045461 | Not found |
| Ta_S58900180 | 2.1 | 0.042857 | Solute carrier family 35 member f1-like |
| Ta_S58887074 | 2.1 | 0.027853 | Protein |
| Ta_S12965080 | 2.0 | 0.031017 | Atp synthase subunit beta |
| Ta_S58865342 | 2.0 | 0.046041 | Protein far1-related sequence 5-like |
| contig_1241 | 2.0 | 0.041959 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S58902295 | 2.0 | 0.03139 | Seven transmembrane domain protein |
| contig_454 | 2.0 | 0.034425 | Cop1-interacting protein |
| Ta_S13135140 | 2.0 | 0.044097 | Not found |
| contig_2564 | 2.0 | 0.009796 | Not found |
| contig_1395 | 2.0 | 0.033116 | Kinesin heavy chain |
| Ta_S12971663 | 2.0 | 0.036675 | Carrier protein |
| contig_857 | 2.0 | 0.035726 | Gdp-mannose pyrophosphorylase |
| contig_395 | 2.0 | 0.043037 | Disease resistance protein rga4-like |
| contig_2601 | 2.0 | 0.021933 | Protein kinase |
| contig_2033 | 2.0 | 0.039417 | Not found |
| contig_3412 | 2.0 | 0.014033 | Not found |
| Ta_S37823504 | 2.0 | 0.040924 | Not found |
| Ta_S12924295 | 2.0 | 0.043982 | Formiminotransferase- expressed |
| contig_1621 | 2.0 | 0.034748 | Nadh-ubiquinone oxidoreductase |
| Ta_S58864643 | (-)ND | 0.002036 | Retrotransposon unclassified |
| Ta_S58849115 | (-)ND | 0.017092 | Retrotransposon unclassified |
| Ta_S13223809 | (-)ND | 0.046522 | Ring-box protein |
| Ta_S13149798 | (-)ND | 0.014972 | Transmembrane bax inhibitor motif-containing protein 4 |
| Ta_S58912535 | (-)ND | 0.033338 | Wak1 - receptor-like cytoplasmic kinase ( -rlck) precursor defense |

| | | | |
|---|---|---|---|
| | | | response to fungus |
| Ta_S32656390 | (-)ND | 0.00326 | Zinc finger protein id1 |
| contig_6889 | (-)ND | 0.005749 | Not found |
| contig_6774 | (-)ND | 0.044708 | Not found |
| Ta_S32605842 | (-)ND | 0.001484 | Not found |
| Ta_S58841817 | (-)ND | 0.001981 | Not found |
| Ta_S13128736 | (-)ND | 0.00209 | Not found |
| Ta_S37864864 | (-)ND | 0.0035 | Not found |
| Ta_S58845207 | (-)ND | 0.003902 | Not found |
| Ta_S58854505 | (-)ND | 0.006751 | Not found |
| Ta_S13181029 | (-)ND | 0.009241 | Not found |
| Ta_S58845845 | (-)ND | 0.009801 | Not found |
| Ta_S58898595 | (-)ND | 0.011382 | Not found |
| Ta_S58852808 | (-)ND | 0.011659 | Not found |
| Ta_S13143288 | (-)ND | 0.014402 | Not found |
| Ta_S32611510 | (-)ND | 0.014905 | Not found |
| Ta_S32629074 | (-)ND | 0.016429 | Not found |
| Ta_S13031432 | (-)ND | 0.018661 | Not found |
| Ta_S32519859 | (-)ND | 0.018718 | Not found |
| Ta_S37936079 | (-)ND | 0.0191 | Not found |
| Ta_S32515094 | (-)ND | 0.028336 | Not found |
| Ta_S58848140 | (-)ND | 0.031894 | Not found |
| Ta_S58912831 | (-)ND | 0.033668 | Not found |
| Ta_S13173968 | (-)ND | 0.033907 | Not found |
| Ta_S13129446 | (-)ND | 0.039654 | Not found |
| contig_1563 | 296.8 | 0.005116 | Hypothetical protein EB105725_31_00165 [Escherichia blattae NBRC 105725] |
| Ta_S17989215 | 224.8 | 0.012153 | Not found |
| Ta_S18007616 | 86.1 | 0.035934 | F-box protein interaction domain containing protein |
| contig_122 | 74.4 | 0.020042 | Kgg repeat-containing stress-induced protein |
| contig_7138 | 47.7 | 0.000812 | PREDICTED: uncharacterized protein LOC100828580 [Brachypodium distachyon] |
| Ta_S58889718 | 34.9 | 0.000155 | Not found |

| | | | |
|---|---|---|---|
| Ta_S22379260 | 33.3 | 2.83E-05 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S58851470 | 29.3 | 0.008616 | Not found |
| Ta_S37803822 | 28.8 | 0.049691 | Upf0481 protein at3g47200-like |
| Ta_S58855143 | 23.4 | 0.005618 | Pentatricopeptide repeat-containing protein |
| Ta_S32562131 | 22.0 | 0.006854 | Not found |
| Ta_S13041446 | 20.0 | 0.036236 | Not found |
| Ta_S58888744 | 19.4 | 0.011021 | Not found |
| Ta_S13119248 | 18.9 | 0.03781 | Not found |
| Ta_S58893909 | 18.8 | 0.01346 | Not found |
| Ta_S58842447 | 17.9 | 0.016019 | PREDICTED: uncharacterized protein LOC100837593 [Brachypodium distachyon] |
| Ta_S13132385 | 17.4 | 0.005321 | Like protein |
| Ta_S58862139 | 16.2 | 0.017777 | Not found |
| Ta_S58869437 | 15.7 | 0.001733 | Not found |
| Ta_S58865123 | 15.2 | 0.002555 | Not found |
| Ta_S58894064 | 15.1 | 0.022629 | Tvp38 tmem64 family membrane protein slr0305-like |
| Ta_S58863212 | 14.9 | 0.042984 | Not found |
| Ta_S50387228 | 14.3 | 0.020233 | Not found |
| Ta_S58846533 | 14.3 | 0.041675 | Nodulin-like protein |
| Ta_S13180058 | 13.8 | 0.038596 | Not found |
| Ta_S58854706 | 13.2 | 0.007929 | Bwf1-like protein |
| contig_2145 | 12.9 | 0.000596 | Elongation factor ts |
| Ta_S58866498 | 11.9 | 0.011321 | Not found |
| contig_6805 | 11.4 | 0.00084 | Not found |
| Ta_S37854435 | 11.4 | 0.000559 | Anthocyanidin -o-glucosyltransferase-like |
| contig_6985 | 10.1 | 0.000141 | Hypothetical protein SORBIDRAFT_03g008680 [Sorghum bicolor] |
| Ta_S58845691 | 9.9 | 0.033479 | Mutant low phytic acid protein 1 |
| Ta_S58849116 | 9.8 | 0.008202 | Not found |
| Ta_S16231538 | 9.5 | 0.000544 | PREDICTED: uncharacterized protein LOC100841809 [Brachypodium distachyon] |
| Ta_S58865733 | 9.1 | 0.010126 | Hypothetical protein osj_31200 [Oryza sativa Japonica Group] |
| Ta_S58896701 | 9.0 | 0.007022 | Not found |
| contig_6324 | 8.9 | 0.032258 | Protein yeez |

| | | | |
|---|---|---|---|
| Ta_S12913717 | 8.8 | 0.00634 | Dna-directed rna polymerases i and iii subunit rpac1-like |
| Ta_S12882577 | 8.6 | 0.009406 | Ring-h2 finger protein atl1n precursor |
| contig_1201 | 8.5 | 0.01555 | Not found |
| Ta_S58848010 | 8.1 | 0.02126 | Not found |
| contig_1642 | 8.0 | 0.041335 | PREDICTED: uncharacterized protein LOC100826907 [Brachypodium distachyon] |
| Ta_S32622948 | 7.9 | 0.000312 | Late embryogenesis abundant protein |
| Ta_S13014352 | 7.8 | 0.017039 | Protein suppressor of gene silencing-like protein |
| contig_6887 | 7.7 | 0.000537 | Not found |
| Ta_S58858052 | 7.7 | 0.019978 | PREDICTED: uncharacterized protein LOC100829225 [Brachypodium distachyon] |
| Ta_S13119076 | 7.7 | 0.027102 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S58909995 | 7.7 | 0.002892 | Bzip transcription factor family expressed |
| contig_2040 | 7.7 | 0.002061 | Transferring glycosyl |
| Ta_S17979419 | 7.5 | 0.019694 | Dna ligase-like |
| Ta_S16246857 | 7.3 | 0.006151 | Disease resistance protein rpm1-like |
| Ta_S13183409 | 7.2 | 0.00982 | Not found |
| Ta_S32568379 | 7.2 | 0.002987 | Not found |
| Ta_S58847149 | 7.0 | 0.009853 | Not found |
| Ta_S13012191 | 6.9 | 0.02941 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S13262842 | 6.9 | 0.014523 | PREDICTED: uncharacterized protein LOC100827899 [Brachypodium distachyon] |
| contig_5628 | 6.8 | 0.023393 | Cytochrome c heme attachment protein |
| Ta_S58839265 | 6.7 | 0.003925 | Not found |
| contig_2680 | 6.7 | 0.015497 | PREDICTED: uncharacterized protein LOC100827734 [Brachypodium distachyon] |
| Ta_S58882413 | 6.6 | 0.000605 | Protein |
| Ta_S12957883 | 6.5 | 0.025181 | Not found |
| contig_4166 | 6.4 | 0.009352 | Not found |
| Ta_S58888286 | 6.4 | 0.002662 | Protein chloroplast import apparatus 2-like |
| contig_1287 | 6.4 | 0.036626 | Protein ddb_g0268328-like |
| Ta_S58852095 | 6.4 | 0.012195 | Not found |
| contig_3460 | 6.3 | 0.04975 | Not found |

| | | | |
|---|---|---|---|
| Ta_S58909884 | 6.3 | 0.007486 | PREDICTED: uncharacterized protein LOC100826789 isoform 2 [Brachypodium distachyon] |
| Ta_S58889807 | 6.2 | 0.039403 | Global transcription factor group |
| contig_2233 | 6.2 | 7.39E-05 | Not found |
| Ta_S58847793 | 6.2 | 0.008982 | Not found |
| Ta_S13179757 | 6.1 | 0.002234 | Not found |
| contig_6194 | 6.0 | 0.000574 | Protein furry homolog-like |
| Ta_S12894932 | 5.9 | 0.003389 | Vip3 protein |
| Ta_S58894572 | 5.9 | 0.028102 | Not found |
| contig_506 | 5.8 | 4.72E-05 | Rna polymerase beta subunit |
| Ta_S58841053 | 5.8 | 0.039817 | Not found |
| Ta_S58890145 | 5.8 | 0.010066 | L-asparaginase |
| contig_6486 | 5.8 | 0.011558 | Not found |
| Ta_S58855771 | 5.7 | 0.037754 | Not found |
| Ta_S13111509 | 5.7 | 0.024983 | Calmodulin |
| Ta_S16248415 | 5.7 | 0.010506 | Not found |
| Ta_S52543421 | 5.6 | 0.002692 | Protein |
| contig_6115 | 5.5 | 0.011847 | Cytochrome c biogenesis protein precursor |
| contig_1932 | 5.5 | 0.032824 | Zinc finger-like |
| Ta_S32564414 | 5.5 | 0.016276 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S19116911 | 5.5 | 0.017142 | Fca protein |
| Ta_S26025255 | 5.4 | 0.012003 | Photosystem ii reaction center w protein |
| Ta_S13179255 | 5.3 | 0.017007 | Not found |
| Ta_S32565615 | 5.2 | 0.00308 | Not found |
| contig_6267 | 5.1 | 8.63E-05 | Not found |
| contig_1068 | 5.1 | 0.00032 | Not found |
| Ta_S58884786 | 5.0 | 0.034851 | Flavonol 3-sulfotransferase |
| Ta_S13043420 | 5.0 | 0.01845 | Protein |
| Ta_S52545275 | 4.9 | 0.008435 | Ulp1+protease+family [Oryza glaberrima] |
| Ta_S13137206 | 4.9 | 0.021794 | Not found |
| Ta_S59490003 | 4.9 | 0.040244 | Myb transcription factor |
| Ta_S58907457 | 4.9 | 0.000209 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S26023560 | 4.8 | 0.014513 | Not found |

|  |  |  |  |
|---|---|---|---|
| Ta_S16213897 | 4.8 | 0.014501 | Insulin-degrading enzyme-like |
| Ta_S17978397 | 4.7 | 0.049031 | Casp-like protein stg-like |
| Ta_S58890169 | 4.7 | 0.017786 | Fk506 binding protein |
| contig_3086 | 4.7 | 9.64E-05 | Coiled-coil domain-containing protein 132-like |
| Ta_S58886646 | 4.7 | 0.016325 | Phytosulfokines 2-like |
| Ta_S53281796 | 4.6 | 0.004466 | Partial |
| Ta_S13194862 | 4.6 | 0.034102 | Not found |
| Ta_S32671427 | 4.6 | 0.00369 | Not found |
| Ta_S37850818 | 4.6 | 0.047891 | Blue copper binding protein |
| contig_387 | 4.5 | 0.015073 | Peroxidase 1 precursor |
| contig_1359 | 4.5 | 0.007121 | Not found |
| Ta_S58869803 | 4.5 | 0.022403 | Something about silencing protein |
| Ta_S58885579 | 4.5 | 0.013609 | Retrotransposon ty3-gypsy expressed |
| Ta_S58886383 | 4.5 | 0.038333 | Not found |
| Ta_S58895529 | 4.4 | 0.013951 | Probable fructokinase-1-like |
| Ta_S58853931 | 4.4 | 0.004754 | Not found |
| contig_3430 | 4.4 | 0.035664 | PREDICTED: uncharacterized protein LOC100835632 [Brachypodium distachyon] |
| Ta_S58854350 | 4.4 | 0.003766 | Not found |
| Ta_S16199865 | 4.4 | 0.005065 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S58839592 | 4.4 | 0.022398 | Not found |
| Ta_S52543823 | 4.4 | 0.014655 | Glycolate oxidase |
| Ta_S37845220 | 4.3 | 0.027409 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S16203218 | 4.3 | 0.031188 | G-patch domain containing protein |
| Ta_S58845015 | 4.3 | 0.035904 | Not found |
| Ta_S13194190 | 4.3 | 0.008729 | Not found |
| Ta_S32602541 | 4.3 | 0.035606 | Wrky45-like transcription factor |
| Ta_S52541979 | 4.3 | 0.005915 | Mazg nucleotide pyrophosphohydrolase domain protein |
| contig_6543 | 4.2 | 0.024677 | Abc transporter g family member 16-like |
| contig_4210 | 4.2 | 0.003053 | Not found |
| contig_2469 | 4.1 | 0.0154 | Not found |
| contig_6647 | 4.1 | 0.022231 | Not found |
| Ta_S58856084 | 4.0 | 0.006992 | Protein raspberry 3 |

|  |  |  |  |
|---|---|---|---|
| contig_2463 | 4.0 | 0.020513 | Nac domain-containing protein 21 22-like |
| Ta_S52546230 | 4.0 | 0.02679 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S55352938 | 4.0 | 0.042183 | Not found |
| Ta_S58894026 | 4.0 | 0.006073 | Protein mei2-like 2-like |
| Ta_S32564964 | 4.0 | 0.015267 | Lob domain-containing protein 12-like |
| Ta_S18008276 | 4.0 | 0.02317 | Metallothionein |
| contig_4435 | 3.9 | 0.001184 | Not found |
| Ta_S52542038 | 3.9 | 0.011996 | Not found |
| contig_3797 | 3.9 | 0.047636 | Not found |
| Ta_S58857043 | 3.9 | 0.046382 | Not found |
| Ta_S13011770 | 3.9 | 0.016041 | Response regulator receiver domain containing expressed |
| Ta_S32529059 | 3.9 | 0.044464 | P-glycoprotein 1 |
| Ta_S58862129 | 3.9 | 0.015591 | Ubiquitin carboxyl-terminal hydrolase 5-like |
| contig_6139 | 3.9 | 0.017725 | PREDICTED: uncharacterized protein LOC100830293 [Brachypodium distachyon] |
| Ta_S37773901 | 3.9 | 0.020961 | Cytochrome p450 |
| contig_4099 | 3.9 | 0.011792 | Not found |
| Ta_S58884172 | 3.8 | 0.019041 | Sugar transporter family expressed |
| Ta_S26022483 | 3.8 | 0.004652 | Mrna turnover protein 4 homolog |
| contig_2117 | 3.8 | 0.036091 | Protein far1-related sequence 6-like |
| Ta_S58900106 | 3.8 | 0.036143 | Light-harvesting complex i chlorophyll a b binding protein 3 |
| contig_177 | 3.8 | 0.021501 | Not found |
| Ta_S22370925 | 3.7 | 0.028464 | Cyclin-dependent protein |
| contig_4121 | 3.7 | 0.003503 | Nadh-plastoquinone oxidoreductase subunit 4 |
| contig_189 | 3.6 | 0.002803 | Hydroxypyruvate reductase |
| contig_3206 | 3.6 | 0.01727 | Not found |
| contig_1921 | 3.6 | 0.031429 | Not found |
| Ta_S17057489 | 3.6 | 0.012101 | Auxin response factor 3-like |
| Ta_S37847348 | 3.6 | 0.046873 | Not found |
| contig_6073 | 3.6 | 0.000429 | Not found |
| Ta_S17984780 | 3.6 | 0.038704 | Rna recognition motif-containing protein |
| Ta_S58847292 | 3.6 | 0.044602 | Not found |
| Ta_S17990036 | 3.5 | 0.012441 | Os01g67210-like protein |

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|---|---|---|---|
| contig_4485 | 3.5 | 0.011469 | Protein |
| contig_34 | 3.5 | 0.007414 | Ac079179_7 dna2-nam7 helicase family protein |
| Ta_S13192404 | 3.5 | 0.002451 | Not found |
| contig_5565 | 3.5 | 0.013811 | Not found |
| Ta_S16265918 | 3.5 | 0.034256 | Not found |
| contig_6371 | 3.5 | 0.003753 | Cleavage and polyadenylation specificity factor subunit 1-like |
| contig_5623 | 3.5 | 0.015428 | Not found |
| Ta_S32623645 | 3.5 | 0.005422 | Not found |
| contig_4508 | 3.5 | 0.026426 | Not found |
| contig_3771 | 3.5 | 0.045802 | Not found |
| Ta_S13051479 | 3.4 | 0.02613 | Serine threonine-protein kinase afc1 |
| contig_667 | 3.4 | 0.007296 | Glucan endo- -beta-glucosidase 3 precursor |
| Ta_S13158111 | 3.4 | 0.038946 | 3 -n-debenzoyl-2 -deoxytaxol n-benzoyltransferase-like |
| contig_6266 | 3.4 | 0.026402 | PREDICTED: uncharacterized protein LOC100846531 [Brachypodium distachyon] |
| Ta_S22368361 | 3.4 | 0.030739 | Not found |
| Ta_S17985298 | 3.4 | 0.030577 | Os03g0806600 [Oryza sativa Japonica Group] |
| contig_6429 | 3.4 | 0.001115 | Atp-dependent clp protease atp-binding subunit -like |
| contig_5972 | 3.4 | 0.036929 | Kinesin-like protein |
| contig_6711 | 3.4 | 0.001579 | Ring finger protein 10-like |
| contig_1657 | 3.4 | 0.001289 | PREDICTED: uncharacterized protein LOC100833724 [Brachypodium distachyon] |
| contig_4494 | 3.4 | 0.004922 | Adomet-dependent rrna methyltransferase spb1-like |
| Ta_S35718003 | 3.3 | 0.034433 | Cbf protein 4 |
| contig_2829 | 3.3 | 0.016477 | Disease resistance protein rpp13-like |
| Ta_S52544017 | 3.3 | 0.000181 | Os11g0205500 [Oryza sativa Japonica Group] |
| Ta_S52541619 | 3.3 | 0.003758 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_976 | 3.3 | 0.017469 | Not found |
| Ta_S32680735 | 3.3 | 0.046318 | Atp-dependent helicase |
| contig_893 | 3.3 | 0.026324 | Hypothetical protein SORBIDRAFT_02g042020 [Sorghum bicolor] |
| contig_7150 | 3.3 | 0.043671 | Pectinacetylesterase precursor |
| contig_5790 | 3.3 | 0.00218 | Atp gtp binding protein |
| Ta_S12937455 | 3.3 | 0.02511 | Caffeic acid 3-o-methyltransferase |

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|---|---|---|---|
| contig_6028 | 3.3 | 0.047501 | Zinc finger-like |
| contig_6790 | 3.2 | 0.002154 | Not found |
| Ta_S58885047 | 3.2 | 0.043247 | Required to maintain repression 1 |
| contig_1204 | 3.2 | 0.020006 | Not found |
| Ta_S58890225 | 3.2 | 0.032208 | Pinus taeda anonymous locus 0_13978_01 genomic sequence |
| Ta_S58892307 | 3.2 | 0.036361 | Protein |
| Ta_S12978479 | 3.2 | 0.025629 | Upf0503 protein chloroplastic-like |
| Ta_S52544593 | 3.2 | 0.008103 | Iaa amidohydrolase |
| Ta_S58891200 | 3.2 | 0.049555 | Probable calcium-binding protein cml45-like |
| Ta_S58843579 | 3.2 | 0.012423 | Zinc finger c-x8-c-x5-c-x3-h type family protein |
| contig_5459 | 3.2 | 0.0118 | Not found |
| contig_6622 | 3.2 | 0.033575 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_1887 | 3.2 | 0.029589 | Nadh-plastoquinone oxidoreductase subunit i |
| contig_1450 | 3.1 | 0.024256 | Not found |
| contig_6247 | 3.1 | 0.031666 | Ubiquitin-protein pub49 |
| contig_5892 | 3.1 | 0.03285 | Tgf-beta type i ii extracellular region |
| Ta_S32611416 | 3.1 | 0.002956 | Not found |
| contig_1268 | 3.1 | 0.004966 | Pre-mrna-processing factor 6-like |
| Ta_S58848668 | 3.1 | 0.022083 | Protein |
| Ta_S58839681 | 3.1 | 0.005448 | Molybdopterin cofactor |
| Ta_S52543429 | 3.1 | 0.048621 | Far-red impaired response |
| contig_510 | 3.1 | 0.016319 | Not found |
| contig_3567 | 3.1 | 0.046643 | Histidine kinase 1 |
| Ta_S12898462 | 3.1 | 0.048414 | Not found |
| contig_595 | 3.1 | 0.016907 | Not found |
| Ta_S16213725 | 3.1 | 0.024768 | Not found |
| contig_206 | 3.1 | 0.040605 | Wall-associated receptor kinase 3-like |
| Ta_S52541449 | 3.1 | 0.015366 | Acc oxidase |
| Ta_S58855004 | 3.0 | 0.022203 | Retrotransposon unclassified |
| Ta_S52541238 | 3.0 | 0.036684 | Protein |
| Ta_S58908965 | 3.0 | 0.04018 | Not found |
| contig_4372 | 3.0 | 0.010219 | PREDICTED: uncharacterized protein LOC100830560 [Brachypodium distachyon] |

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|---|---|---|---|
| contig_6211 | 3.0 | 0.023654 | Not found |
| contig_1319 | 3.0 | 0.001602 | Protein |
| Ta_S58849836 | 3.0 | 0.019897 | Transposon en spm sub-class |
| Ta_S12971695 | 3.0 | 0.038384 | Not found |
| Ta_S52545353 | 3.0 | 0.026062 | Gene product |
| contig_2007 | 3.0 | 0.002687 | S-locus protein 4 |
| contig_4736 | 3.0 | 0.04582 | Transparent testa 12 protein |
| contig_4368 | 3.0 | 0.025215 | Pleckstrin homology domain-containing protein |
| Ta_S58863463 | 3.0 | 0.044705 | Not found |
| contig_1928 | 3.0 | 0.003062 | Protein kinase |
| Ta_S58850183 | 3.0 | 0.043876 | Protein rrp5 homolog |
| Ta_S32571600 | 3.0 | 0.019429 | Aaa atpase containing von willebrand factor type a precursor |
| Ta_S26018764 | 3.0 | 0.028686 | Not found |
| Ta_S16207731 | 2.9 | 0.024887 | Aspartic proteinase nepenthesin-1-like |
| Ta_S37827906 | 2.9 | 0.039072 | Not found |
| contig_6944 | 2.9 | 0.011773 | Not found |
| contig_5588 | 2.9 | 0.040374 | Auxilin-related protein 2-like |
| contig_1953 | 2.9 | 0.006278 | Not found |
| contig_3846 | 2.9 | 0.002502 | Not found |
| Ta_S22381029 | 2.9 | 0.03341 | Cytochrome p450 |
| Ta_S16262691 | 2.9 | 0.024578 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_4488 | 2.8 | 0.042037 | Not found |
| Ta_S17897290 | 2.8 | 0.003737 | Nascent polypeptide associated complex alpha chain |
| Ta_S26023404 | 2.8 | 0.041541 | Plastid protein |
| contig_1298 | 2.8 | 0.035525 | Low quality protein: 1-phosphatidylinositol-3-phosphate 5-kinase-like |
| Ta_S26026252 | 2.8 | 0.027495 | 50s ribosomal protein l9 |
| Ta_S17987500 | 2.8 | 0.043801 | Cytochrome p450 probable 6-deoxoteasterone to 3-dehydro 6-deoxoteasterone or teasterone to 3-dehydro teasterone |
| contig_85 | 2.8 | 0.018126 | Not found |
| Ta_S26022199 | 2.8 | 0.038098 | Not found |
| contig_6724 | 2.8 | 0.03668 | Os05g0207900 [Oryza sativa Japonica Group] |
| contig_2320 | 2.8 | 0.00944 | Not found |

| | | | |
|---|---|---|---|
| Ta_S58849094 | 2.8 | 0.036562 | Not found |
| contig_1882 | 2.8 | 0.026119 | Not found |
| contig_2188 | 2.8 | 0.028778 | Dynamin-like protein |
| Ta_S58907153 | 2.8 | 0.045212 | Post-illumination chlorophyll fluorescence increase protein |
| Ta_S32591420 | 2.8 | 0.026478 | C-terminal zinc-finger |
| Ta_S17988916 | 2.8 | 0.00575 | Probable atp-dependent rna helicase dhx36-like |
| contig_1923 | 2.8 | 0.012786 | Not found |
| contig_1955 | 2.8 | 0.049442 | Not found |
| Ta_S18012554 | 2.8 | 0.043176 | At5g16250 t21h19_170 |
| Ta_S12880675 | 2.7 | 0.019579 | Af385697_1 at5g10580 f12b17_70 |
| contig_4145 | 2.7 | 0.046526 | Not found |
| Ta_S58886363 | 2.7 | 0.013311 | Stearoyl-acyl-carrier protein desaturase |
| Ta_S32628058 | 2.7 | 0.014778 | Protein mitochondrial-like |
| Ta_S37846208 | 2.7 | 0.015742 | Anthocyanidin -o-glucosyltransferase-like |
| Ta_S58902249 | 2.7 | 0.032019 | Not found |
| Ta_S16058277 | 2.7 | 0.003438 | Cinnamyl alcohol dehydrogenase |
| contig_4117 | 2.7 | 0.028115 | Not found |
| Ta_S58888109 | 2.7 | 0.015363 | Tpa: nac transcription factor |
| Ta_S52545220 | 2.7 | 0.024114 | Chloroplast omega-6 fatty acid desaturase |
| Ta_S58900624 | 2.7 | 0.028533 | Serine hydroxymethyltransferase |
| contig_4744 | 2.7 | 0.043444 | Probable fructokinase-2 |
| Ta_S58885157 | 2.7 | 0.007421 | Retrotransposon expressed |
| Ta_S37889954 | 2.7 | 0.038063 | Not found |
| contig_5322 | 2.7 | 0.005918 | Not found |
| Ta_S32537167 | 2.7 | 0.033359 | Not found |
| Ta_S58861966 | 2.7 | 0.044648 | Diacylglycerol acyltransferase |
| Ta_S26027242 | 2.7 | 0.026064 | Chaperonin 20 |
| contig_5307 | 2.7 | 0.01233 | PREDICTED: uncharacterized protein LOC100838094 [Brachypodium distachyon] |
| contig_132 | 2.7 | 0.01751 | Not found |
| contig_7151 | 2.7 | 0.015553 | Not found |
| contig_347 | 2.7 | 0.005414 | Not found |
| Ta_S58863091 | 2.7 | 0.022328 | Not found |

| | | | |
|---|---|---|---|
| contig_2278 | 2.7 | 0.037931 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S17987196 | 2.7 | 0.03366 | Alpha 3 subunit of 20s proteasome |
| Ta_S13179831 | 2.7 | 0.0085 | Not found |
| contig_179 | 2.7 | 0.027104 | Choline ethanolamine kinase |
| Ta_S52543551 | 2.7 | 0.010257 | Basic region leucine zipper protein |
| contig_4596 | 2.7 | 0.027564 | Protein kinase and pp2c-like domain-containing isoform 2 |
| contig_2341 | 2.6 | 0.004378 | Not found |
| Ta_S32661131 | 2.6 | 0.011714 | Wir1b_wheat ame: full=protein wir1b |
| Ta_S58865460 | 2.6 | 0.031304 | Aaa family atpase cdc48 subfamily |
| Ta_S58904389 | 2.6 | 0.017919 | Clp-like energy-dependent protease |
| contig_3754 | 2.6 | 0.047926 | Not found |
| contig_5733 | 2.6 | 0.041474 | Not found |
| Ta_S58855639 | 2.6 | 0.037345 | Not found |
| Ta_S58850763 | 2.6 | 0.048262 | PREDICTED: uncharacterized protein At2g39910-like [Brachypodium distachyon] |
| Ta_S26022932 | 2.6 | 0.035619 | Grassy tillers 1 |
| Ta_S52546220 | 2.6 | 0.038764 | Tonoplast intrinsic |
| contig_3687 | 2.6 | 0.020669 | Not found |
| Ta_S32660720 | 2.6 | 0.038125 | Not found |
| Ta_S58902262 | 2.6 | 0.00681 | Tonoplast intrinsic protein |
| Ta_S58853104 | 2.6 | 0.044161 | Probable lrr receptor-like serine threonine-protein kinase at3g47570-like |
| contig_1468 | 2.6 | 0.007515 | Not found |
| contig_3564 | 2.6 | 0.028809 | Not found |
| Ta_S58850272 | 2.5 | 0.044373 | Not found |
| Ta_S58867334 | 2.5 | 0.044755 | 1 domain containing expressed |
| contig_2492 | 2.5 | 0.048355 | Rna polymerase beta partial |
| contig_1864 | 2.5 | 0.029312 | Probable atp-dependent rna helicase ythdc2-like |
| contig_5660 | 2.5 | 0.041875 | Not found |
| Ta_S13567817 | 2.5 | 0.02858 | Rubisco subunit binding-protein alpha subunit |
| contig_5786 | 2.5 | 0.00571 | Not found |
| Ta_S13137675 | 2.5 | 0.024318 | Not found |
| Ta_S26018735 | 2.5 | 0.033949 | Ribosome biogenesis protein bop1 homolog |

| | | | |
|---|---|---|---|
| Ta_S52546131 | 2.5 | 0.049751 | Not found |
| contig_1896 | 2.5 | 0.003622 | Not found |
| Ta_S12922871 | 2.5 | 0.012976 | Nucleic acid-binding protein |
| Ta_S22391033 | 2.5 | 0.040161 | Ser thr-rich protein t10 in dgcr region |
| Ta_S18012285 | 2.5 | 0.009965 | Not found |
| Ta_S52545881 | 2.5 | 0.022684 | Anthocyanin 5-aromatic acyltransferase-like |
| Ta_S24513426 | 2.5 | 0.046717 | G1-like3 protein |
| contig_7038 | 2.5 | 0.04571 | Argininosuccinate lyase |
| Ta_S58853020 | 2.5 | 0.045993 | PREDICTED: uncharacterized protein LOC100833596 [Brachypodium distachyon] |
| Ta_S32541082 | 2.5 | 0.039925 | Not found |
| Ta_S13205638 | 2.4 | 0.017913 | Not found |
| contig_1250 | 2.4 | 0.00939 | Not found |
| contig_4290 | 2.4 | 0.006712 | Not found |
| Ta_S13049499 | 2.4 | 0.030413 | Non-specific lipid-transfer protein at2g13820-like |
| contig_1177 | 2.4 | 0.04838 | Not found |
| contig_5852 | 2.4 | 0.00586 | Importin subunit beta-1-like |
| contig_956 | 2.4 | 0.028589 | Not found |
| Ta_S12923244 | 2.4 | 0.009896 | Ribulose -bisphosphate carboxylase activase |
| contig_6317 | 2.4 | 0.035749 | Not found |
| Ta_S13163819 | 2.4 | 0.036475 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S37811723 | 2.4 | 0.028953 | Not found |
| Ta_S58886850 | 2.4 | 0.015067 | Apurinic endonuclease-redox protein |
| Ta_S26020605 | 2.3 | 0.003917 | Not found |
| Ta_S58855596 | 2.3 | 0.025724 | Protein nlrc3-like |
| Ta_S17987082 | 2.3 | 0.020748 | Aquaporin tip4-1 |
| Ta_S17890271 | 2.3 | 0.039185 | H+ ca2+ exchanger |
| Ta_S26025478 | 2.3 | 0.02849 | Dehydrin 5 |
| Ta_S52547012 | 2.3 | 0.016971 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1-like |
| Ta_S17987611 | 2.3 | 0.030724 | Protein kinase chloroplast |
| contig_1672 | 2.3 | 0.006677 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S58896564 | 2.3 | 0.037143 | Not found |
| Ta_S17987213 | 2.3 | 0.046563 | Rna polymerase beta subunit |

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|---|---|---|---|
| contig_3666 | 2.3 | 0.025692 | Calcium-dependent protein kinase |
| contig_2386 | 2.3 | 0.043744 | Type i inositol- -trisphosphate 5-phosphatase cvp2-like |
| contig_4893 | 2.3 | 0.025021 | Not found |
| contig_329 | 2.3 | 0.01921 | Not found |
| contig_4 | 2.3 | 0.041515 | Nadh dehydrogenase subunit 2 |
| contig_6090 | 2.3 | 0.041248 | Abscisic acid receptor pyl8-like |
| Ta_S22381224 | 2.3 | 0.044987 | Potassium transporter 25-like |
| Ta_S17889976 | 2.3 | 0.036853 | Chlorophyll a b binding protein |
| Ta_S50379630 | 2.3 | 0.036224 | Casp-like protein at3g53850-like |
| Ta_S13232890 | 2.3 | 0.016033 | Adp-ribosylation factor |
| Ta_S22368999 | 2.3 | 0.038426 | Not found |
| contig_984 | 2.2 | 0.038863 | Not found |
| contig_4802 | 2.2 | 0.025676 | Ap-2 complex subunit sigma-like |
| Ta_S17888862 | 2.2 | 0.014477 | Cysteine-rich repeat secretory protein 55-like |
| Ta_S58842296 | 2.2 | 0.045837 | Copine (calcium-dependent phospholipid-binding protein) family |
| Ta_S35138743 | 2.2 | 0.014374 | Fasciclin-like arabinogalactan protein 11-like |
| Ta_S52546553 | 2.2 | 0.001782 | Subtilisin-like protease |
| contig_3386 | 2.2 | 0.012737 | Heavy metal p-type atpase |
| contig_1812 | 2.2 | 0.026186 | Not found |
| contig_264 | 2.2 | 0.044341 | O-methyltransferase family expressed |
| Ta_S26019852 | 2.2 | 0.033632 | Not found |
| Ta_S58897752 | 2.2 | 0.04849 | Not found |
| Ta_S13127316 | 2.2 | 0.028718 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| contig_1333 | 2.2 | 0.047689 | Nadh-plastoquinone oxidoreductase subunit 4 |
| Ta_S22390999 | 2.2 | 0.032546 | Not found |
| Ta_S52542749 | 2.2 | 0.015284 | Hexokinase 2 |
| contig_300 | 2.2 | 0.026097 | Kelch motif family protein |
| Ta_S17988496 | 2.2 | 0.002513 | Sex determination protein tasselseed 2 |
| Ta_S17989302 | 2.2 | 0.042233 | Adenylate kinase |
| Ta_S16203131 | 2.2 | 0.046073 | Ribosomal protein l29 family protein |
| Ta_S58884885 | 2.2 | 0.041543 | Predicted protein [Hordeum vulgare subsp. Vulgare] |
| Ta_S17890391 | 2.2 | 0.031877 | Vacuolar sorting receptor 1 expressed |
| Ta_S58863494 | 2.1 | 0.044972 | Retrotransposon protein |

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|---|---|---|---|
| contig_4909 | 2.1 | 0.006443 | Not found |
| Ta_S37822414 | 2.1 | 0.034591 | Pentatricopeptide repeat-containing protein |
| Ta_S52544010 | 2.1 | 0.045153 | 3 -n-debenzoyl-2 -deoxytaxol n-benzoyltransferase-like |
| contig_2559 | 2.1 | 0.042846 | At1g03060-like partial |
| Ta_S13110644 | 2.1 | 0.019238 | Not found |
| Ta_S17888161 | 2.1 | 0.031418 | Chlorophyll a-b binding protein of lhcii type iii |
| Ta_S37752627 | 2.1 | 0.006329 | Not found |
| Ta_S26023930 | 2.1 | 0.027836 | High mobility group b protein 7-like |
| Ta_S26027971 | 2.1 | 0.037103 | Calmodulin-like protein 6-like |
| Ta_S32686907 | 2.1 | 0.008878 | Not found |
| contig_6052 | 2.1 | 0.042806 | Uncharacterized membrane protein at1g16860-like |
| contig_1648 | 2.1 | 0.024846 | Isoleucyl-trna cytoplasmic-like |
| Ta_S53111501 | 2.1 | 0.037225 | Uncharacterized cdp-alcohol phosphatidyltransferase class-i family protein 3-like |
| Ta_S12926531 | 2.1 | 0.03622 | Deoxyuridine 5 -triphosphate nucleotidohydrolase |
| Ta_S58893991 | 2.1 | 0.020919 | Receptor-like protein kinase feronia-like |
| contig_2368 | 2.1 | 0.035919 | Not found |
| contig_1504 | 2.1 | 0.03768 | E3 ubiquitin-protein ligase rnf14-like |
| contig_1845 | 2.1 | 0.008551 | Not found |
| contig_1554 | 2.1 | 0.046294 | Actin-related protein 2 3 complex subunit 2-like |
| contig_2934 | 2.1 | 0.043022 | Transmembrane protein 87b |
| Ta_S16058462 | 2.1 | 0.015165 | Tryptophansynthase subunit beta |
| Ta_S13000024 | 2.1 | 0.049558 | Homeobox protein hox-c4 |
| contig_1033 | 2.1 | 0.009665 | Not found |
| Ta_S18008953 | 2.1 | 0.040356 | Not found |
| Ta_S52542397 | 2.1 | 0.037953 | Rhodanese homology domain-containing protein |
| Ta_S12977017 | 2.1 | 0.034287 | Sialyltransferase-like protein |
| Ta_S26028954 | 2.1 | 0.019628 | Cysteine-rich receptor-like protein kinase 10-like |
| Ta_S32566041 | 2.1 | 0.035432 | Not found |
| contig_4518 | 2.1 | 0.0373 | Tbcc domain-containing protein 1-like isoform 2 |
| contig_2912 | 2.1 | 0.047699 | Not found |
| Ta_S58885203 | 2.0 | 0.013504 | Auxin-induced protein pcnt115-like isoform 1 |
| Ta_S52542430 | 2.0 | 0.001997 | Nitrile-specifier protein 5-like |

| | | | |
|---|---|---|---|
| contig_2364 | 2.0 | 0.035622 | Not found |
| Ta_S52541388 | 2.0 | 0.017841 | Not found |
| contig_5468 | 2.0 | 0.034603 | Not found |
| contig_5536 | 2.0 | 0.023919 | Not found |
| Ta_S13109609 | 2.0 | 0.009045 | Glutathione s-transferase 4-like |
| Ta_S58849569 | 2.0 | 0.041587 | Eukaryotic aspartyl protease family expressed |
| Ta_S58867749 | 2.0 | 0.043975 | Glutamyl-trna synthetase |
| contig_4742 | 2.0 | 0.049874 | Not found |
| Ta_S13146959 | 2.0 | 0.045941 | Hypothetical protein [Zea mays] |
| Ta_S58865230 | 2.0 | 0.030608 | Protein binding |
| Ta_S52542697 | 2.0 | 0.033319 | Hypothetical protein SORBIDRAFT_09g022220 [Sorghum bicolor] |
| Ta_S13057957 | 2.0 | 0.02364 | Hydroquinone glucosyltransferase |
| Ta_S58900435 | 2.0 | 0.040822 | Cobw domain-containing protein 2-like isoform 2 |
| Ta_S58857859 | 2.0 | 0.035993 | Tsn1 |
| Ta_S58896684 | 2.0 | 0.004458 | Thiamine biosynthetic enzyme |
| contig_2355 | 2.0 | 0.040908 | Not found |
| Ta_S52544123 | 2.0 | 0.038415 | Short chain alcohol |
| Ta_S17889067 | 2.0 | 0.01788 | Phosphoenolpyruvate carboxykinase |

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[a] Fold-change in red indicates down-regulation in colonized wheat roots (CWR); (+)ND not expressed in the N-IWR libraries; (-) ND not expressed in the CWR libraries.