**Supplementary Table 2.** Differentially abundant proteins in mite tolerant *Oryza sativa* cv. Nipponbare (control x early infested condition).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| ***Oryza sativa* cv. Nipponbare Control x Early infested - Proteins unique or more expressed in control leaves** | | | | | | |
| **Functional categories** | **Description** | **Uniprot** | **Locus** | **Reported peptides** | **t-Test** | **Log2 Fold Change** |
| **Photosynthesis** | photosystem II 47 kDa protein (chloroplast) | PSBB\_ORYSJ | LOC\_Os06g39708 | 8 | 0.004 | -1.672 |
| carboxyvinyl-carboxyphosphonate phosphorylmutase, chloroplastic | Q0IPL3\_ORYSJ | LOC\_Os12g08760 | 5 | 0.002 | -1.292 |
| photosystem II protein D2 (chloroplast) | PSBD\_ORYSJ | LOC\_Osp1g00170 | 5 | 0.018 | -1.253 |
| photosystem II CP43 chlorophyll apoprotein (chloroplast) | PSBC\_ORYSJ | LOC\_Osp1g00180 | 7 | 0.024 | -1.198 |
| protochlorophyllide reductase B, chloroplastic | PORB\_ORYSJ | LOC\_Os10g35370 | 2 | 0.000 | -1.077 |
| phosphoenolpyruvate carboxylase | Q5QNA5\_ORYSJ | LOC\_Os01g11054 | 2 | 0.001 | -0.998 |
| photosystem II protein D1 (chloroplast) | PSBA\_ORYSJ | LOC\_Osp1g00110 | 3 | 0.014 | -0.993 |
| protein TIC110, chloroplastic | Q0IWS0\_ORYSJ | LOC\_Os10g35030 | 4 | 0.046 | -0.976 |
| transketolase, chloroplastic | Q7XWP9\_ORYSJ | LOC\_Os04g19740 | 3 | 0.001 | -0.764 |
| chlorophyll a-b binding protein 7, chloroplastic | Q6ZL95\_ORYSJ | LOC\_Os07g38960 | 5 | 0.011 | -0.761 |
| chlorophyll a-b binding protein CP29.1, chloroplastic | Q6Z411\_ORYSJ | LOC\_Os07g37240 | 3 | 0.007 | -0.739 |
| chlorophyll a-b binding protein of LHCII type III, chloroplastic | Q6ZF30\_ORYSJ | LOC\_Os07g37550 | 8 | 0.017 | -0.537 |
| **Translation** | 50S ribosomal protein L11, chloroplastic | A0A0P0VSE5\_ORYSJ | LOC\_Os03g03020 | 2 | 0.012 | -1.109 |
| ribosomal protein L2 (chloroplast) | RK2\_ORYSJ | LOC\_Osp1g01100 | 3 | 0.000 | -0.910 |
| ribosomal protein L16 (chloroplast) | RK16\_ORYSJ | LOC\_Os05g22724 | 3 | 0.000 | -0.879 |
| elongation factor G-2, chloroplastic | A0A0N7KJF4\_ORYSJ | LOC\_Os04g45490 | 4 | 0.000 | -0.792 |
| 50S ribosomal protein L4, chloroplastic | Q10NM5\_ORYSJ | LOC\_Os03g15870 | 2 | 0.001 | -0.722 |
| 30S ribosomal protein S1, chloroplastic | Q0DSD6\_ORYSJ | LOC\_Os03g20100 | 9 | 0.018 | -0.516 |
| **Cytoskeleton** | tubulin alpha-1 chain | TBA2\_ORYSJ | LOC\_Os11g14220 | 15 | 0.003 | -1.170 |
| tubulin beta-5 chain | TBB1\_ORYSJ | LOC\_Os01g18050 | 16 | 0.005 | -0.100 |
| tubulin alpha-1 chain | TBA1\_ORYSJ | LOC\_Os07g38730 | 13 | 0.017 | -0.656 |
| tubulin beta chain | TBB7\_ORYSJ | LOC\_Os03g56810 | 17 | 0.014 | -0.650 |
| tubulin beta chain | TBB3\_ORYSJ | LOC\_Os06g46000 | 17 | 0.020 | -0.581 |
| **Carbohydrate metabolism and energy production** | sucrose synthase 3 | SUS3\_ORYSJ | LOC\_Os07g42490 | 11 | Unique Control | Unique Control |
| ATP synthase CF0 subunit I (chloroplast) | ATPF\_ORYSJ | LOC\_Os10g38272 | 2 | 0.021 | -1.137 |
| sucrose synthase 1 | SUS1\_ORYSJ | LOC\_Os03g28330 | 26 | 0.001 | -0.687 |
| **Antioxidant system** | ferredoxin--nitrite reductase, chloroplastic | NIR\_ORYSJ | LOC\_Os01g25484 | 11 | 0.000 | -1.872 |
| peroxidase 70 | Q5U1Q2\_ORYSJ | LOC\_Os03g22010 | 4 | 0.019 | -1.480 |
| peroxidase 1-like | Q0DCP0\_ORYSJ | LOC\_Os06g20150 | 7 | 0.028 | -0.885 |
| **Amino acid metabolism** | glycine dehydrogenase (decarboxylating), mitochondrial | A0A0P0V7A3\_ORYSJ | LOC\_Os01g51410 | 11 | 0.009 | -0.717 |
| glycine dehydrogenase (decarboxylating), mitochondrial | A0A0P0WYZ5\_ORYSJ | LOC\_Os06g40940 | 18 | 0.005 | -0.659 |
| **General metabolic processes** | probable pyridoxal 5'-phosphate synthase subunit PDX1.1 | Q53NW9\_ORYSJ | LOC\_Os11g48080 | 5 | 0.004 | -0.669 |
| **Protein modification/degradation** | serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform X1 | A0A0P0XJR1\_ORYSJ | LOC\_Os09g07510 | 3 | 0.002 | -0.600 |
| **Transport** | Aquaporin PIP1-2 | PIP12\_ORYSJ | LOC\_Os04g47220 | 4 | 0.006 | -1.666 |
| putative cellular retinaldehyde-binding/triple function | Q5TKJ2\_ORYSJ | LOC\_Os05g35460 | 6 | 0.004 | -0.834 |
| **Stress response** | heat shock protein 90-5, chloroplastic | Q6ZCV7\_ORYSJ | LOC\_Os08g38086 | 4 | 0.035 | -0.545 |
| **Others** | putative beta-D-glucan exohydrolase | Q6ZG89\_ORYSJ | LOC\_Os02g03870 | 2 | Unique Control | Unique Control |
| ***Oryza sativa* cv. Nipponbare Control x Early infested - Proteins unique or more expressed in early infested leaves** | | | | | | |
| **Functional categories** | **Description** | **Uniprot** | **Locus** | **Reported peptides** | **t-Test** | **Log2 Fold Change** |
| **Antioxidant system** | peroxidase 2 | PER2\_ORYSJ | LOC\_Os07g48030 | 3 | Unique Infested | Unique Infested |
| GDP-mannose 3,5-epimerase 2 | GME2\_ORYSJ | LOC\_Os11g37890 | 4 | Unique Infested | Unique Infested |
| peroxidase P7-like | Q5Z7J2\_ORYSJ | LOC\_Os06g35520 | 2 | 0.026 | 3.482 |
| probable glutathione S-transferase GSTU6 | GSTU6\_ORYSJ | LOC\_Os10g38740 | 5 | 0.015 | 2.430 |
| peroxidase BP1 precursor [*Oryza nivara*] | Q94DM2\_ORYSJ | LOC\_Os01g73200 | 5 | 0.001 | 1.926 |
| glutathione transferase GST 23 | Q93WY5\_ORYSJ | LOC\_Os09g29200 | 4 | 0.001 | 1.884 |
| peroxidase 2 | Q7F1U0\_ORYSJ | LOC\_Os07g48020 | 7 | 0.005 | 1.833 |
| probable L-gulonolactone oxidase 4 | Q6YXT5\_ORYSJ | LOC\_Os08g02230 | 2 | 0.042 | 1.812 |
| anionic peroxidase | Q7XSV2\_ORYSJ | LOC\_Os04g59150 | 11 | 0.005 | 1.491 |
| protein disulfide isomerase | A0A0P0XZP3\_ORYSJ | LOC\_Os11g09280 | 9 | 0.001 | 1.232 |
| lactoylglutathione lyase | LGUL\_ORYSJ | LOC\_Os08g09250 | 11 | 0.000 | 1.193 |
| superoxide dismutase | SODC1\_ORYSJ | LOC\_Os03g22810 | 4 | 0.030 | 1.165 |
| superoxide dismutase [Cu-Zn] 4A | SODC2\_ORYSJ | LOC\_Os07g46990 | 3 | 0.034 | 1.081 |
| ferredoxin | FER1\_ORYSJ | LOC\_Os08g01380 | 3 | 0.038 | 1.054 |
| peroxidase 1 | Q5U1S8\_ORYSJ | LOC\_Os01g22352 | 6 | 0.004 | 0.996 |
| peroxiredoxin-2C | PRX2C\_ORYSJ | LOC\_Os01g48420 | 7 | 0.009 | 0.915 |
| ferredoxin-NADP+ reductase, embryo isozyme, chloroplastic | FENR3\_ORYSJ | LOC\_Os07g05400 | 2 | 0.001 | 0.893 |
| probable NADPH:quinone oxidoreductase 1 | NQR1\_ORYSJ | LOC\_Os01g72430 | 3 | 0.002 | 0.891 |
| glutathione reductase, cytosolic | GSHRC\_ORYSJ | LOC\_Os02g56850 | 9 | 0.030 | 0.792 |
| Cu/Zn superoxide dismutase (chloroplast) | SODCP\_ORYSJ | LOC\_Os08g44770 | 7 | 0.015 | 0.718 |
| cationic peroxidase SPC4-like | Q5JMS4\_ORYSJ | LOC\_Os01g73170 | 10 | 0.013 | 0.652 |
| thioredoxin H-type | Q6L4X5\_ORYSJ | LOC\_Os05g43252 | 2 | 0.034 | 0.615 |
| **General metabolic processes** | S-adenosylmethionine synthase 3 | METK3\_ORYSJ | LOC\_Os01g18860 | 12 | Unique Infested | Unique Infested |
| CBS domain-containing protein CBSX1, chloroplastic | Q6YYV0\_ORYSJ | LOC\_Os09g02710 | 2 | 0.004 | 1.492 |
| phosphoserine aminotransferase 2, chloroplastic-like | Q8LMR0\_ORYSJ | LOC\_Os03g06200 | 5 | 0.008 | 1.325 |
| soluble inorganic pyrophosphatase | Q7XTL6\_ORYSJ | LOC\_Os04g59040 | 5 | 0.006 | 1.189 |
| D-3-phosphoglycerate dehydrogenase 1, chloroplastic | Q7XMP6\_ORYSJ | LOC\_Os04g55720 | 2 | 0.046 | 1.108 |
| nucleoside diphosphate kinase 1 | NDK1\_ORYSJ | LOC\_Os07g30970 | 7 | 0.015 | 0.993 |
| nucleoside diphosphate kinase 1 | Q7XC37\_ORYSJ | LOC\_Os10g41410 | 5 | 0.008 | 0.875 |
| probable methylenetetrahydrofolate reductase | MTHR\_ORYSJ | LOC\_Os03g60090 | 9 | 0.026 | 0.860 |
| cysteine synthase | CYSK1\_ORYSJ | LOC\_Os12g42980 | 15 | 0.003 | 0.779 |
| 6-phosphogluconate dehydrogenase, decarboxylating 1 | 6PGD1\_ORYSJ | LOC\_Os06g02144 | 13 | 0.005 | 0.652 |
| adenine phosphoribosyltransferase 1 | Q2QMV8\_ORYSJ | LOC\_Os12g39860 | 2 | 0.003 | 0.627 |
| nucleoside diphosphate kinase 3-like | Q5TKF4\_ORYSJ | LOC\_Os05g51700 | 3 | 0.001 | 0.613 |
| cysteine synthase | Q7XS58\_ORYSJ | LOC\_Os04g08350 | 2 | 0.009 | 0.610 |
| glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic | G3PC1\_ORYSJ | LOC\_Os08g03290 | 12 | 0.004 | 0.565 |
| reactive Intermediate Deaminase A, chloroplastic | Q8H4B9\_ORYSJ | LOC\_Os07g33240 | 4 | 0.037 | 0.550 |
| adenylate kinase 4 | KAD4\_ORYSJ | LOC\_Os11g20790 | 5 | 0.038 | 0.521 |
| 2,3-dimethylmalate lyase-like | Q7XLP7\_ORYSJ | LOC\_Os04g31700 | 5 | 0.021 | 0.520 |
| cysteine synthase | CYSK2\_ORYSJ | LOC\_Os03g53650 | 6 | 0.003 | 0.513 |
| **Carbohydrate metabolism and energy production** | glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative, expressed | GLGS1\_ORYSJ | LOC\_Os09g12660 | 4 | Unique Infested | Unique Infested |
| NADP-dependent malic enzyme, chloroplastic | MAOC\_ORYSJ | LOC\_Os01g09320 | 3 | Unique Infested | Unique Infested |
| UTP--glucose-1-phosphate uridylyltransferase | Q6ZGL5\_ORYSJ | LOC\_Os02g02560 | 5 | Unique Infested | Unique Infested |
| probable 6-phosphogluconolactonase 4, chloroplastic | B9G4P3\_ORYSJ | LOC\_Os09g35970 | 6 | 0.014 | 1.517 |
| aspartic proteinase | ASPRX\_ORYSJ | LOC\_Os05g04630 | 5 | 0.001 | 1.321 |
| enolase | Q10P35\_ORYSJ | LOC\_Os03g14450 | 13 | 0.000 | 0.852 |
| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | Q5QMK7\_ORYSJ | LOC\_Os01g60190 | 14 | 0.002 | 0.754 |
| NAD-dependent epimerase/dehydratase | Q852A3\_ORYSJ | LOC\_Os03g60740 | 3 | 0.015 | 0.678 |
| UDP-glucose pyrophosphorylase | Q93X08\_ORYSJ | LOC\_Os09g38030 | 16 | 0.024 | 0.637 |
| enolase | ENO\_ORYSJ | LOC\_Os10g08550 | 18 | 0.001 | 0.615 |
| phosphoglycerate kinase, cytosolic | Q6H6C7\_ORYSJ | LOC\_Os02g07260 | 10 | 0.014 | 0.605 |
| NADP-dependent malic enzyme isoform X1 | A0A0P0V7M3\_ORYSJ | LOC\_Os01g52500 | 9 | 0.007 | 0.501 |
| **Protein modification/degradation** | aspartic proteinase nepenthesin-1-like | Q8LNN1\_ORYSJ | LOC\_Os10g39260 | 5 | 0.000 | 2.213 |
| aspartyl protease family protein At5g10770 | Q69QQ2\_ORYSJ | LOC\_Os09g30414 | 3 | 0.000 | 1.713 |
| oryzain alpha chain | ORYA\_ORYSJ | LOC\_Os04g55650 | 4 | 0.002 | 1.340 |
| peptidylprolyl isomerase ROF1-like | Q657L6\_ORYSJ | LOC\_Os01g38229 | 2 | 0.005 | 1.069 |
| probable carboxylesterase 15 | Q8GSJ3\_ORYSJ | LOC\_Os07g06830 | 4 | 0.010 | 0.754 |
| ubiquitin-conjugating enzyme E2 36 | Q8W0I1\_ORYSJ | LOC\_Os01g48280 | 3 | 0.026 | 0.733 |
| putative Calreticulin precursor | CALR\_ORYSJ | LOC\_Os07g14270 | 4 | 0.004 | 0.719 |
| proteasome subunit beta type-2 | PSB2\_ORYSJ | LOC\_Os03g48930 | 4 | 0.004 | 0.663 |
| peptidyl-prolyl cis-trans isomerase | Q6ZH98\_ORYSJ | LOC\_Os02g02890 | 5 | 0.002 | 0.538 |
| proteasome subunit alpha type-5 | PSA5\_ORYSJ | LOC\_Os11g40140 | 2 | 0.000 | 0.526 |
| **Stress response** | chitinase 8 | CHI8\_ORYSJ | LOC\_Os10g39680 | 3 | 0.003 | 4.267 |
| pathogenesis-related protein 1 | Q6YT69\_ORYSJ | LOC\_Os07g03730 | 3 | 0.000 | 3.623 |
| pathogenesis-related maize seed protein | Q8W084\_ORYSJ | LOC\_Os01g28500 | 3 | 0.013 | 2.090 |
| osmotin-like protein | Q2QND6\_ORYSJ | LOC\_Os12g38170 | 5 | 0.004 | 1.524 |
| ricin B-like lectin R40G2 | 40G2\_ORYSJ | LOC\_Os07g48490 | 9 | 0.001 | 1.290 |
| xylanase inhibitor protein 2-like | Q5WMX0\_ORYSJ | LOC\_Os05g15770 | 7 | 0.013 | 1.107 |
| heat shock cognate 70 kDa protein 2 | Q84TA1\_ORYSJ | LOC\_Os03g60620 | 11 | 0.015 | 0.999 |
| ricin B-like lectin R40G3 | Q9FTY4\_ORYSJ | LOC\_Os01g01450 | 2 | 0.010 | 0.997 |
| chitin elicitor-binding protein-like | CEBIP\_ORYSJ | LOC\_Os03g04110 | 4 | 0.001 | 0.936 |
| stress-response A/B barrel domain-containing protein UP3 | A0A0P0X8Q0\_ORYSJ | LOC\_Os07g41820 | 2 | 0.001 | 0.926 |
| osmotin-like protein | Q2QND8\_ORYSJ | LOC\_Os12g38150 | 3 | 0.037 | 0.741 |
| chalcone--flavonone isomerase | CFI\_ORYSJ | LOC\_Os03g60509 | 6 | 0.050 | 0.652 |
| heat shock cognate 70 kDa protein 2 | Q10NA9\_ORYSJ | LOC\_Os03g16860 | 14 | 0.050 | 0.623 |
| **Translation** | putative RNase S-like protein precursor | Q69JF3\_ORYSJ | LOC\_Os09g36700 | 5 | 0.000 | 2.267 |
| ribonuclease 3 | Q69JX7\_ORYSJ | LOC\_Os09g36680 | 11 | 0.001 | 1.669 |
| glycine-rich RNA binding protein | A0A0P0W1Y6\_ORYSJ | LOC\_Os03g46770 | 6 | 0.010 | 1.014 |
| glycine-rich RNA binding protein | Q2QLR2\_ORYSJ | LOC\_Os12g43600 | 5 | 0.004 | 0.857 |
| ribosome-recycling factor, chloroplastic | RRFC\_ORYSJ | LOC\_Os07g38300 | 4 | 0.030 | 0.636 |
| elongation factor 1-delta 1 | EF1D1\_ORYSJ | LOC\_Os07g42300 | 4 | 0.000 | 0.566 |
| ADP-ribosylation factor 2 | ARF2\_ORYSJ | LOC\_Os05g41060 | 10 | 0.027 | 0.564 |
| elongation factor 1-delta-like | EF1B\_ORYSJ | LOC\_Os07g46750 | 7 | 0.040 | 0.530 |
| **Lipid metabolism** | lipoxygenase 2.1, chloroplastic | Q2QNN5\_ORYSJ | LOC\_Os12g37260 | 16 | 0.001 | 4.707 |
| non-specific lipid-transfer protein 1 | Q2QYL0\_ORYSJ | LOC\_Os12g02330 | 2 | 0.017 | 2.275 |
| lipid transfer protein | NLT2B\_ORYSJ | LOC\_Os12g02310 | 3 | 0.035 | 1.253 |
| 3-ketoacyl-CoA thiolase 2, peroxisomal | Q94LR9\_ORYSJ | LOC\_Os10g31950 | 3 | 0.015 | 1.003 |
| probable plastid-lipid-associated protein 6, chloroplastic | Q2R1S1\_ORYSJ | LOC\_Os11g38260 | 5 | 0.014 | 0.674 |
| acyl transferase 9 | Q9FTG9\_ORYSJ | LOC\_Os01g42880 | 3 | 0.018 | 0.501 |
| **Photosynthesis** | psbP domain-containing protein 4, chloroplastic | Q2QWM6\_ORYSJ | LOC\_Os12g08830 | 6 | 0.036 | 0.628 |
| ruBisCO large subunit-binding protein subunit beta, chloroplastic | Q6ZFJ9\_ORYSJ | LOC\_Os02g01280 | 5 | 0.014 | 0.544 |
| psbP domain-containing protein 1, chloroplastic | Q2QNI4\_ORYSJ | LOC\_Os12g37710 | 2 | 0.045 | 0.517 |
| **Protease inhibitor** | putative Bowman Birk trypsin inhibitor | A5HEI2\_ORYSJ | LOC\_Os01g03340 | 4 | 0.026 | 3.248 |
| putative Bowman Birk trypsin inhibitor | Q0JR29\_ORYSJ | LOC\_Os01g03310 | 3 | 0.001 | 3.024 |
| **Hormone-related** | allene oxide cyclase, chloroplastic | AOC\_ORYSJ | LOC\_Os03g32314 | 3 | 0.002 | 1.260 |
| putative Tryptophan synthase beta chain | Q67VM2\_ORYSJ | LOC\_Os06g42560 | 4 | 0.003 | 1.032 |
| **Amino acid metabolism** | aspartate aminotransferase, cytoplasmic | AATC\_ORYSJ | LOC\_Os01g55540 | 2 | 0.010 | 0.846 |
| peptide methionine sulfoxide reductase A4, chloroplastic | MSRA4\_ORYSJ | LOC\_Os10g41400 | 4 | 0.006 | 0.811 |
| **Others** | temperature-induced lipocalin-1 | Q6K623\_ORYSJ | LOC\_Os02g39930 | 4 | 0.000 | 1.911 |
| legumin-like protein | Q65XA1\_ORYSJ | LOC\_Os05g02520 | 6 | 0.003 | 0.798 |
| mannose/glucose-specific lectin | Q306J3\_ORYSJ | LOC\_Os12g14440 | 11 | 0.000 | 4.968 |
| transaldolase 2 | Q5JK10\_ORYSJ | LOC\_Os01g70170 | 12 | 0.003 | 1.273 |
| PLAT domain-containing protein 3 | Q6ZGP5\_ORYSJ | LOC\_Os02g51710 | 4 | 0.009 | 1.261 |
| PLAT domain-containing protein 3 | Q7XRE7\_ORYSJ | LOC\_Os04g38390 | 4 | 0.002 | 1.185 |
| putative F8K7.10 protein | Q6AVR6\_ORYSJ | LOC\_Os03g62370 | 4 | 0.001 | 1.179 |
| protein C2-DOMAIN ABA-RELATED 8-like | Q69RN2\_ORYSJ | LOC\_Os07g31720 | 3 | 0.009 | 0.907 |
| luminal-binding protein 2 | BIP1\_ORYSJ | LOC\_Os02g02410 | 7 | 0.002 | 0.617 |
| putative PrMC3 | A0A0P0WTX9\_ORYSJ | LOC\_Os06g11135 | 4 | 0.026 | 0.613 |
| heme-binding protein 2 | Q9LD82\_ORYSJ | LOC\_Os01g11230 | 6 | 0.010 | 0.609 |
| 14-3-3-like protein | 14336\_ORYSJ | LOC\_Os03g50290 | 12 | 0.010 | 0.533 |