Suppl. Table S3. Heat-responsive proteins identified in leaves from spinach variety Sp73 revealed by proteomic analysis

| **Accession No. (a)** | **Protein name(b)** | **Abbre. (c)** | **Relative protein abundance(d)** | | |
| --- | --- | --- | --- | --- | --- |
| **24h/0h** | **48h/0h** | **72h/0h** |
|  | **1 Signaling and Membrane and transport（16）** |  |  |  |  |
|  | **1.1 Signaling (1)** |  |  |  |  |
| XP\_021834948.1 | Calnexin homolog | CNX | 1.199±0.023 | 1.685±0.009\* | 2.078±0.078**\*** |
|  | **Membrane and transport--Ion and metabolite transport (6)** |  |  |  |  |
| XP\_021866217.1 | Plasma membrane ATPase 1 | AHA1 | 0.668±0.052**\*** | 0.67±0.044**\*** | 0.956±0.052 |
| XP\_021845145.1 | Plasma membrane ATPase 4 | AHA4 | 0.612±0.018**\*** | 0.543±0.007**\*** | 0.647±0.045**\*** |
| XP\_021838582.1 | V-type proton ATPase subunit E | VHA | 0.641±0.063**\*** | 0.837±0.008 | 0.676±0.078**\*** |
| XP\_006833313.1# | V-type proton ATPase subunit B 2 | VHA | 0.56±0.0743\* | 0.47±0.1511\* | 0.73±0.037 |
| KNA24871.1# | V-type proton ATPase subunit B 2☆ | VHA | 1.89±0.4425\* | 2.4±0.7808\* | 1.23±0.2007 |
| XP\_021854515.1 | ABC transporter C family member 15 | ABC-C△ | 3.198±0.962**\*** | 22.15±3.548**\*** | 18.483±1.082**\*** |
|  | **1.2 Membrane and transport--Ran GTPase-mediated nuclear trafficking (2)** |  |  |  |  |
| XP\_021856406.1 | Rho GTPase 1-like | Rho GTPase | 2.185±1.197**\*** | 1.877±0.181**\*** | 1.913±0.069**\*** |
| PIN12430.1 | GTP-binding protein | G-protein | 0.476±0.259**\*** | 0.363±0.136**\*** | 0.391±0.236**\*** |
|  | **Membrane and transport--Other membrane and transport-related proteins (7)** |  |  |  |  |
| XP\_021838660.1 | Remorin | REM | 0.645±0.015**\*** | 0.647±0.027**\*** | 0.64±0.071**\*** |
| XP\_021842374.1 | Remorin-like isoform X1 | REM | 1.433±0.579**\*** | 3.145±0.443**\*** | 2.731±0.141**\*** |
| XP\_021837681.1 | Annexin D5-like | ANN | 1.171±0.166 | 1.502±0.101**\*** | 1.732±0.131**\*** |
| XP\_021846939.1 | Plasma membrane-associated cation-binding protein 1-like | PCAP1 | 0.555±0.037**\*** | 0.558±0.025**\*** | 0.488±0.085**\*** |
| XP\_021843426.1 | Mitochondrial proton/calcium exchanger protein | PCEP△ | 1.118±0.071 | 1.305±0.110 | 1.497±0.22**\*** |
| XP\_021867585.1 | Protein TIC 62, chloroplastic isoform X1 | TIC62 | 0.78±0.029\* | 0.692±0.029\* | 0.641±0.012\* |
| XP\_021845588.1 | Patellin-3-like | PATL3 | 0.718±0.026**\*** | 0.542±0.041**\*** | 0.752±0.012**\*** |
|  | **2 ROS scavenging（15）** |  |  |  |  |
| XP\_021848666.1 | Superoxide dismutase [Fe], chloroplastic-like isoform X2 | FeSOD | 4.826±0.246\* | 4.826±0.246\* | 5.925±1.025\* |
| KNA07766.1# | Superoxide dismutase [Fe] ☆ | FeSOD | 1.69±0.2833\* | 3.97±1.0875\* | 4.24±0.7567\* |
| KNA07394.1# | Superoxide dismutase [Mn] ☆ | Mn SOD | 0.92±0.327 | 2.02±0.3469\* | 1.01±0.2947 |
| XP\_021850716.1 | L-ascorbate peroxidase | APX 3 | 1.233±1.306 | 24.109±4.939\* | 2.059±1.606 |
| KNA16919.1# | Ascorbate peroxidase☆ | APX | 1.55±0.0496 | 1.72±0.2584\* | 1.97±0.4016\* |
| KNA06206.1# | Thioredoxin-like protein CDSP32☆ | Trx-lp | 0.5±0.1175\* | 0.37±0.1125\* | 0.4±0.137\* |
| XP\_021845231.1 | Catalase | CAT | 1.128±0.055 | 1.351±0.088 | 1.682±0.085\* |
| XP\_021858785.1 | Peroxidase 3-like | POD3 | 0.532±0.075\* | 0.521±0.060\* | 0.598±0.072\* |
| XP\_021835551.1 | Peroxidase 27-like | POD27 | 2.376±1.569\* | 1.230±0.159 | 1.833±0.275\* |
| XP\_021856126.1 | Glutathione S-transferase-like | GST | 6.737±1.424\* | 14.397±2.682**\*** | 14.793±3.390\* |
| XP\_021866953.1 | Glutathione S-transferase parC | GST | 2.529±0.618\* | 5.044±0.855\* | 5.521±0.983\* |
| XP\_021840069.1 | Glutathione S-transferase U17-like | GST | 1.265±0.158 | 2.115±0.030\* | 1.777±0.097\* |
| KNA21418.1# | Glutathione S-transferase☆ | GST | 1.97±0.6952\* | 3.4±1.0183\* | 3.25±1.8588\* |
| KNA21418.1# | Glutathione S-transferase☆ | GST | 2.37±0.1951\* | 4.86±1.1884\* | 5.06±0.9615\* |
| KNA20674.1# | Monodehydroascorbate reductase☆ | MDHAR | 0.4±0.1557\* | 0.39±0.1991\* | 0.39±0.2645\* |
|  | **3 Stress defense（17）** |  |  |  |  |
| XP\_021855446.1 | NADPH-dependent aldo-keto reductase | AKR | 1.489±0.117 | 3.778±0.355\* | 3.771±0.070\* |
| XP\_021865287.1 | Aldo-keto reductase 2 | AKR2 | 0.880±0.049 | 4.962±0.613\* | 2.616±0.554\* |
| KNA12253.1# | Aldo-keto reductases 2 ☆ | AKR2 | 1.15±0.1653 | 2.47±0.7444\* | 1.77±0.2198\* |
| KNA04779.1# | Ferritin-3☆ | FER3 | 0.6±0.0383\* | 0.54±0.0879\* | 0.19±0.1719\* |
| XP\_021866075.1 | Ferritin-4 | FER4 | 0.634±0.044**\*** | 0.416±0.029**\*** | 0.431±0.019**\*** |
| XP\_021842944.1 | Polyphenol oxidase | PPO | 3.082±0.371**\*** | 1.924±0.196**\*** | 2.122±0.227**\*** |
| KNA18659.1# | Polyphenol oxidase ☆ | PPO | 4.34±2.7005\* | 2.73±0.8366\* | 2.7±1.214\* |
| XP\_021843006.1 | Jasmonate-induced protein homolog | JIP | 1.938±0.239**\*** | 2.122±0.290**\*** | 2.315±0.651**\*** |
| XP\_021843386.1 | Jasmonate-induced protein homolog | JIP | 1.016±0.051 | 0.778±0.036 | 0.555±0.050**\*** |
| XP\_021848701.1 | Jasmonate-induced protein homolog | JIP | 2.143±0.096**\*** | 2.476±0.280**\*** | 1.399±0.092 |
| KNA21726.1# | Jasmonate-induced protein homolog ☆ | JIP | 2.49±0.3033\* | 3.25±0.9722\* | 2.3±0.6266\* |
| KNA21726.1# | Jasmonate-induced protein homolog ☆ | JIP | 2.7±0.5083\* | 2.67±0.5748\* | 2.08±0.6581\* |
| XP\_021851175.1 | Mannose/glucose-specific lectin-like | MGSL△ | 1.303±0.224 | 0.696±0.064**\*** | 0.399±0.142**\*** |
| XP\_021849180.1 | Mannose/glucose-specific lectin-like | MGSL△ | 5.225±2.303**\*** | 3.741±2.604**\*** | 4.090±1.655**\*** |
| XP\_021843280.1 | Glucan endo-1,3-beta-glucosidase-like | Glu-ase△ | 0.857±0.071 | 0.601±0.014\* | 1.176±0.069 |
| XP\_021843281.1 | Glucan endo-1,3-beta-glucosidase-like | Glu-ase△ | 0.248±0.111\* | 0.164±0.118\* | 0.216±0.086\* |
| XP\_021864256.1 | Glucan endo-1,3-beta-glucosidase A6 | Glu-ase△ | 0.438±0.072\* | 0.265±0.023\* | 0.32±0.017\* |
|  | **4 Ethylene synthesis pathway（3）** |  |  |  |  |
| XP\_021865012.1 | 1-aminocyclopropane-1-carboxylate oxidase 4-like | ACO | 0.293±0.342\* | 0.165±0.016\* | 0.19±0.111\* |
| XP\_021837634.1 | 1-aminocyclopropane-1-carboxylate oxidase-like | ACO | 0.284±0.108**\*** | 0.199±0.04\* | 0.161±0.054\* |
| KNA04023.1# | 1-aminocyclopropane-1-carboxylate oxidase-like☆ | ACO | 0.52±0.1147\* | 0.48±0.0348\* | 0.48±0.0885\* |
|  | **5 Photosynthesis (43)** |  |  |  |  |
|  | **5.1 Photosynthetic electron transfer chain (13)** |  |  |  |  |
|  | **Chlorophyll a/b binding protein** |  |  |  |  |
| CB23\_ORYSI # | Chloroplastic chlorophyll a-b binding protein | CAB | 0.38±0.1235\* | 0.3±0.1622\* | 0.4±0.1247\* |
| BAA24493.1# | Chlorophyll a-b binding protein of LHCII type 1 | CAB | 0.39±0.1625\* | 0.28±0.0736\* | 0.38±0.2448\* |
| KNA08160.1# | Chloroplastic chlorophyll a-b binding protein 5☆ | CAB5 | 0.22±0.2091\* | 0.28±0.2779\* | 0.21±0.2324\* |
| CDP05852.1# | Chloroplastic chlorophyll a-b binding protein 13☆ | CAB13 | 0.19±0.1971\* | 0.2±0.1969\* | 0.19±0.1616\* |
| XP\_021854771.1 | Chlorophyll a-b binding protein CP24 | CP24 | 0.472±0.100\* | 0.494±0.036\* | 0.409±0.04\* |
| XP\_021835308.1 | Chlorophyll a-b binding protein CP29.1 | CP29.1 | 0.569±0.067 | 0.439±0.030\* | 0.533±0.047 |
|  | **PSII oxygen-evolving complex protein** |  |  |  |  |
| KNA05109.1# | Chloroplastic psbP domain-containing protein 6☆ | PsbP | 0.93±0.1461 | 1.96±0.3581\* | 1.24±0.206 |
| XP\_021850205.1 | PsbP domain-containing protein 3 | PsbP3 | 0.411±0.034 | 0.352±0.035 | 0.27±0.032\* |
| P12302.1# | Oxygen-evolving enhancer protein 2 | OEE2 | 0.52±0.0192\* | 0.15±0.1275\* | 0.3±0.13\* |
| XP\_021843617.1 | Oxygen-evolving enhancer protein 2 | OEE2 | 0.682±0.123 | 0.729±0.055 | 0.52±0.139\* |
| XP\_021850099.1 | Oxygen-evolving enhancer protein 3 | OEE3 | 0.453±0.041 | 0.937±0.072 | 0.46±0.036\* |
|  | **PSII assembly and/or stability** |  |  |  |  |
| NP\_054929.1 | Photosystem II 44 kDa protein | PSII P△ | 0.456±0.030\* | 0.431±0.024\* | 0.49±0.029\* |
| KNA22712.1# | Photosystem II stability/assembly factor HCF136☆ | HCF136 | 0.33±0.0804\* | 0.24±0.0168\* | 0.33±0.0575\* |
|  | **5.2 Calvin cycle (23)** |  |  |  |  |
| XP\_021860182.1 | Carbonic anhydrase | CA | 7.056±9.795\* | 1.188±0.056 | 1.121±0.047 |
| P16016.2 # | Carbonic anhydrase | CA | 0.20±0.1812\* | 0.24±0.2091\* | 0.27±0.2412\* |
| P16016.2# | Carbonic anhydrase | CA | 3.37±0.6859\* | 3.26±1.2824\* | 1.88±0.3234\* |
| KNA02995.1# | Ribulose bisphosphate carboxylase /oxygenase activase ☆ | RCA | 1.28±0.0737 | 0.97±0.0671 | 0.43±0.1602\* |
| XP\_021835474.1 | Ribulose bisphosphate carboxylase/oxygenase activase | RCA | 0.812±0.034 | 0.565±0.009\* | 0.325±0.058\* |
| XP\_021864876.1 | RuBisCO large subunit-binding protein subunit alpha | RBPα | 19.183±32.495\* | 5.547±1.331\* | 5.497±1.178\* |
| XP\_021862888.1 | RuBisCO large subunit-binding protein subunit beta | RBPβ | 3.756±4.673\* | 1.81±0.098\* | 1.872±0.102\* |
| KNA12027.1# | RuBisCO large subunit-binding protein subunit beta☆ | RBPβ | 1.34±0.1202 | 1.17±0.4241 | 1.87±0.4322\* |
| XP\_021854666.1 | RuBisCO large subunit-binding protein subunit beta | RBPβ | 22.011±39.271\* | 3.923±0.618**\*** | 3.695±0.787\* |
| AEM04561.1# | Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | RubisCO LSU | 0.09±0.1637\* | 0.16±0.2876\* | 0.12±0.2097\* |
| CAB10739.2# | Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | RubisCO LSU | 0±0 | 0.19±0.3314\* | 0.15±0.2668\* |
| AFP20630.1 # | Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | RubisCO LSU | 1.67±0.1353\* | 1.74±0.1337\* | 2.18±0.2599\* |
| Q9XQJ6.1# | Ribulose bisphosphate carboxylase large chain | RubisCO LSU | 1.77±0.2285\* | 1.79±0.2693\* | 1.51±0.0249 |
| KNA25347.1# | Phosphoglycerate kinase ☆ | PGK | 5.88±2.2825\* | 10.06±5.1545\* | 7.15±1.2103\* |
| KNA25347.1# | Phosphoglycerate kinase ☆ | PGK | 0.46±0.1914\* | 0.27±0.1614\* | 0.51±0.1826\* |
| XP\_021865698.1 | Phosphoglycerate kinase 3 | PGK3 | 0.943±0.12 | 2.254±0.317\* | 2.08±0.254\* |
| KNA15190.1# | Glyceraldehyde-3-phosphate dehydrogenase A ☆ | GAPDH-A | 1.11±0.2415 | 2.03±0.2604\* | 1.03±0.2803 |
| P12860.1 # | Glyceraldehyde-3-phosphate dehydrogenase B | GAPDH-B | 0.24±0.3069\* | 0.29±0.2678\* | 0.14±0.2564\* |
| KNA12216.1# | Fructose-bisphosphate aldolase 1☆ | FBA | 1.78±0.3003\* | 0.59±0.0156\* | 0.94±0.3313 |
| KNA05413.1# | Fructose-bisphosphate aldolase 1☆ | FBA | 0.49±0.1194\* | 0.43±0.1153\* | 0.46±0.1497\* |
| KNA17728.1# | Transketolase☆ | TK | 0.73±0.0557 | 0.46±0.1496\* | 0.61±0.0383\* |
| KNA17728.1# | Transketolase☆ | TK | 0.45±0.0923\* | 0.44±0.0572\* | 0.52±0.0523\* |
| Q94KU2.1# | 6-phosphogluconate dehydrogenase, decarboxylating | 6PGDH | 0.35±0.1119\* | 0.39±0.1809\* | 0.52±0.1483\* |
|  | **5.3 Photosynthetic other proteins (7)** |  |  |  |  |
|  | **Chlorophyll biosynthesis** |  |  |  |  |
| XP\_021846014.1 | Magnesium-chelatase subunit ChlI | MgCh | 0.15±0.021\* | 0.185±0.009\* | 0.237±0.018\* |
|  | **Chlorophyll degradation** |  |  |  |  |
| XP\_021848289.1 | Pheophorbide a oxygenase | PaO | 1.782±0.074\* | 2.131±0.087\* | 2.906±0.427\* |
|  | **Xanthophyll cycle** |  |  |  |  |
| XP\_021837806.1 | Zeaxanthin epoxidase | ZE | 0.599±0.014\* | 0.477±0.028\* | 0.47±0.004\* |
| Q9SM43.2# | Violaxanthin de-epoxidase | VDE | 0.27±0.2405\* | 0.24±0.2246\* | 0.22±0.248\* |
|  | **Carotenoid biosynthesis** |  |  |  |  |
| PSS29531.1 | Zeta-carotene desaturase | ZDS | 1.52±0.302 | 1.664±0.311 | 3.261±2.16**\*** |
|  | **Thylakoid lumenal protein** |  |  |  |  |
| XP\_021856837.1 | Thylakoid lumenal 16.5 kDa protein | TL16.5△ | 0.42±0.022\* | 0.562±0.028 | 0.396±0.03\* |
| XP\_021855928.1 | Thylakoid lumenal protein TL20.3, chloroplastic isoform X1 | TL20.3△ | 0.63±0.032 | 0.647±0.428 | 0.454±0.073\* |
|  | **6 Carbohydrate and energy metabolism（26）** |  |  |  |  |
|  | **Glycolysis（6）** |  |  |  |  |
| XP\_021847260.1 | Fructose-bisphosphate aldolase | FBA | 0.925±0.072 | 2.898±0.204\* | 2.497±0.183\* |
| KNA08949.1# | Fructose-bisphosphate aldolase☆ | FBA | 1.56±0.0574 | 2.02±0.5767\* | 1.92±0.4023\* |
| KNA11348.1# | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase☆ | PGAM-i | 0.59±0.0875\* | 0.38±0.2498\* | 0.73±0.0648 |
| XP\_021857227.1 | Enolase | ENO | 0.963±0.077 | 2.347±0.204\* | 1.603±0.255\* |
| XP\_021865530.1 | Pyruvate kinase 1 | PK1 | 5.343±0.087\* | 1.62±0.038\* | 1.581±0.056\* |
| XP\_021849973.1 | Phosphoenolpyruvate carboxylase 2 | PEPC 2 | 12.664±22.596\* | 1.170±0.046 | 1.130±0.044 |
|  | **TCA cycle（2）** |  |  |  |  |
| XP\_021843297.1 | Citrate synthase | CS | 1.044±0.022 | 1.411±0.151\* | 1.446±0.147\* |
| KNA20426.1# | Mitochondrial succinate dehydrogenase [ubiquinone] flavoprotein subunit ☆ | SDHS△ | 1.27±0.1975 | 1.21±0.3295 | 1.55±0.0317 |
|  | **Glyoxylic cycle（1）** |  |  |  |  |
| XP\_021866315.1 | Malate synthase | MS | 1.911±0.188\* | 1.843±0.043\* | 2.344±0.199\* |
|  | **Other Sugar metabolism (13)** |  |  |  |  |
| KNA15981.1# | Fructokinase-6☆ | FK-6△ | 0.93±0.1344 | 0.59±0.0768\* | 0.48±0.1283\* |
| XP\_021859174.1 | Beta-glucosidase 13-like | BGLU | 3.864±0.811\* | 6.605±0.686\* | 6.136±0.873\* |
| XP\_021838803.1 | Beta-galactosidase | β- GAL | 2.313±0.237\* | 1.633±0.279\* | 3.157±0.369\* |
| KNA07682.1# | Xylose isomerase ☆ | XI | 1.62±0.066\* | 1.68±0.2607\* | 1.8±0.3756\* |
| XP\_021842301.1 | Sorbitol dehydrogenase | SDH | 0.235±0.092\* | 0.411±0.093\* | 0.411±0.027\* |
| KNA11613.1# | Sorbitol dehydrogenase ☆ | SDH | 0.25±0.2277\* | 0.34±0.3184\* | 0.18±0.158\* |
| XP\_021836757.1 | Mannitol dehydrogenase | MDH | 2.152±0.506\* | 3.552±0.12\* | 3.885±0.241\* |
| XP\_021844627.1 | Alpha-amylase 3 | AMY3 | 0.553±0.071\* | 0.576±0.011\* | 0.305±0.039\* |
| XP\_021837616.1 | Starch synthase 3 | StSy3△ | 2.089±1.226\* | 1.599±0.208\* | 1.616±0.178\* |
| XP\_021856044.1 | UTP--glucose-1-phosphate uridylyltransferase | UGP | 21.962±36.129\* | 1.354±2.330\* | 1.447±0.082\* |
| XP\_021842618.1 | UDP-glycosyltransferase 74G1-like | UGT | 1.544±0.407\* | 4.899±1.402\* | 4.924±1.849\* |
| XP\_021839259.1 | Crocetin glucosyltransferase | GT | 1.035±0.033 | 1.572±0.17\* | 1.348±0.094\* |
| XP\_021853290.1 | Beta-D-xylosidase 5 | BXL5 | 3.2±0.682\* | 4.05±0.796\* | 4.193±0.735\* |
|  | **Carbohydrate and energy metabolism--ATP synthesis (4)** |  |  |  |  |
| P05435.2# | ATP synthase gamma chain | ATPase-γ | 0.41±0.3608\* | 0.31±0.2878\* | 0.07±0.1358\* |
| Q4PLI6.1# | ATP synthase subunit beta | ATPase-β | 2.41±0.8822\* | 15.59±8.8597\* | 7.27±5.4912\* |
| KNA26060.1# | ATP synthase CF1 alpha subunit (plastid) ☆ | ATP CF1α | 0.02±0.0431\* | 0±0 | 0.09±0.0859\* |
| NP\_054943.1# | ATP synthase CF1 beta subunit | ATP CF1β | 0.35±0.0493\* | 0.35±0.0506\* | 0.32±0.1156\* |
|  | **7 DNA and chromatin assembly（2）** |  |  |  |  |
|  | **DNA repair（1）** |  |  |  |  |
| EOY02839.1 | DNA double-strand break repair rad50 ATPase | DSBR | 2.377±1.415**\*** | 12.385±7.443**\*** | 11.366±6.872**\*** |
|  | **Chromatin assembly（1）** |  |  |  |  |
| XP\_021843257.1 | HMG-Y-related protein A-like | HMG | 2.518±0.789**\*** | 14.375±2.98**\*** | 13.058±2.969**\*** |
|  | **8 Transcription related（7）** |  |  |  |  |
|  | **Transcription--transcriptional regulation (4)** |  |  |  |  |
| XP\_021837354.1 | RNA-binding protein CP29B | RBP | 0.215±0.019**\*** | 0.313±0.076 | 0.247±0.071**\*** |
| XP\_021863490.1 | RNA-binding protein FUS-like isoform X1 | RBP | 1.652±0.479**\*** | 5.547±1.094**\*** | 3.957±1.250**\*** |
| KNA17125.1 # | Glycine-rich RNA-binding protein 7-like ☆ | RBP | 3.95±0.6979\* | 4.4±1.5333\* | 4.95±3.324\* |
| XP\_021845829.1 | Cold shock protein CS66-like | CSP | 0.700±0.024**\*** | 0.892±0.078 | 0.319±0.042**\*** |
|  | **Transcription--RNA processing (1)** |  |  |  |  |
| XP\_021835826.1 | Nuclear poly(A) polymerase 1 | PAP1 | 29.941±50.196**\*** | 73.152±25.548**\*** | 68.574±24.844**\*** |
|  | **Transcription--RNA cleaveage(2)** |  |  |  |  |
| XP\_021842969.1 | Ribonuclease 1-like | RNS1 | 0.401±0.042\* | 0.323±0.055\* | 0.307±0.062\* |
| XP\_021842659.1 | Cleavage and polyadenylation specificity factor subunit 6 | CPSF6 | 13.494±14.221**\*** | 11.096±10.156**\*** | 15.313±8.3**\*** |
|  | **9 Protein synthesis and fate (78)** |  |  |  |  |
|  | **9.1 Ribosome assembly (17）** |  |  |  |  |
| XP\_021835218.1 | 30S ribosomal protein 2 | RP2 | 0.452±0.017**\*** | 0.679±9.914 | 0.493±0.034**\*** |
| P29344.1# | 30S ribosomal protein S1 | RPS1 | 0.56±0.0954\* | 0.52±0.1776\* | 0.54±0.1753\* |
| XP\_021854510.1 | 30S ribosomal protein S1 | RPS1 | 0.618±0.089\* | 0.644±0.071\* | 0.425±0.117**\*** |
| XP\_021861431.1 | 30S ribosomal protein S5 | RPS5 | 0.563±0.046\* | 0.587±0.038\* | 0.452±0.106\* |
| XP\_021835051.1 | 40S ribosomal protein S6-1 | RPS6-1 | 0.655±0.03 | 0.789±0.008 | 0.545±0.048\* |
| XP\_021850506.1 | 50S ribosomal protein L3 | RPL3 | 0.552±0.044\* | 0.669±0.031 | 0.42±0.044\* |
| XP\_021850402.1 | 50S ribosomal protein L5 | RPL5 | 0.591±0.068 | 0.675±0.019 | 0.409±0.029\* |
| XP\_021848290.1 | 50S ribosomal protein L9 | RPL9 | 0.511±0.073 | 0.577±0.011\* | 0.27±0.072\* |
| XP\_021865443.1 | 50S ribosomal protein L10 | RPL10 | 0.596±0.026 | 0.665±0.031 | 0.425±0.017\* |
| XP\_021856730.1 | 50S ribosomal protein L11 | RPL11 | 0.517±0.026 | 0.700±0.055 | 0.427±0.057\* |
| XP\_021842736.1 | 50S ribosomal protein L12 | RPL12 | 0.508±0.058\* | 0.764±0.055 | 0.296±0.05\* |
| XP\_021859407.1 | 50S ribosomal protein L15 | RPL15 | 0.609±0.046 | 0.663±0.025 | 0.518±0.005\* |
| XP\_021841114.1 | Ribosome-inactivating protein PD-L3/PD-L4-like | RIPs | 2.277±0.227\* | 3.143±0.183\* | 2.559±0.047\* |
| XP\_021841867.1 | Antiviral protein MAP-like | AP△ | 0.208±0.046\* | 0.225±0.015\* | 0.297±0.018\* |
| XP\_021841706.1 | Antiviral protein I-like | AP△ | 1.786±0.167\* | 2.427±0.391\* | 1.960±0.166\* |
| XP\_021858263.1 | Ribosome-binding factor PSRP1 | RPF1 | 0.498±0.041\* | 0.618±0.062 | 0.383±0.134\* |
| XP\_021859462.1 | Ribosome-recycling factor | RRF | 0.59±0.035\* | 0.747±0.074 | 0.557±0.041\* |
|  | **9.2 Protein synthesis（8）** |  |  |  |  |
| KNA07603.1 # | 28 kDa ribonucleoprotein☆ | 28RNP | 0.34±0.3188\* | 0.47±0.1587\* | 0.23±0.2084\* |
| KNA07603.1# | 28 kDa ribonucleoprotein☆ | 28RNP | 0.5±0.0756\* | 0.51±0.1121\* | 0.41±0.1383\* |
| XP\_021852447.1 | 33 kDa ribonucleoprotein | 33RNP | 0.476±0.046**\*** | 0.602±0.027 | 0.393±0.021**\*** |
| EOY30721.1 | Elongation factor Ts isoform 2 | EF-Ts | 0.683±0.01 | 0.659±0.004**\*** | 0.565±0.047\* |
| KNA13787.1# | Elongation factor TuA ☆ | EF-Tu | 0.48±0.2364\* | 0.37±0.2229\* | 0.24±0.1211\* |
| XP\_021855924.1 | Elongation factor G-2 | EF-G | 0.742±0.054 | 0.603±0.054\* | 0.597±0.031\* |
| XP\_021852251.1 | Alanine--tRNA ligase | AlaRS | 0.631±0.055 | 0.517±0.058\* | 0.509±0.034\* |
| KNA06975.1# | Obg-like ATPase 1☆ | OLA1 | 0.14±0.1435\* | 0.19±0.172\* | 0.18±0.1727\* |
|  | **9.3 Protein folding（37）** |  |  |  |  |
| XP\_021857906.1 | Protein disulfide-isomerase | PDI | 1.978±0.276 | 5.041±0.55\* | 4.755±0.855\* |
| KNA24506.1# | Protein disulfide-isomerase ☆ | PDI | 1.72±0.2656\* | 2.36±0.4588\* | 2.29±0.2809\* |
| XP\_021863789.1 | Protein disulfide-isomerase-like | PDI | 1.608±0.131\* | 2.22±0.134\* | 2.063±0.049\* |
| XP\_021851928.1 | protein disulfide isomerase-like 2-3 | PDI | 1.619±0.314 | 2.492±0.232\* | 2.631±0.373\* |
| XP\_021866122.1 | Peptidyl-prolyl cis-trans isomerase CYP19-3 | PPI | 0.221±0.027 | 0.236±0.02\* | 0.184±0.012\* |
| KNA05585.1 # | Peptidyl-prolyl cis-trans isomerase CYP26-2 ☆ | PPI | 0.58±0.1337\* | 0.5±0.1419\* | 0.4±0.049\* |
| Q42434.1# | Luminal-binding protein | BiP | 1.72±0.175\* | 1.13±0.304 | 1.89±0.3428\* |
| XP\_021843141.1 | Luminal-binding protein | BiP | 2.635±0.196 | 5.357±1.154\* | 4.948±0.599\* |
| XP\_021855337.1 | Luminal-binding protein 4-like | BiP | 1.787±0.182 | 2.211±0.417 | 2.502±0.52\* |
| XP\_021845929.1 | Neurofilament medium polypeptide-like | NEFM | 2.179±0.276 | 3.957±0.219\* | 2.227±1.470 |
| XP\_021857548.1 | 20 kDa chaperonin | CPN20 | 1.746±0.976 | 2.284±0.34\* | 2.258±0.249\* |
| XP\_021864904.1 | Chaperonin CPN60 | CPN60 | 0.739±0.099 | 1.716±0.132\* | 1.716±0.059\* |
| XP\_021850292.1 | Chaperone protein ClpB1 | ClpB1 | 10.599±4.531\* | 10.863±4.949\* | 9.145±2.876\* |
| XP\_021838854.1 | Chaperone protein ClpB3 | ClpB3 | 1.817±0.125\* | 2.006±0.086\* | 2.108±0.174\* |
| PSR85306.1 | Protein GrpE like | GrpE | 1.378±0.083 | 2.115±0.030 | 2.365±0.134\* |
| XP\_021848615.1 | Small heat shock protein | sHSP | 13.188±8.049\* | 24.06±5.625\* | 20.393±8.489\* |
| XP\_021845591.1 | 18.3 kDa class I heat shock protein | HSP18.3 | 15.604±14.489\* | 21.481±8.116\* | 22.214±8.466\* |
| XP\_021855806.1 | 17.1 kDa class II heat shock protein-like | HSP17.1 | 9.849±10.077\* | 11.514±5.991\* | 9.43±5.369\* |
| AAB91472.1# | Heat shock 70 protein | HSP70 | 0.93±0.1784 | 1.85±0.2215\* | 2.15±0.1978\* |
| AAB91472.1# | Heat shock 70 protein | HSP70 | 4.62±2.4786\* | 4.52±0.4919\* | 3.99±1.408\* |
| XP\_021848099.1 | Heat shock 70 kDa protein 15-like | HSP 70 | 1.117±0.031 | 1.531±0.135\* | 1.413±0.033\* |
| XP\_021846134.1 | Stromal 70 kDa heat shock-related protein | HSP 70 | 20.839±6.742\* | 18.661±8.549\* | 20.25±7.818\* |
| XP\_021866290.1 | Heat shock cognate 70 kDa protein 2-like | HSP 70 | 7.594±2.214\* | 8.174±1.681\* | 6.79±2.628\* |
| XP\_021865550.1 | Heat shock 70 kDa protein | HSP 70 | 2.973±0.975 | 4.018±0.935\* | 4.61±1.27\* |
| XP\_021858516.1 | Heat shock cognate 70 kDa protein | HSP 70 | 22.054±1.675\* | 27.605±1.59\* | 28.846±2.226\* |
| XP\_021844209.1 | Heat shock protein 83 | HSP83 | 7.589±3.366\* | 10.437±2.149\* | 9.895±5.622\* |
| KQL02373.1# | Heat shock protein 81-1☆ | HSP81-1 | 0.3±0.274\* | 0.37±0.3338\* | 0.27±0.2416\* |
| XP\_021857345.1 | Activator of 90 kDa heat shock protein ATPase homolog 2 | HSP90 | 1.985±0.383 | 1.997±0.303**\*** | 1.919±0.282\* |
| KNA16992.1# | Heat shock protein 90-5 ☆ | HSP90-5 | 1.86±0.3177\* | 2.64±0.4068\* | 2.21±0.4545\* |
| XP\_021860107.1 | Heat shock protein 90-5 | HSP90-5 | 24.296±39.987 | 1.66±0.087 | 1.996±0.196**\*** |
| XP\_021867040.1 | Heat shock protein 90-6 | HSP90-6 | 3.292±2.783\* | 3.705±0.558\* | 4.379±0.834\* |
| EMT11425.1# | Heat shock cognate 70 kDa protein 1 | HSC70-1 | 1.86±0.2872\* | 2.3±0.9071\* | 2.49±0.3992\* |
| CDP09035.1# | Heat shock cognate 70 kDa protein 2☆ | HSC70-2 | 2.5±0.1758\* | 4.55±1.1975\* | 4.31±0.5788\* |
| XP\_021841811.1 | Heat shock cognate protein 80 | HSC80 | 34.046±56.324 | 3.442±0.639\* | 3.278±0.552\* |
| XP\_021855925.1 | Hsp70-Hsp90 organizing protein 2 | HOP2 | 2.304±1.048**\*** | 2.584±1.250**\*** | 2.787±0.438**\*** |
| KNA12705.1# | Hsp70-Hsp90 organizing protein 2☆ | HOP3 | 2.05±0.5205\* | 2.55±0.6602\* | 2.31±0.7112\* |
| XP\_021843089.1 | Protein BOBBER 1 | BOB1 | 1.504±0.356 | 1.989±0.106\* | 1.702±0.17\* |
|  | **9.4 Protein Degradation（16）** |  |  |  |  |
| XP\_021841474.1 | Ion protease homolog 2 | Ion Pase△ | 9.104±12.907 | 23.45±18.42\* | 17.625±10.06\* |
| XP\_021847456.1 | 26S proteasome regulatory subunit 7 | PRS | 1.019±0.104 | 1.605±0.162\* | 1.437±0.031\* |
| AAS01048.1 # | Proteasome 20S beta1 subunit | PSB-20S△ | 2.12±0.355\* | 2.65±0.2154\* | 2.4±0.2583\* |
| XP\_021842711.1 | 26S proteasome non-ATPase regulatory subunit 2 homolog A-like | PARS2 | 0.822±0.142 | 1.097±0.133 | 1.545±0.253\* |
| XP\_021864618.1 | 26S proteasome non-ATPase regulatory subunit 8 homolog A | PARS8 | 1.122±0.084 | 1.331±0.054**\*** | 1.207±0.068 |
| O24362.1# | Proteasome subunit alpha type-3 | PSBα3 | 1.71±0.133\* | 2.25±0.1336\* | 2.22±0.4082\* |
| O24362.1# | Proteasome subunit alpha type-3 | PSBα3 | 1.69±0.144\* | 1.88±0.3153\* | 1.64±0.0846\* |
| XP\_021842195.1 | proteasome subunit alpha type-5 | PSBα5 | 0.982±0.018 | 1.553±0.093**\*** | 1.424±0.090 |
| XP\_021843794.1 | ATP-dependent zinc metalloprotease FTSH2 | FTSH2 | 0.5±0.088 | 0.579±0.005\* | 0.36±0.052\* |
| KNA17405.1# | ATP-dependent zinc metalloprotease FTSH2☆ | FTSH2 | 0.53±0.0822\* | 0.56±0.0934\* | 0.58±0.0258\* |
| KNA05787.1# | Petal death protein-like☆ | PDP | 0.24±0.2147\* | 0.27±0.2446\* | 0.26±0.3123\* |
| XP\_021845104.1 | Puromycin-sensitive aminopeptidase-like | PSA | 0.781±0.054 | 0.654±0.042\* | 0.649±0.076 |
| XP\_021844772.1 | ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B | Clp P△ | 0.516±0.02\* | 0.472±0.009\* | 0.572±0.023\* |
| XP\_021857685.1 | Subtilisin-like protease SBT5.4 | SBT5.4 | 7.05±1.603\* | 7.086±0.636\* | 6.122±0.7\* |
| XP\_021836534.1 | Ubiquitin-activating enzyme E1 1-like | E1 | 1.685±0.269 | 2.487±0.208 | 2.638±0.266\* |
| XP\_021858284.1 | Cysteine protease RD21B | CP | 0.32±0.095 | 0.284±0.069\* | 0.34±0.108 |
|  | **10 Amino acid metabolism（17）** |  |  |  |  |
| XP\_021837924.1 | 3-dehydroquinate synthase | DHQS | 0.496±0.034\* | 0.703±0.01\* | 0.563±0.105\* |
| XP\_021845465.1 | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase | MHMT | 1.041±0.061 | 0.581±0.061**\*** | 0.509±0.056**\*** |
| XP\_021858044.1 | S-adenosylmethionine synthase 1 | SAM -M | 0.478±0.059**\*** | 0.48±0.047**\*** | 0.522±0.037**\*** |
| XP\_021845773.1 | Methyltransferase DDB\_G0268948 | MT | 2.083±0.283**\*** | 3.362±0.281**\*** | 2.741±0.336**\*** |
| XP\_021860504.1 | Alpha-aminoadipic semialdehyde synthase | AASS | 2.361±0.141**\*** | 1.468±0.15**\*** | 1.777±0.074**\*** |
| XP\_021842540.1 | Ketol-acid reductoisomerase | KARI | 0.707±0.042**\*** | 0.637±0.048**\*** | 0.54±0.06**\*** |
| Q01292.1# | Ketol-acid reductoisomerase | KARI | 0.72±0.0392 | 0.71±0.0494 | 0.38±0.344\* |
| AAF17703.1# | Glutamine synthetase | GS | 0.21±0.1906\* | 0.12±0.1099\* | 0.19±0.2366\* |
| ABL89188.2# | Glutamine synthetase 2 | GS2 | 0.89±0.1891 | 0.49±0.1241\* | 0.87±0.1899 |
| KNA14203.1# | Aspartate-semialdehyde dehydrogenase ☆ | ASADH | 0.19±0.3436\* | 0.22±0.3822\* | 0.17±0.3017\* |
| XP\_021862303.1 | Aspartate aminotransferase | AST | 1.489±0.029**\*** | 3.232±1.214**\*** | 3.266±0.914**\*** |
| CDP06749.1# | 3-isopropylmalate dehydrogenase ☆ | IPMDH | 1.82±0.3271\* | 2.09±0.3472\* | 1.87±0.3985\* |
| XP\_021842724.1 | Tyrosine aminotransferase | GOT | 3.407±1.933**\*** | 4.349±2.123**\*** | 6.043±3.038**\*** |
| KNA10703.1# | Argininosuccinate synthase ☆ | ASS | 0.19±0.3445\* | 0.12±0.2222\* | 0.1±0.1805\* |
| XP\_021864269.1 | Arginase 1 | Arginase-1 | 1.122±0.148 | 1.789±0.115**\*** | 1.412±0.093**\*** |
| KNA16731.1# | Arginase 1☆ | Arginase-1 | 1.19±0.4426 | 1.27±0.1481 | 1.86±0.2391\* |
| KNA10343.1# | Omega-amidase☆ | ω- amidase | 0.9±0.1689 | 0.62±0.0342\* | 0.56±0.0939\* |
|  | **11 Other metabolic (15)** |  |  |  |  |
|  | **Fatty acid metabolism（1）** |  |  |  |  |
| XP\_021849524.1 | Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | ACC α | 0.749±0.095**\*** | 0.573±0.062\* | 0.346±0.069\* |
|  | **Nitrogen metabolism（2）** |  |  |  |  |
| XP\_002866603.1 | Nitronate monooxygenase | NMO | 4.15±2.52\* | 5.148±3.784\* | 5.947±1.466\* |
| XP\_021866794.1 | Ferredoxin--nitrite reductase | Fd-NiR | 0.43±0.094\* | 0.378±0.019\* | 0.298±0.012\* |
|  | **Sulfur metabolism（1）** |  |  |  |  |
| XP\_021857221.1 | ATP sulfurylase 1 | ATPS | 1.665±0.708\* | 5.756±2.814\* | 5.54±3.135\* |
|  | **Lignin synthesis（1）** |  |  |  |  |
| XP\_021842512.1 | Caffeoyl-CoA O-methyltransferase 5 | COMT5 | 1.366±0.207\* | 2.804±0.295\* | 2.248±0.552 |
|  | **Storage protein（2）** |  |  |  |  |
| XP\_021845066.1 | Basic 7S globulin-like | Bg | 0.676±0.078 | 0.739±0.48 | 0.462±0.075\* |
| XP\_021835696.1 | Glutelin type-B 5-like | GLN△ | 1.265±0.099 | 1.354±0.08\* | 1.588±0.196\* |
|  | **Other (8)** |  |  |  |  |
| KNA12569.1# | Methylenetetrahydrofolate reductase 2-like ☆ | MTHFR | 2.98±0.455\* | 2.65±0.6983\* | 2.18±0.3228\* |
| XP\_021855131.1 | REF/SRPP-like protein At1g67360 | REF/SRPP | 8.978±1.148\* | 13.898±2.021\* | 12.844±2.228\* |
| KNA14859.1# | Haloalkane dehalogenase ☆ | HLD | 0.34±0.3187\* | 0.31±0.2891\* | 0.31±0.2796\* |
| KNA12844.1# | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase ☆ | HDS | 1.89±0.1316\* | 2.27±0.9461\* | 2.58±0.3805\* |
| XP\_021842915.1 | 2-methylene-furan-3-one reductase-like | MTFOR△ | 1.043±0.043 | 1.355±0.033**\*** | 1.466±0.119**\*** |
| XP\_021842589.1 | UDP-4-keto-L-rhamnose-reductase RHM1 | RHM | 0.487±0.064\* | 0.528±0.046\* | 0.473±0.005\* |
| XP\_021855793.1 | Golgin subfamily A member 4 | Golga4 | 0.936±0.188 | 0.62±0.038\* | 0.472±0.115\* |
| XP\_021836661.1 | Selenium-binding protein 2-like | SBP1 | 1.103±0.149 | 1.4184±0.110 | 1.597±0.112\* |
|  | **12 Cytoskeleton and Cell cycle (4)** |  |  |  |  |
|  | **Cytoskeleton（2）** |  |  |  |  |
| XP\_021860086.1 | Tubulin alpha-2 chain-like | Tubulin-α | 0.293±0.036\* | 0.563±0.018\* | 0.428±0.116 |
| XP\_021862576.1 | Tubulin alpha-2 chain isoform X1 | Tubulin-α | 0.204±0.056\* | 0.41±0.08\* | 0.145±0.065\* |
|  | **Cell cycle（2）** |  |  |  |  |
| XP\_021863243.1 | Protein P21 | P21 | 1.850±0.380**\*** | 2.313±0.507**\*** | 4.487±0.677**\*** |
| XP\_021863278.1 | Cell division cycle protein 48 homolog | CDC48 | 1.717±0.341 | 3.068±0.516\* | 2.534±0.709 |
|  | **13 Function unknown（14）** |  |  |  |  |
| XP\_021859565.1 | Osteocalcin 2 | - | 0.425±0.045\* | 0.766±0.041 | 0.525±0.037 |
| XP\_021862039.1 | FK506-binding protein 5 | - | 0.717±0.09 | 0.752±1.954 | 0.519±0.125\* |
| XP\_021855769.1 | Uncharacterized protein LOC110795099 isoform X1 | - | 0.591±0.134 | 0.742±0.092 | 0.468±0.101\* |
| XP\_021865075.1 | Cilia- and flagella-associated protein 251-like | - | 0.526±0.123 | 0.279±0.102\* | 0.133±0.08\* |
| XP\_021859434.1 | Uncharacterized protein LOC110798553 | - | 0.428±0.020**\*** | 0.378±0.058**\*** | 0.352±0.042**\*** |
| XP\_021838103.1 | Uncharacterized protein LOC110777824 | - | 0.318±0.044\* | 0.252±0.648\* | 0.189±0.057\* |
| XP\_021858729.1 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic | - | 22.636±36.055\* | 2.198±0.207\* | 2.718±0.344**\*** |
| XP\_021863188.1 | Protein seele | - | 1.148±0.99 | 3.37±0.797\* | 1.706±0.042 |
| XP\_010678098.1# | NAD\_binding\_10 domain-containing protein ☆ | - | 1.16±0.1561 | 1.71±0.1539\* | 2.01±0.6858\* |
| XP\_021846851.1 | Uncharacterized protein LOC110786609 | - | 51.171±43.436\* | 52.35±37.148\* | 55.954±30.046\* |
| XP\_021858578.1 | Uncharacterized protein LOC110797770 | - | 3.740±0.450**\*** | 4.638±0.672**\*** | 3.902±0.535**\*** |
| XP\_021858556.1 | Uncharacterized protein LOC110797749 | - | 2.700±0.185**\*** | 3.829±0.203**\*** | 3.022±0.204**\*** |
| XP\_021837930.1 | Uncharacterized protein LOC110777646 | - | 1.398±0.227 | 1.594±0.209\* | 1.463±0.235\* |
| KNA12985.1# | Unknown protein☆ | - | 2.13±0.5437\* | 2.74±0.7077\* | 1.84±0.307\* |

a Database accession numbers marked with a pound sign (#) from NCBInr identified by 2DE-based analysis, the other database accession numbers from NCBInr identified by iTRAQ-based analysis.

b The names and functional categories of the proteins identified by proteomics analysis. Protein names marked with a pentagram (☆) have been edited by us according to functional domain annotations from NCBI non-redundant protein database.

c The abbreviations for the protein names. The abbreviations marked with a triangle (△) are defined by us.

d Relative protein abundances under 24 HHT, 48 HHT, and 72 HHT compared with control condition, respectively. The ratios were presented as means ± standard deviation. The asterisks indicate significant differences (p < 0.05).