**Supplementary Table S1.** Anthocyanins determined in strawberry samples by LC-DAD-ESI-MS/MS analysis, including peak number, retention time (RT), precursor and product ions, their tentative identification and abbreviation.

| Peak | RT (min) | Precursor ion [M-H]^+ | Product ion | Tentative identification | Abbreviation |
|------|----------|-----------------------|-------------|--------------------------|--------------|
| 1    | 11.2     | 449                   | 287         | cyanidin 3-O-glucoside   | cya 3-O-glc |
| 2    | 12.8     | 433                   | 271         | pelargonidin 3-O-glucoside | pel 3-O-glc |
| 3    | 13.5     | 579                   | 271         | pelargonidin 3-O-rutinoside | pel 3-O-rut |
| 4    | 14.5     | 519                   | 271         | pelargonidin 3-O-malonyl-glucoside | pel 3-O-mal-glc |
| 5    | 15.1     | 475                   | 271         | pelargonidin 3-O-acetyl-glucoside | pel 3-O-ac-glc |
| 6    | 17.0     | 449                   | 287         | cyanidin derivative      | cya der     |
**Supplementary Table S2.** Identification and quantification details of the proteins quantified in this study. Protein accession and description, exp. \(q\)-value, sum posterior error probability (PEP) score, sequence coverage (%), number of identified peptides, peptide spectrum matches (PSMs), protein groups, number of identified unique peptides, number of razor peptides and Mascot identification score are reported, together with protein theoretical values (number of amino acids, molecular mass, pI). Specific information on protein quantification are reported including: Found in file, Found in sample, modification(s), abundance ratios, abundance (grouped), abundance (scaled), abundance, abundance (normalized). TAIR accession number for homologues counterparts in *Arabidopsis thaliana* and results of Blast alignments are reported for the identified proteins.

**Supplementary Table S3.** Protein quantitative changes ascertained in fruits from plants treated with different *Trichoderma* strains, with respect to control. Functional assignment of proteins was performed as reported in the experimental section. Figures containing resulting outputs are also reported.
**Supplementary Table S4.** Top-15 entries deriving from functional enrichment analysis of strawberry DRPs after *Trichoderma* strain treatments. Results from Biological process (GO), Molecular function (GO) and KEGG pathways enrichment are shown.

### Biological Process (GO)

| GO-term        | Description                                                      | Count in gene set | False-discovery rate |
|----------------|------------------------------------------------------------------|-------------------|----------------------|
| GO:0010035     | response to inorganic substance                                  | 59 of 795         | 2.33e-25             |
| GO:0010038     | response to metal ion                                            | 44 of 414         | 2.98e-24             |
| GO:0046686     | response to cadmium ion                                          | 38 of 286         | 5.61e-24             |
| GO:0042221     | response to chemicals                                           | 90 of 2654        | 1.82e-17             |
| GO:0050896     | response to stimulus                                            | 124 of 5064       | 3.16e-14             |
| GO:0051179     | localization                                                    | 75 of 2244        | 8.12e-14             |
| GO:0006810     | transport                                                       | 71 of 2140        | 7.59e-13             |
| GO:0044281     | small molecule metabolic process                                 | 58 of 1503        | 7.90e-13             |
| GO:0055086     | nucleobase-containing small molecule metabolic process           | 29 of 414         | 1.31e-11             |
| GO:0009117     | nucleotide metabolic process                                     | 26 of 323         | 1.31e-11             |
| GO:0055114     | oxidation-reduction process                                      | 52 of 1348        | 1.62e-11             |
| GO:0006950     | response to stress                                              | 81 of 2932        | 4.76e-11             |
| GO:0019752     | carboxylic acid metabolic process                                | 40 of 863         | 5.70e-11             |
| GO:0033036     | macromolecule localization                                       | 38 of 818         | 2.00e-10             |
| GO:0019637     | organophosphate metabolic process                                | 31 of 547         | 2.01e-10             |

### Molecular Function (GO)

| GO-term        | Description                                                      | Count in gene set | False-discovery rate |
|----------------|------------------------------------------------------------------|-------------------|----------------------|
| GO:0043167     | ion binding                                                      | 120 of 5070       | 2.55e-12             |
| GO:0005488     | binding                                                          | 170 of 8611       | 2.55e-12             |
| GO:003824      | catalytic activity                                               | 148 of 7239       | 1.82e-11             |
| GO:0036904     | small molecule binding                                           | 76 of 2633        | 4.31e-11             |
| GO:0043168     | anion binding                                                    | 74 of 2629        | 2.55e-10             |
| GO:0000166     | nucleotide binding                                               | 70 of 2461        | 6.15e-10             |
| GO:0016491     | oxidoreductase activity                                          | 45 of 1201        | 1.19e-09             |
| GO:0032553     | ribonucleotide binding                                           | 64 of 2204        | 1.74e-09             |
| GO:0043169     | cation binding                                                   | 75 of 2949        | 8.74e-09             |
GO:0046872  metal ion binding  74 of 2940  1.74e-08
GO:0032555  purine ribonucleotide binding  60 of 2179  4.23e-08
GO:0035639  purine ribonucleoside triphosphate binding  59 of 2147  5.59e-08
GO:0005507  copper ion binding  15 of 157  6.34e-08
GO:0016874  ligase activity  16 of 185  6.54e-08
GO:0019829  cation-transporting ATPase activity  10 of 74  1.50e-06

KEGG Pathways

| Pathway   | Description                                      | Count in gene set | False-discovery rate |
|-----------|--------------------------------------------------|-------------------|----------------------|
| ath01100  | Metabolic pathways                              | 70 of 1899        | 2.51e-15             |
| ath01110  | Biosynthesis of secondary metabolites            | 44 of 1063        | 5.48e-11             |
| ath00190  | Oxidative phosphorylation                        | 17 of 149         | 3.40e-10             |
| ath01200  | Carbon metabolism                               | 19 of 261         | 1.99e-08             |
| ath04141  | Protein processing in endoplasmic reticulum      | 15 of 205         | 8.89e-07             |
| ath00970  | Aminoacyl-tRNA biosynthesis                      | 8 of 57           | 1.20e-05             |
| ath00710  | Carbon fixation in photosynthetic organisms      | 8 of 69           | 3.80e-05             |
| ath04144  | Endocytosis                                      | 10 of 142         | 0.00013              |
| ath00620  | Pyruvate metabolism                             | 8 of 85           | 0.00013              |
| ath03013  | RNA transport                                    | 9 of 161          | 0.0015               |
| ath00480  | Glutathione metabolism                           | 7 of 98           | 0.0017               |
| ath00010  | Glycolysis / Gluconeogenesis                     | 7 of 115          | 0.0039               |
| ath03050  | Proteasome                                       | 5 of 58           | 0.0052               |
| ath00640  | Propanoate metabolism                            | 4 of 33           | 0.0052               |
| ath00030  | Pentose phosphate pathway                        | 5 of 58           | 0.0052               |
### Supplementary Table S5. Bridged and non-linked nodes identified during STRING analysis of DRPs present in strawberry fruits after plant treatment with *Trichoderma* strains (T22, TH1 and GV41). Functional protein associations were based on data recorded for *A. thaliana* protein homologues, whose name is also provided in the table.

| TAIR entry   | Symbol | Description                                                                 |
|--------------|--------|-----------------------------------------------------------------------------|
| AT1G01470    | LEA14  | Probable desiccation-related protein LEA14;                                 |
| AT1G01800    | AT1G01800 | Short-chain dehydrogenase/reductase 2b-like;                                |
| AT1G02140    | MAGO   | Protein mago nashi homolog;                                                 |
| AT1G02500    | SAM1   | S-adenosylmethionine synthetase 1;                                          |
| AT1G03860    | PHB2   | Prohibitin-2, mitochondrial;                                                |
| AT1G04510    | MAC3A  | Pre-mRNA-processing factor 19 homolog 1;                                    |
| AT1G04760    | VAMP726 | Putative vesicle-associated membrane protein 726;                           |
| AT1G07040    | AT1G07040 | Methyltransferase PMT9;                                                |
| AT1G07810    | ECA1   | Calcium-transporting ATPase 1, endoplasmic reticulum-type;                  |
| AT1G07990    | AT1G07990 | SIT4 phosphatase-associated family protein;                                |
| AT1G08420    | BS1    | Serine/threonine-protein phosphatase BSL2;                                  |
| AT1G08830    | CSD1   | Cytosolic copper/zinc superoxide dismutase;                                 |
| AT1G09080    | BIP3   | Probable mediator of RNA polymerase II transcription subunit 37b;           |
| AT1G09210    | CRT1b  | Calreticulin 1b;                                                           |
| AT1G09620    | AT1G09620 | Leucine-tRNA ligase, cytoplasmic;                                           |
| AT1G09630    | RAB11c | Ras-related protein RABA2a;                                                  |
| AT1G10390    | AT1G10390 | Nuclear pore complex protein NUP98a;                                       |
| AT1G10950    | TMN1   | Transmembrane 9 superfamily member 1;                                      |
| AT1G12310    | AT1G12310 | Calcium-binding EF-hand family protein;                                    |
| AT1G12640    | LPLAT1 | MBOAT (membrane bound O-acyl transferase) family protein;                  |
| AT1G12900    | GAPA-2 | Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic;             |
| AT1G13440    | GAPC2  | Glyceraldehyde-3-phosphate dehydrogenase GAPC2, cytosolic;                 |
| AT1G13700    | PGL1   | Probable 6-phosphoglucuronolactonase 1;                                    |
| AT1G14610    | TWN2   | Valyl-tRNA synthetase/valine-tRNA ligase (VALRS);                           |
| AT1G15520    | ABCG40 | Pleiotropic drug resistance protein 1-like;                                 |
| AT1G15690    | AVP1   | Pyrophosphate-energized vacuolar membrane proton pump 1;                    |
| AT1G16030    | Hsp70b | Heat shock 70 kDa protein 5;                                                 |
| AT1G16780    | VHP2-2 | Pyrophosphate-energized membrane proton pump 3;                            |
| AT1G17260    | AHA10  | Autoinhibited H(+)-ATPase isofrom 10;                                      |
| AT1G17880    | BTF3   | Basic transcription factor 3 (BTF3);                                       |
| AT1G18080    | ATARCA | Transducin/WD40 repeat-like superfamily protein;                           |
| AT1G20200    | EMB2719 | 26S Proteasome non-ATPase regulatory subunit 3 homolog A;                   |
| AT1G20330    | SMT2   | 24-Methylenosterol C-methyltransferase 2;                                   |
| AT1G20950    | AT1G20950 | Pyrophosphate-6-phosphate 1-phosphotransferase subunit alpha 1;           |
| AT1G21750    | PDIL1-1 | Protein disulfide isomerase-like (PDIL) protein;                           |
| AT1G23100    | AT1G23100 | Putative 10kDa chaperonin (CPN10) protein;                   |
| AT1G23000    | AOR    | NADPH-dependent alkanone/one oxidoreductase, chloroplastic;                |
| AT1G24360    | AT1G24360 | 3-Oxoacyl-[acyl-carrier-protein] reductase, chloroplastic;                   |
| AT1G25480    | AT1G25480 | Aluminum activated malate transporter family protein;                       |
| AT1G26110    | DCP5   | Protein decapping 5;                                                       |
| AT1G26880    | AT1G26880 | Ribosomal protein L34e superfamily protein;                             |
| AT1G27310    | NTF2A  | Nuclear transport factor 2A;                                                |
| AT1G29880    | AT1G29880 | Glycyl-tRNA synthetase/glycine-tRNA ligase;                             |
| AT1G29900    | CARB   | Carbamoyl-phosphate synthase large chain, chloroplastic;                   |
| AT1G29990    | PFD6   | Prefoldin 6;                                                              |
| AT1G31812    | ACBP6  | Acyl-CoA-binding domain-containing protein 6;                               |
| AT1G31850    | AT1G31850 | S-adenosyl-L-methionine-dependent methyltransferase superfamily protein;   |
| AT1G32900    | GBSS1  | Granule-bound starch synthase 1, chloroplastic/amylolytic;                  |
| AT1G35620    | PDIL5-2 | Protein disulfide-isomerase 5-2;                                           |
| AT1G36160    | ACC1   | Acetyl-CoA carboxylase 1;                                                   |
| AT1G36180    | ACC2   | Acetyl-CoA carboxylase 2;                                                   |
| AT1G47550    | SEC3A  | Exocyst complex component SEC3A;                                           |
| AT1G47710    | SERPIN | Serine protease inhibitor (SERPIN) family protein;                          |
| AT1G48410    | AGO1   | Stabilizer of iron transporter SufD/Polymerotidyl transferase;             |
| Accession   | Description                                                                 |
|------------|-------------------------------------------------------------------------------|
| AT2G36250  | FTSZ2-1 Cell division protein FtsZ homolog 2-1, chloroplastic;               |
| AT2G36380  | ABCG34 Pleiotropic drug resistance protein 2-like;                            |
| AT2G36530  | LOS2 Bifunctional enolase 2/transcriptional activator;                        |
| AT2G37170  | PIP2B Plasma membrane intrinsic protein 2;                                    |
| AT2G37270  | RPS5B Ribosomal protein S;                                                     |
| AT2G39390  | AT2G39390 60S Ribosomal L29 family protein;                                    |
| AT2G39730  | RCA Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic;     |
| AT2G39770  | CYT1 Mannose-1-phosphate guanylyltransferase 1;                               |
| AT2G39780  | RNS2 Ribonuclease 2;                                                          |
| AT2G40800  | AT2G40800 Import inner membrane translocase subunit;                          |
| AT2G41680  | CYP98A3 Cytochrome P450, family 98, subfamily A, polypeptide 3;               |
| AT2G41790  | NTRC NADPH-dependent thioredoxin reductase 3;                                 |
| AT2G44060  | AT2G441790 Insulinase (Peptidase family M16) family protein;                  |
| AT2G44990  | AT2G44060 Late embryogenesis abundant protein, group 2;                       |
| AT2G45590  | AT2G45590 Ribosomal RNA small subunit methyltransferase G;                    |
| AT2G46520  | AT2G46520 Cellular apoptosis susceptibility protein, putative/importin-alpha re-exporter; |
| AT3G01390  | VMA10 V-type proton ATPase subunit G1;                                       |
| AT3G01480  | CYP38 Peptidyl-prolyl cis-trans isomerase CYP38,                             |
| AT3G01640  | GLCAK Glucuronokinase 1;                                                      |
| AT3G01680  | SEOR1 Protein sieve element occlusion B;                                      |
| AT3G01780  | TPLEATE ARM repeat superfamily protein;                                      |
| AT3G03070  | AT3G03070 NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial; |
| AT3G04790  | EMB3119 Probable ribose-5-phosphate isomerase 3, chloroplastic;             |
| AT3G05040  | HASTY Exportin-1/importin-beta;                                               |
| AT3G06050  | PRXIIF Peroxiredoxin-2F, mitochondrial;                                      |
| AT3G07100  | ERM02 Protein transport protein Sec24-like At3g07100;                        |
| AT3G09980  | AT3G09980 RAB6-interacting golgin;                                            |
| AT3G10920  | MSD1 Superoxide dismutase [Mn] 1, mitochondrial;                              |
| AT3G11050  | FER2 Ferritin-2, chloroplastic;                                               |
| AT3G11130  | AT3G11130 Clathrin heavy chain 1;                                             |
| AT3G11400  | EIF3G1 Eukaryotic translation initiation factor 3 subunit G;                  |
| AT3G11830  | AT3G11830 T-complex protein 1 subunit et;                                     |
| AT3G11910  | UBP13 Ubiquitin carboxyl-terminal hydrolase 13;                               |
| AT3G12490  | CYSB Cysteine proteinase inhibitor 6;                                         |
| AT3G12580  | HSP70 Mediator of RNA polymerase II transcription subunit 37c;               |
| AT3G13330  | PA200 Proteasome activating protein 200;                                     |
| AT3G14420  | GOX1 Peroxiosomal (S)-2-hydroxy-acid oxidase-like;                            |
| AT3G14940  | PPC3 Cytosolic phosphoenolpyruvate carboxylase;                              |
| AT3G15660  | GRX4 Monothiol glutaredoxin-S15, mitochondrial;                              |
| AT3G15730  | PLDALPHA1 Phospholipase D alpha 1;                                            |
| AT3G15880  | WSIP2 Topless-related protein 4;                                              |
| AT3G16640  | TCTP Translationally controlled tumor protein;                               |
| AT3G16810  | PUM24 Pumilio homolog 24;                                                     |
| AT3G17210  | HS1 Stress-response A/B barrel domain-containing protein HS1;                 |
| AT3G17390  | MTO3 S-adenosylmethionine synthetase family protein;                         |
| AT3G19000  | AT3G19000 2-Oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein; |
| AT3G19240  | AT3G19240 Vacuolar import/degradation, Vid27-related protein;                |
| AT3G20390  | AT3G20390 Reactive intermediate deaminase A, chloroplastic;                  |
| AT3G20920  | AT3G20920 Translocation protein Sec62;                                        |
| AT3G21790  | AT3G21790 UDP-glucose flavonoid 3-O-glucosyltransferase 3;                    |
| AT3G22630  | PBD1 Proteasome subunit beta type 2-A;                                       |
| AT3G22640  | PAP85 Vicilin-like seed storage protein At3g22640;                           |
| AT3G25800  | PP2AA2 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A β isoform; |
| AT3G26060  | PRXQ Peroxiredoxin Q protein;                                                 |
| AT3G29360  | UDPG2 UDP-glucose 6-dehydrogenase family protein;                            |
| AT3G42170  | DAYSLEEPER Zinc finger BED domain-containing protein DAYSLEEPER;             |
| AT3G42640  | HA8 ATPase 8, plasma membrane-type;                                           |
| AT3G43190  | SUS4 Sucrose synthase 4;                                                      |
| AT3G43300  | ATMIN7 Brefeldin A-inhibited guanine nucleotide-exchange protein 5;           |
| AT3G43810  | CAM7 Calmodulin-7;                                                           |
| AT3G45140  | LOX2 Linoleate 13S-lipoxygenase 2-1;                                          |
| Gene ID   | Protein Name                                    | Description                                                                 |
|----------|------------------------------------------------|-----------------------------------------------------------------------------|
| AT3G45600| TET3                                           | Tetraspanin-3;                                                             |
| AT3G47950| HA4                                            | ATPase 4, plasma membrane-type;                                             |
| AT3G48140| AT3G48140                                      | B12D protein;                                                              |
| AT3G48890| MAPR3                                          | Putative progesterone-binding protein homolog (Atmp2) mRNA;                 |
| AT3G50590| AT3G50590                                      | Transducin/WD40 repeat-like superfamily protein;                            |
| AT3G51730| AT3G51730                                      | Saposin B domain-containing protein;                                        |
| AT3G51810| EMI                                            | Stress induced protein;                                                    |
| AT3G52140| NOXY38                                         | Tetratricopeptide repeat (TPR)-containing protein;                          |
| AT3G52300| ATPQ                                           | ATP synthase subunit d, mitochondrial;                                      |
| AT3G52730| AT3G52730                                      | Cytochrome b-c1 complex subunit 9;                                         |
| AT3G52990| ArCDC48B                                       | Pyruvate kinase 1;                                                         |
| AT3G53230| PAL2                                           | Cell division control protein 48 homolog D;                                |
| AT3G53260| PIP2A                                          | Phenylalanine ammonia-lyase 2;                                             |
| AT3G53420| AT3G53990                                      | Universal stress protein A;                                                |
| AT3G54440| AT3G54440                                      | Beta-galactosidase;                                                        |
| AT3G54820| PIP2,5                                         | Plasma membrane intrinsic protein 2,5;                                     |
| AT3G55410| AT3G55410                                      | 2-Oxoglutarate dehydrogenase, E1 component;                                |
| AT3G56070| ROC2                                           | Peptidyl-prolyl cis-trans isomerase CYP19-3;                                |
| AT3G57520| SIP2                                           | Probable galactinol-sucrose galactosyltransferase 2;                        |
| AT3G60860| AT3G60860                                      | Brefeldin A-inhibited guanine nucleotide-exchange protein 2;                |
| AT3G61220| AT3G61220                                      | Proline-tRNA ligase;                                                       |
| AT3G62560| AT3G62560                                      | GTP-binding protein SAR1A-like;                                            |
| AT3G63460| AT3G63460                                      | Transport protein SEC31 homolog B;                                         |
| AT4G00430| PIP1,4                                         | Plasma membrane intrinsic protein 1,4;                                     |
| AT4G01900| ATST2E24                                       | Peptidase family M48 family protein;                                       |
| AT4G02080| SAR2                                           | Secretion-associated RAS super family 2;                                  |
| AT4G02350| SEC15B                                         | Exocyst complex component EXOC6/SEC15B;                                   |
| AT4G02450| AT4G02450                                      | HSP20-like chaperones superfamily protein;                                 |
| AT4G02570| CUL1                                           | Cullin-1;                     |
| AT4G02620| AT4G02620                                      | H(+)-transporting two-sector ATPase;                                       |
| AT4G03240| FH                                             | Frataxin, mitochondrial;                                                   |
| AT4G04020| FIB                                            | Probable plastid-lipid-associated protein 1, chloroplastic;                |
| AT4G05050| UBQ11                                          | Polyubiquitin 11;                                                          |
| AT4G09320| NDPK1                                          | Nucleoside diphosphate kinase B-like isoform;                              |
| AT4G10040| CYTC-2                                         | Cytochrome c-2;                                                            |
| AT4G10320| AT4G10320                                      | Isoleucine-tRNA ligase;                                                    |
| AT4G11600| GPX6                                           | Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial;|
| AT4G11740| SAY1                                           | Plant UBX domain-containing protein 8;                                     |
| AT4G12400| Hop3                                           | Stress-inducible protein, putative;                                       |
| AT4G13200| AT4G13200                                      | Uncharacterized protein At4g13200, chloroplastic;                          |
| AT4G13780| AT4G13780                                      | Methionine-tRNA ligase, putative/methionyl-tRNA synthetase,                |
| AT4G16130| ARA1                                           | Arabinose kinase;                                                          |
| AT4G16720| AT4G16720                                      | 60S ribosomal protein L23/L15e family protein;                             |
| AT4G18100| AT4G18100                                      | Ribosomal protein L32e;                                                    |
| AT4G18360| GOX3                                           | Peroxosomal (S)-2-hydroxy-acid oxidase GLO5;                               |
| AT4G19006| AT4G19006                                      | 26S proteasome non-ATPase regulatory subunit 13 homolog B;                 |
| AT4G19120| ERD3                                           | Methyltransferase PMT21;                                                   |
| AT4G20980| AT4G20980                                      | Eukaryotic translation initiation factor 3 subunit 7 (eIF-3);              |
| AT4G21580| AT4G21580                                      | Quinone oxidoreductase PIG3-like;                                          |
| AT4G23460| AT4G23460                                      | Beta-adaptin-like protein C;                                               |
| AT4G26910| AT4G26910                                      | Dihydrolipoamide succinyltransferase;                                     |
| AT4G27130| AT4G27130                                      | Translation initiation factor SU11 family protein;                         |
| AT4G27270| AT4G27270                                      | NAD(P)H dehydrogenase (quinone) FQR1-like 1;                               |
| AT4G29900| ACA10                                          | Calcium-transporting ATPase 10, plasma membrane-type;                      |
| AT4G30440| GAE1                                           | UDP-D-glucuronate 4-epimerase 1;                                           |
| AT4G30600| AT4G30600                                      | Signal recognition particle receptor alpha subunit family protein;         |
| AT4G31080| AT4G31080                                      | Integral membrane metal-binding family protein (DUF2296);                  |
| AT4G31480| AT4G31480                                      | Coatomer subunit beta-1 (COPB1);                                          |
| AT4G32910| AT4G32910                                      | Nuclear pore complex protein NUP85;                                       |
| AT4G33070| AT4G33070                                      | Thiamine pyrophosphate dependent pyruvate decarboxylase family protein;   |
| Gene ID    | Description                                                                 |
|-----------|------------------------------------------------------------------------------|
| AT4G33090 | APM1 Aminopeptidase M1;                                                      |
| AT4G33150 | AT4G33150 Alpha-aminoadipic semialdehyde synthase;                           |
| AT4G33640 | Costar family protein AT4g33640;                                            |
| AT4G34450 | AT4G34450 Coatomer gamma-2 subunit, putative/gamma-2 coat protein;           |
| AT4G34640 | SQS1 Squalene synthase;                                                      |
| AT4G35220 | AT4G35220 Cyclase family protein;                                            |
| AT4G36910 | LEI2 CBS domain-containing protein CBSX1, chloroplastic;                    |
| AT4G37980 | ELI3-1 Cinnamyl alcohol dehydrogenase 7/mannitol dehydrogenase;             |
| AT4G37990 | ELI3-2 Cinnamyl alcohol dehydrogenase 8/mannitol dehydrogenase;             |
| AT4G38600 | SQS1 Squalene synthase;                                                      |
| AT4G39230 | AT4G39230 NmrA-like negative transcriptional regulator family protein;       |
| AT4G39260 | GRP8 Glycine-rich RNA-binding, abscisic acid-inducible protein;              |
| AT5G01600 | FER1 Ferritin-1, chloroplastic;                                              |
| AT5G02500 | HSC70-1 Heat shock cognate 70 kDa protein 2-like;                           |
| AT5G02790 | GSTL3 Glutathione S-transferase family protein;                              |
| AT5G05010 | AT5G05010 Coatomer subunit delta-like;                                       |
| AT5G06460 | UBA2 Ubiquitin/SUMO-activating enzyme E1 2;                                  |
| AT5G06970 | AT5G06970 Protein of unknown function (DUF810);                             |
| AT5G07350 | Tudor1 Ribonuclease TUDOR 1;                                                 |
| AT5G08290 | YLS8 mRNA splicing factor, thioredoxin-like U5 snRNP;                       |
| AT5G09650 | PPα6 Soluble inorganic pyrophosphatase 6, chloroplastic;                    |
| AT5G10840 | CBSX3 CBS domain-containing protein CBSX3, mitochondrial;                   |
| AT5G10860 | TRS120 TRAPP II complex, Trs120 protein;                                   |
| AT5G11520 | ASP3 Aspartate aminotransferase 3, chloroplastic;                           |
| AT5G13560 | AT5G13560 Structural maintenance of chromosomes protein;                     |
| AT5G13930 | TT4 Chalcone and stilbene synthase family protein;                          |
| AT5G15270 | AT5G15270 RNA-binding KH domain-containing protein;                         |
| AT5G17020 | XPO1A Protein exportin 1A;                                                   |
| AT5G17330 | GAD Glutamate decarboxylase 1;                                               |
| AT5G19820 | emb2734 Importin 5/uncharacterized protein At5g19820;                      |
| AT5G20280 | SPRS1 Sucrose phosphate synthase 1F;                                        |
| AT5G20490 | XIK Myosin family protein with Dil domain having ATPase activity;           |
| AT5G20720 | CPN20 20 kDa Chaperonin, chloroplastic;                                     |
| AT5G20890 | AT5G20890 TCP-1/cpn60 chaperonin family protein;                            |
| AT5G22780 | AT5G22780 Adaptor protein complex AP-2, alpha subunit;                      |
| AT5G25450 | AT5G25450 Cytochrome bd ubiquinol oxidase, 14kDa subunit;                   |
| AT5G25757 | AT5G25757.1 Eukaryotic translation initiation factor 3 subunit L;            |
| AT5G25880 | NADP-ME3 NADP-dependent malic enzyme (EC 1.1.1.40);                         |
| AT5G26710 | AT5G26710 Glutamyl/glutaminyl-tRNA synthetase, class 1c;                    |
| AT5G26830 | AT5G26830 Threonine-tRNA ligase, mitochondrial 1;                           |
| AT5G27030 | F2P16.14 Topless-related protein 3;                                          |
| AT5G27120 | AT5G27120 NOP56-like pre RNA processing ribonucleoprotein;                  |
| AT5G28830 | AT5G28830 Calcium-binding EF hand family protein;                           |
| AT5G34850 | Pap26 Bifunctional purple acid phosphatase 26;                              |
| AT5G35160 | AT5G35160 Endomembrane protein 70 protein family;                           |
| AT5G35360 | CA2 Acetyl Co-enzyme a carboxylase biotin carboxylase subunit;              |
| AT5G35500 | FIM5 Fimbrin-like protein 2;                                                 |
| AT5G36110 | CYP716A1 Cytochrome P450, family 716, subfamily A, polypeptide 1;           |
| AT5G36210 | AT5G36210 Peptidase belonging to the alpha/beta-Hydrolases superfamily;     |
| AT5G37780 | CAM1 Calmodulin involved in thigmomorphogenesis;                            |
| AT5G39410 | AT5G39410 Mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410; |
| AT5G39850 | AT5G39850 Ribosomal protein S4;                                              |
| AT5G40770 | PHB3 Prohibitin-3, mitochondrial;                                            |
| AT5G41670 | AT5G41670 6-Phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic;|
| AT5G42420 | AT5G42420 Nucleotide-sugar phosphate transporter family protein;             |
| AT5G45160 | RL2 Root hair defective 3 GTP-binding protein;                              |
| AT5G46070 | AT5G46070 Guanylate-binding family protein;                                 |
| AT5G47030 | AT5G47030 ATP synthase subunit delta’, mitochondrial;                        |
| AT5G50530 | CBS/CBSBPB4 CBS/octicosapetide/Phox/Bemp1 domains-containing protein CBS/CBSBPB4; |
| AT5G51970 | AT5G51970 Sorbitol dehydrogenase;                                           |
AT5G53480  AT5G53480  Armadillo-like helical, importin subunit beta-1;
AT5G53530  VPS26A  Vacuolar protein sorting-associated protein 26A;
AT5G53560  CB5-E  Cytochrome b5 isoform E;
AT5G54500  FQR1  NAD(P)H dehydrogenase (quinone) FQR1-like protein;
AT5G54960  PDC2  Pyruvate decarboxylase-2; belongs to the TPP enzyme family
AT5G55160  SUMO2  Small ubiquitin-like modifier (SUMO) polypeptide;
AT5G555240  ATPXG2  Arabidopsis thaliana peroxigenase 2;
AT5G55940  emb2731  ER membrane protein complex subunit 8/9 homolog;
AT5G58070  TIL  Temperature-induced lipocalin-1;
AT5G59240  AT5G59240 40S ribosomal protein S8;
AT5G59970  At1g07660  Histone superfamily protein;
AT5G60390  At1g07940  Elongation factor 1-alpha;
AT5G62390  BAG7  BAG family molecular chaperone regulator 7;
AT5G62670  HA11  ATPase 11, plasma membrane-type;
AT5G62890  AT5G62890  Xanthine/uracil/vitamin C permease family protein;
AT5G63400  At5g63400  Adenylate kinase 4;
AT5G64130  AT5G64130  cAMP-regulated phosphoprotein 19-related protein;
AT5G64250  AT5G64250  2-Nitropropane dioxygenase-like protein;
AT5G67500  VDAC2  Mitochondrial outer membrane protein porin 2;
ATMG0066  NAD5B  NADH-ubiquinone oxidoreductase chain 5;
AT2G47780  REF  Rubber elongation factor protein.

Figure legends

Supplementary Figure S1. HPLC-DAD chromatogram of an exemplificative strawberry dried extract recorded at 520 nm. Putative compound identification was performed according to the scientific literature (Holzwarth 2012; Carbone et al., 2009). (1) cyanidin 3-O-glucoside; (2) pelargonidin 3-O-glucoside; (3) pelargonidin 3-O-rutinoside; (4) pelargonidin 3-O-malonyl-glucoside; (5) pelargonidin 3-O-acetyl-glucoside; (6) cyanidin derivative.

Supplementary Figure S2. Heat-map representation and hierarchical clustering analysis of proteins involved in solute transport (upper panel), calcium metabolism (middle panel) and nutrient uptake (lower panel), which were differentially represented in strawberry fruits produced by plants subjected to the treatments with Trichoderma strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log2 transformed abundance ratio values.

Supplementary Figure S3. Heat-map representation and hierarchical clustering analysis of proteins involved in carbon and energy metabolism that were differentially represented in strawberry fruits produced by plants subjected to the treatments with Trichoderma strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log2 transformed abundance ratio values.

Supplementary Figure S4. Heat-map representation and hierarchical clustering analysis of proteins involved in stress response that were differentially represented in strawberry fruits produced by plants subjected to the treatments with Trichoderma strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log2 transformed abundance ratio values.

Supplementary Figure S5. Heat-map representation and hierarchical clustering analysis of proteins involved in amino acid metabolism (upper panel), coenzyme metabolism (middle panel), nucleotide metabolism (middle panel) or lipid metabolism (lower panel), which were differentially
represented in strawberry fruits produced by plants subjected to the treatments with *Trichoderma* strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log₂ transformed abundance ratio values.

**Supplementary Figure S6.** Heat-map representation and hierarchical clustering analysis of proteins involved in RNA biosynthesis (upper panel), RNA processing (middle panel) and protein biosynthesis (lower panel), which were differentially represented in strawberry fruits produced by plants subjected to the treatments with *Trichoderma* strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log₂ transformed abundance ratio values.

**Supplementary Figure S7.** Heat-map representation and hierarchical clustering analysis of proteins involved in protein modification (upper panel), protein translocation (middle panel) and protein degradation (lower panel), which were differentially represented in strawberry fruits produced by plants subjected to the treatments with *Trichoderma* strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log₂ transformed abundance ratio values.

**Supplementary Figure S8.** Heat-map representation and hierarchical clustering analysis of proteins involved in cytoskeleton (upper panel), cell wall (middle upper panel), chromatin organization (middle panel), cell cycle (middle lower panel) and vesicle trafficking (lower panel), which were differentially represented in strawberry fruits produced by plants subjected to the treatments with *Trichoderma* strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log₂ transformed abundance ratio values.

**Supplementary Figure S9.** Heat-map representation of hierarchical clustering analysis of proteins with unknown function that were differentially represented in strawberry fruits produced by plants subjected to the treatments with *Trichoderma* strains (T22, TH1 and GV41), as compared to control (Ctr). Shown are proteins presenting abundance fold changes ≥1.50 or ≤0.66 with respect to control (P≤ 0.05) (Supplementary Table S3). Data are reported as log₂ transformed abundance ratio values. Results related to proteins with unknown function are shown.

**References**

Holzwarth, M., Korhummel, S., Carle, R., and Kammerer, D. R. (2012). Evaluation of the Effects of Different Freezing and Thawing Methods on Color, Polyphenol and Ascorbic Acid Retention in Strawberries (*Fragaria × Ananassa* Duch.). *Food Res. Int.* 48, 241–248. doi: 10.1016/j.foodres.2012.04.004

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