**S1\_Table. Differentially expressed proteins identified from resistant (R) and susceptible (S) leaves**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Spot No.** | **Spot % volume variation** | **Mr (kDa) /pI** | **Accession****No.** | **Description** | **Functional****categories** | **Protein Score** | **Protein Score C.I.%** | **Pep Count.** | **Species** |
| **Metabolism and energy production** |
| **7** |   | 55.44/5.09 | gi|346683279 | ATP synthase CF1 alpha subunit | Ι | 192 | 100 | 6 | *Pyrus pyrifolia* |
| **8** |  | 52.10/5.02 | gi|7708676 | ATP synthase beta subunit | Ι | 262 | 100 | 2 | *Thunbergia coccinea* |
| **9** |  | 56.89/7.1 | gi|295684201 | ADP glucose pyrophosphorylase small subunit 1-likeprotein | Ι | 349 | 100 | 8 | *Malus x domestica* |
| **12** |  | 43.84/6.11 | gi|211906520 | UDP-D-apiose/UPD-D-xylose synthetase | Ι | 140 | 100 | 7 | *Gossypium hirsutum* |
| **14** |  | 50.75/6.36 | gi|297816078 | glutamate-1-semialdehyde 2,1-aminomutase 2 | Ι | 121 | 100 | 5 | *Arabidopsis lyrata subsp. lyrata* |
| **16** |  | 42.83/6.06 | gi|118175929 | chloroplast sedoheptulose-1,7-bisphosphatase | Ι | 306 | 100 | 8 | *Morus alba var. multicaulis* |
| **18** |  | 97.45/6.4 | gi|55585585 | phosphoribulokinase-like protein 2 | Ι | 171 | 100 | 1 | *Elaeis guineensis* |
| **20** |  | 30.86/6.2 | gi|60101357 | glutamine synthetase | Ι | 167 | 100 | 3 | *Vigna radiata* |
| **21** |  | 37.04/7.06 | gi|211906470 | glyceraldehyde-3-phosphate dehydrogenase | Ι | 344 | 100 | 9 | *Gossypium hirsutum* |
| **22** |  | 41.09/7.98 | gi|41052915 | putative ferredoxin-NADP(H) oxidoreductase | Ι | 321 | 100 | 11 | *Oryza sativa Japonica Group* |
| **29** |  | 27.37/5.24 | gi|414550 | cytosolic triose phosphate isomerase | Ι | 150 | 100 | 4 | *Arabidopsis thaliana* |
| **33** |  | 26.79/7.01 | gi|9909636 | ribulose 1,5-bisphosphate carboxylase | Ι | 137 | 100 | 5 | *Elatine hydropiper* |
| **34** |  | 24.60/8.45 | gi|315364830 | chloroplast Rieske-type iron-sulfur protein | Ι | 155 | 100 | 6 | *Citrullus lanatus* |
| **42** |  | 51.99/5.91 | gi|75758075 | carboxylase/oxygenase large subunit | Ι | 406 | 100 | 20 | *Eryngium giganteum* |
| **Protein synthesis** |
| **30** |  | 33.97/6.69 | gi|170131 | ribosomal protein 30S subunit | ΙΙ | 114 | 100 | 6 | *Spinacia oleracea* |
| **35** |  | 14.59/6.4 | gi|14594929 | putative beta4 proteasome subunit | ΙΙ | 182 | 100 | 4 | *Nicotiana tabacum* |
| **43** |  | 30.92/5.48 | gi|255564051 | amino acid-binding protein, putative | ΙΙ | 180 | 100 | 3 | *Ricinus communis* |
| **Defense response** |
| **1**  |  | 71.52/5.17 | gi|359486799 | heat-shock cognate 70 kDa proteinisoform 2 | ΙΙΙ | 921 | 100 | 19 | *Vitis vinifera* |
| **2** |  | 71.57/5.17 | gi|6969976 | high-molecular-weight heat-shock protein | ΙΙΙ | 763 | 100 | 18 | *Malus xdomestica* |
| **3** |  | 72.04/5.27 | gi|186898205 | heat-shock protein 70 | ΙΙΙ | 436 | 100 | 13 | *Hevea brasiliensis* |
| **4** |  | 72.04/5.27 | gi|186898205 | heat-shock protein 70 | ΙΙΙ | 573 | 100 | 15 | *Hevea brasiliensis* |
| **5** |  | 72.04/5.27 | gi|186898205 | heat-shock protein 70 | ΙΙΙ | 551 | 100 | 17 | *Hevea brasiliensis* |
| **10** |  | 43.68/5.83 | gi|356539350 | bifunctional polymyxin resistance protein ArnA-like | ΙΙΙ | 204 | 100 | 5 | *Glycine max* |
| **11** |  | 43.61/5.5 | gi|224108858 | s-adenosylmethionine synthetase 3 | ΙΙΙ | 411 | 100 | 12 | *Populus trichocarpa* |
| **13** |  | 43.61/5.5 | gi|224101473 | s-adenosylmethionine synthetase 1 | ΙΙΙ | 487 | 100 | 13 | *Populus trichocarpa* |
| **15** |  | 21.76/9.21 | gi|226789714 | beta-1,3-glucanase | ΙΙΙ | 153 | 100 | 3 | *Malus x domestica* |
| **17** |  | 41.02/5.24 | gi|82697951 | CXE carboxylesterase | ΙΙΙ | 157 | 100 | 5 | *Malus pumila* |
| **19** |  | 36.53/5.28 | gi|27372289 | ACC oxidase | ΙΙΙ | 130 | 100 | 5 | *Malus x domestica* |
| **23** |  | 18.42/4.53 | gi|138753498 | pathogenesis-related protein 8 | ΙΙΙ | 124 | 100 | 2 | *Malus x domestica* |
| **27** |  | 22.21/4.92 | gi|327422155 | 2-cys-peroxiredoxin | ΙΙΙ | 135 | 100 | 4 | *Vigna unguiculata* |
| **28** |  | 27.71/5.53 | gi|145581388 | ascorbate peroxidase | ΙΙΙ | 155 | 100 | 5 | *Malus x domestica* |
| **31** |  | 25.05/8.37 | gi|300078580 | peroxiredoxin | ΙΙΙ | 393 | 100 | 7 | *Jatropha curcas* |
| **32** |  | 21.96/4.93 | gi|47027073 | 2-cys peroxiredoxin-like protein | ΙΙΙ | 139 | 100 | 4 | *Hyacinthus orientalis* |
| **36** |  | 18.69/6.14 | gi|33308408 | glutathione peroxidase | ΙΙΙ | 507 | 100 | 12 | *Malus x domestica* |
| **37** |  | 18.11/5.54 | gi|255558882 | heat-shock protein, putative | ΙΙΙ | 149 | 100 | 6 | *Ricinus communis* |
| **38** |  | 17.69/5.67 | gi|4590376 | major allergen mal d 1 | ΙΙΙ | 163 | 100 | 6 | *Malus x domestica* |
| **39** |  | 17.69/5.67 | gi|4590376 | major allergen mal d 1 | ΙΙΙ | 418 | 100 | 8 | *Malus x domestica* |
| **40** |  | 17.70/5.67 | gi|15418742 | ribonuclease-like PR-10c | ΙΙΙ | 525 | 100 | 9 | *Malus x domestica* |
| **41** |  | 17.51/5.62 | gi|2443824 | major allergen Mal d 1 | ΙΙΙ | 244 | 100 | 6 | *Malus x domestica* |
| **Cell division** |
| **6** |  | 75.50/6.43 | gi|255558698 | cell division protein ftsH, putative | ΙV | 880 | 100 | 13 | *Ricinus communis* |
| **Unclear classification** |
| **24** |  | 38.07/6.51 | gi|356545090 | uncharacterised protein | V | 107 | 100 | 1 | *Glycine max* |
| **25** |  | 26.34/5.29 | gi|227204455 | AT2G37660 | V | 167 | 100 | 2 | *Arabidopsis thaliana* |
| **26** |  | 26.65/9.62 | gi|226747930 | Mdfwg2100K20.g1 Apple\_EST\_ | V | 389 | 100 | 6 | *Malus x domestica* |

\* Y axis: Relative expression of the spot (V%);

\* X axis: column1: S-CK, 2: S-48h, 3: R-CK, 4: R-48h; CK: Control leaf; 48 h: Inoculation for 48 h

Data are representative of three independent biological replicates and given as intensity means ± S.D.