

**Additional file 3**

**File format: PDF**

**Title: Supplementary Table S2**

**Description:**

**Table S2. Proteins identified in poplar (*P. deltoides*) leaf apoplast using 2-D LC MS/MS.**

| Poplar Protein ID                   | Poplar transcript ID             | Poplar new ID      | Mr/pl ( theor.) | Number of matched peptides total/unique | Protein score | Protein identity/similarity                   | Sequence similarity | Accession number | Organism                                              | Signal peptide (SP) | Non-classical SP |
|-------------------------------------|----------------------------------|--------------------|-----------------|-----------------------------------------|---------------|-----------------------------------------------|---------------------|------------------|-------------------------------------------------------|---------------------|------------------|
| <b>Cell wall metabolism</b>         |                                  |                    |                 |                                         |               |                                               |                     |                  |                                                       |                     |                  |
| 422858 <sup>#</sup>                 | gw1.XII.1318.1                   | POPTR_0012s10830.1 | 112.5/5.7       | 3/2                                     | 28.19         | Alpha-mannosidase                             | 70%                 | Q8LPJ3           | <i>Arabidopsis thaliana</i>                           | yes                 |                  |
| 816882*                             | estExt_fgenes4_pg.C_LG_II2363    | POPTR_0002s23920.1 | 114.8/5.8       | 23/21                                   | 198.32        | Alpha-mannosidase                             | 71%                 | P94078           | <i>Arabidopsis thaliana</i>                           | yes                 |                  |
| 757134                              | fgenes4_pg.C_LG_III000676        | POPTR_0007s09730.1 | 114.0/5.5       | 2/2                                     | 14.24         | Alpha-mannosidase                             | 67%                 | Q9FKW9           | <i>Arabidopsis thaliana</i>                           | SA                  | yes              |
| 572859*                             | eugene3.00140904                 | POPTR_0014s14050.1 | 113.8/6.3       | 4/3                                     | 26.19         | Alpha-mannosidase                             | 70%                 | Q9FFX7           | <i>Arabidopsis thaliana</i>                           | yes                 |                  |
| 786149*                             | fgenes4_pg.C_scaffold_164000005  | POPTR_0018s14920.1 | 40.0/4.9        | 4/3                                     | 30.20         | Alpha-galactosidase                           | 83%                 | Q84VQ7           | <i>Helianthus annuus</i>                              | no                  | yes              |
| 204338 <sup>#</sup> *               | gw1.IX.4803.1                    | POPTR_0009s01780.1 | 90.0/6.3        | 9/8                                     | 90.26         | Beta-galactosidase                            | 77%                 | Q93X57           | <i>Fragaria ananassa</i>                              | yes                 |                  |
| 297914 <sup>#</sup> *               | gw1.88.36.1                      | POPTR_0017s08470.1 | 98.5/6.2        | 3/3                                     | 30.21         | Beta-galactosidase                            | 77%                 | Q5CCQ1           | <i>Pyrus pyrifolia</i>                                | SA                  | yes              |
| 207219 <sup>#</sup> *               | gw1.V.2620.1                     | POPTR_0005s07020.1 | 71.2/4.9        | 12/9                                    | 78.33         | Beta-galactosidase                            | 72%                 | A5AXS9           | <i>Vitis vinifera</i>                                 | no                  | yes              |
| 798675                              | fgenes4_pm.C_LG_II000364         | POPTR_0002s08120.1 | 89.6/9.4        | 2/2                                     | 18.17         | Beta-galactosidase 16                         | 66%                 | Q8GX69           | <i>Arabidopsis thaliana</i>                           | no                  | yes              |
| 228333 <sup>#</sup>                 | gw1.X.3030.1                     | POPTR_0010s26170.1 | 41.1/6.8        | 2/2                                     | 18.12         | Acid alpha galactosidase 1                    | 83%                 | Q2MK92           | <i>Cucumis sativus</i>                                | no                  | yes              |
| 209602 <sup>#</sup> *               | gw1.V.5003.1                     | POPTR_0005s16590.1 | 32.8/5.0        | 7/7                                     | 40.24         | Glucan 1,3-beta-glucosidase                   | 68%                 | Q8RU06           | <i>Oryza sativa subsp. japonica</i>                   | no                  | yes              |
| 171426 <sup>#</sup>                 | gw1.I.26.1                       | POPTR_0001s21430.1 | 79.5/6.0        | 11/2                                    | 70.25         | Xylan 1,4-beta-xylosidase                     | 93%                 | Q2MCJ5           | <i>Populus tremula x Populus alba</i>                 | no                  | yes              |
| 799561                              | fgenes4_pm.C_LG_III000026        | POPTR_0003s01730.1 | 83.4/5.7        | 10/1                                    | 78.25         | Xylan 1,4-beta-xylosidase                     | 96%                 | Q2MCJ6           | <i>Populus tremula x Populus alba</i>                 | yes                 |                  |
| 255102*                             | gw1.XVI.1041.1                   | POPTR_0016s02620.2 | 73.3/5.5        | 30/21                                   | 240.37        | Alpha-L-arabinofuranosidase                   | 74%                 | Q7X9G7           | <i>Malus domestica</i>                                | yes                 |                  |
| 204508 <sup>#</sup>                 | gw1.IX.4973.1                    | POPTR_0009s01240.1 | 51.5/4.9        | 3/3                                     | 20.23         | Alpha-L-fucosidase 1                          | 73%                 | Q8GW72           | <i>Arabidopsis thaliana</i>                           | no                  | yes              |
| 830063*                             | estExt_fgenes4_pm.C_LG_II0164    | POPTR_0002s03580.1 | 33.9/5.5        | 3/1                                     | 30.18         | Phenylcoumaran benzylic ether reductase       | 100%                | O65904           | <i>Populus trichocarpa</i>                            | no                  | no               |
| 718566*                             | estExt_Genewise1_v1.C_LG_VII1401 | POPTR_0007s04020.1 | 62.1/6.3        | 6/3                                     | 50.27         | Pectin methylesterase-like protein            | 66%                 | Q9FXW9           | <i>Arabidopsis thaliana</i>                           | yes                 |                  |
| 253960 <sup>#</sup>                 | gw1.XV.3396.1                    | POPTR_0015s12990.1 | 39.9/8.3        | 2/1                                     | 20.26         | Pectinacetyl esterase                         | 68%                 | Q9FF93           | <i>Arabidopsis thaliana</i>                           | no                  | no               |
| 827492                              | estExt_fgenes4_pg.C_860139       | POPTR_0004s24220.4 | 44.2/9.1        | 1/1                                     | 10.14         | Pectinacetyl esterase                         | 64%                 | Q41695           | <i>Phaseolus aureus</i>                               | yes                 |                  |
| 570444*                             | eugene3.00121097                 | POPTR_0012s13090.1 | 43.3/5.1        | 7/6                                     | 60.30         | Pectinacetyl esterase                         | 64%                 | Q9FF93           | <i>Arabidopsis thaliana</i>                           | yes                 |                  |
| 755730                              | fgenes4_pg.C_LG_II001910         | POPTR_0002s18800.1 | 50.7/4.9        | 4/3                                     | 38.19         | Polygalacturonase                             | 68%                 | Q75LI0           | <i>Oryza sativa subsp. japonica</i>                   | yes                 |                  |
| 644497                              | grail3.0039009101                | POPTR_0002s16390.1 | 51.5/5.9        | 5/5                                     | 40.30         | Polygalacturonase-like protein                | 80%                 | Q84LI7           | <i>Fragaria ananassa</i>                              | yes                 |                  |
| 662785*                             | grail3.0016022201                | POPTR_0013s02730.2 | 41.7/6.1        | 7/3                                     | 50.31         | Lipolytic enzyme, G-D-S-L                     | 75%                 | Q2HTP0           | <i>Medicago truncatula</i>                            | yes                 |                  |
| 225922 <sup>#</sup>                 | gw1.X.619.1                      | POPTR_0010s15510.1 | 61.8/8.9        | 1/1                                     | 6.13          | O-linked GlcNAc transferase                   | 69%                 | Q9LSP3           | <i>Arabidopsis thaliana</i>                           | no                  | no               |
| 551701                              | eugene3.00021016                 | POPTR_0002s11090.1 | 72.9/4.8        | 6/5                                     | 40.18         | LG27/30-like gene (rhamnogalacturonate lyase) | 67%                 | Q9STV1           | <i>Arabidopsis thaliana</i>                           | no                  | yes              |
| 836412                              | estExt_fgenes4_pm.C_400050       | POPTR_0014s04360.1 | 20.2/8.0        | 1/1                                     | 10.14         | Sts15 protein                                 | 59%                 | P93569           | <i>Solanum tuberosum</i>                              | yes                 |                  |
| 272681 <sup>#</sup> *               | gw1.152.150.1                    | POPTR_0006s06100.1 | 56.8/6.0        | 4/4                                     | 40.33         | Heparanase-like protein 3                     | 66%                 | Q9FZP1           | <i>Arabidopsis thaliana</i>                           | no                  | yes              |
| 262951 <sup>#</sup>                 | gw1.XVIII.3492.1                 | POPTR_0025s00410.1 | 55.9/8.0        | 2/2                                     | 16.33         | Heparanase-like protein 3                     | 68%                 | Q9FZP1           | <i>Arabidopsis thaliana</i>                           | no                  | yes              |
| <b>Cell wall and stress related</b> |                                  |                    |                 |                                         |               |                                               |                     |                  |                                                       |                     |                  |
| 774930                              | fgenes4_pg.C_LG_XIV000840        | POPTR_0014s14000.1 | 33.5/9.1        | 1/1                                     | 18.19         | Peroxidase                                    | 98%                 | Q58GF4           | <i>Populus alba x Populus tremula var. glandulosa</i> | yes                 |                  |
| 825400*                             | estExt_fgenes4_pg.C_LG_XVI1240   | POPTR_0016s14030.1 | 33.4/8.1        | 5/4                                     | 40.29         | Cationic peroxidase 1                         | 69%                 | P22195           | <i>Arachis hypogaea</i>                               | yes                 |                  |
| 817694*                             | estExt_fgenes4_pg.C_LG_III1873   | POPTR_0003s21660.1 | 33.4/5.8        | 12/10                                   | 106.30        | Peroxidase N                                  | 67%                 | Q42517           | <i>Armoracia rusticana</i>                            | no                  | yes              |

Table S2. continued

|                       |                                  |                    |          |       |        |                                                                             |     |        |                                       |     |     |
|-----------------------|----------------------------------|--------------------|----------|-------|--------|-----------------------------------------------------------------------------|-----|--------|---------------------------------------|-----|-----|
| 718485*               | estExt_Genewise1_v1.C_LG_VII1054 | POPTR_0007s02580.1 | 35.9/8.6 | 6/4   | 60.22  | Peroxidase                                                                  | 74% | Q9ZNZ5 | <i>Glycine max</i>                    | yes |     |
| 777213*               | fgenes4_pg.C_LG_XVI000455        | POPTR_0149s00200.1 | 33.0/5.3 | 4/3   | 40.30  | Peroxidase                                                                  | 93% | Q08IT3 | <i>Populus alba</i>                   | no  | yes |
| 208491 <sup>#</sup>   | gw1.V.3892.1                     | POPTR_0005s14190.1 | 32.6/5.2 | 3/2   | 28.27  | Peroxidase 10                                                               | 66% | Q9FX85 | <i>Arabidopsis thaliana</i>           | no  | yes |
| 547681*               | eugene3.00010122                 | POPTR_0001s05050.1 | 36.8/4.5 | 4/1   | 38.25  | Peroxidase                                                                  | 98% | Q43101 | <i>Populus trichocarpa</i>            | yes |     |
| <b>Stress/defense</b> |                                  |                    |          |       |        |                                                                             |     |        |                                       |     |     |
| 249950 <sup>#</sup>   | gw1.XIX.2350.1                   | POPTR_0019s12350.1 | 27.9/4.5 | 2/1   | 18.13  | Class IV chitinase                                                          | 75% | Q9M2U5 | <i>Arabidopsis</i>                    | yes |     |
| 270686 <sup>**</sup>  | gw1.142.209.1                    | POPTR_0013s12870.1 | 27.1/4.4 | 7/7   | 60.41  | Class IV chitinase                                                          | 80% | Q9M2U5 | <i>Arabidopsis thaliana</i>           | no  | yes |
| 574380*               | eugene3.00190854                 | POPTR_0019s12360.1 | 28.9/4.7 | 4/1   | 30.29  | Class IV chitinase                                                          | 70% | Q7X9F8 | <i>Galega orientalis</i>              | yes |     |
| 746640*               | estExt_Genewise1_v1.C_1970084    | POPTR_0015s05990.1 | 30.8/4.4 | 6/3   | 60.48  | Acidic class III chitinase                                                  | 72% | Q09Y38 | <i>Citrullus lanatus</i>              | yes |     |
| 828660*               | estExt_fgenes4_pg.C_1970027      | POPTR_0015s05980.1 | 31.7/8.4 | 8/7   | 60.25  | Hevamine-A                                                                  | 80% | P23472 | <i>Hevea brasiliensis</i>             | yes |     |
| 203165 <sup>#</sup>   | gw1.IX.3630.1                    | POPTR_0001s26210.1 | 33.7/5.4 | 8/2   | 20.30  | Beta-1,3-glucanase                                                          | 67% | Q56AP0 | <i>Fragaria ananassa</i>              | no  | yes |
| 652688*               | grail3.0024032801                | POPTR_0006s04670.1 | 31.6/4.7 | 4/4   | 30.16  | Beta-1,3 glucanase                                                          | 80% | Q9M5I9 | <i>Populus tremula x Populus alba</i> | yes |     |
| 669475*               | grail3.0020019002                | POPTR_0018s10490.1 | 24.7/7.8 | 5/4   | 100.30 | Thaumatococin-like protein                                                  | 76% | Q5ND92 | <i>Actinidia deliciosa</i>            | yes |     |
| 747341                | estExt_Genewise1_v1.C_4720001    | POPTR_0001s09000.1 | 24.1/5.6 | 4/1   | 40.26  | Thaumatococin-like protein isoform 2                                        | 71% | Q2VAC9 | <i>Ficus awkeotsang</i>               | yes |     |
| 649635                | grail3.0001063901                | POPTR_0009s09760.1 | 25.1/5.0 | 4/1   | 38.15  | NIPRP27                                                                     | 73% | Q9XIY9 | <i>Nicotiana tabacum</i>              | yes |     |
| 549955*               | eugene3.00012396                 | POPTR_0001s30680.1 | 25.0/7.0 | 10/5  | 100.37 | NIPRP27                                                                     | 72% | Q9XIY9 | <i>Nicotiana tabacum</i>              | yes |     |
| 669494                | grail3.0020020701                | POPTR_0018s10730.1 | 13.6/4.7 | 2/2   | 20.32  | Blight-associated protein p12                                               | 60% | Q653F1 | <i>Oryza sativa subsp. japonica</i>   | yes |     |
| 781921                | fgenes4_pg.C_scaffold_44000051   | POPTR_0003s02750.1 | 20.1/9.3 | 1/1   | 8.15   | Pathogenesis-related transcriptional factor                                 | 70% | Q2HUA6 | <i>Medicago truncatula</i>            | no  | no  |
| 579227                | eugene3.10400001                 | POPTR_0185s00200.1 | 34.9/5.4 | 1/1   | 8.13   | Resistance protein RGC2                                                     | 25% | Q6Y136 | <i>Lactuca sativa</i>                 | no  | yes |
| 198468                | gw1.IV.3557.1                    | POPTR_0004s08710.1 | 58.2/6.5 | 1/1   | 8.17   | Disease resistance protein                                                  | 49% | Q9C784 | <i>Arabidopsis thaliana</i>           | no  | yes |
| 819386*               | estExt_fgenes4_pg.C_LG_VI1270    | POPTR_0006s19310.1 | 13.8/8.9 | 4/4   | 40.20  | Blight-associated protein p12                                               | 49% | Q6K4C4 | <i>Oryza sativa subsp. japonica</i>   | yes |     |
| 825296*               | estExt_fgenes4_pg.C_LG_XVI0953   | POPTR_0016s10140.1 | 11.9/8.1 | 6/6   | 60.30  | Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | 74% | A9XNQ1 | <i>Sonneratia caseolaris</i>          | yes |     |
| 648132                | grail3.0038010001                | POPTR_0004s08500.1 | 11.8/9.2 | 1/1   | 10.24  | Non-specific lipid-transfer protein                                         | 91% | A9PJG2 | <i>Populus jackii</i>                 | yes |     |
| 761882                | fgenes4_pg.C_LG_VI000192         | POPTR_0006s02260.1 | 23.5/5.4 | 2/2   | 20.18  | Abrin-a                                                                     | 33% | P11140 | <i>Abrus precatorius</i>              | SA  | yes |
| 294386 <sup>#</sup>   | gw1.6840.1.1                     | POPTR_0001s09570.1 | 7.3/7.7  | 1/1   | 10.20  | Osmotin-like protein linusitin                                              | 92% | Q8GUQ2 | <i>Linum usitatissimum</i>            | no  | yes |
| 811643*               | fgenes4_pm.C_scaffold_163000009  | POPTR_0011s01280.1 | 21.6/6.4 | 3/2   | 30.23  | Superoxide dismutase [Cu-Zn]                                                | 99% | A9PJW9 | <i>Populus jackii</i>                 | no  | yes |
| <b>Proteolysis</b>    |                                  |                    |          |       |        |                                                                             |     |        |                                       |     |     |
| 740448                | estExt_Genewise1_v1.C_400832     | POPTR_0014s02630.1 | 79.5/5.1 | 9/9   | 60.22  | Subtilase                                                                   | 51% | Q84TR6 | <i>Casuarina glauca</i>               | no  | yes |
| 781559*               | fgenes4_pg.C_scaffold_40000309   | POPTR_0014s02650.1 | 83.4/5.3 | 8/8   | 70.27  | Subtilase                                                                   | 50% | Q84TR6 | <i>Casuarina glauca</i>               | yes |     |
| 208844                | gw1.V.4245.1                     | POPTR_0005s18880.1 | 80.4/6.6 | 1/1   | 10.17  | Subtilisin-like protease                                                    | 77% | 9XG40  | <i>Nicotiana tabacum</i>              | yes |     |
| 709916*               | estExt_Genewise1_v1.C_LG_II0461  | POPTR_0002s02010.1 | 77.2/5.3 | 16/16 | 110.33 | Subtilisin-like serine protease                                             | 61% | Q8LAE1 | <i>Arabidopsis thaliana</i>           | no  | yes |
| 551801*               | eugene3.00021116                 | POPTR_0002s12130.1 | 82.0/6.6 | 15/15 | 148.39 | Serine protease                                                             | 98% | Q8RVJ7 | <i>Populus canadensis</i>             | yes |     |
| 675847*               | grail3.0028002001                | POPTR_0006s14400.1 | 39.3/6.3 | 4/4   | 40.31  | Cysteine protease CP1                                                       | 79% | A5HIJ1 | <i>Actinidia deliciosa</i>            | yes |     |
| 781583*               | fgenes4_pg.C_scaffold_40000333   | POPTR_0014s02410.1 | 50.4/5.4 | 3/3   | 20.16  | Cysteine protease CP1                                                       | 82% | Q52QX8 | <i>Manihot esculenta</i>              | yes |     |
| 560367*               | eugene3.00060326                 | POPTR_0006s03490.1 | 51.1/4.9 | 9/8   | 88.24  | Serine carboxypeptidase family protein                                      | 65% | Q2R3G8 | <i>Oryza sativa subsp. japonica</i>   | yes |     |
| 835003*               | estExt_fgenes4_pm.C_LG_XIV0520   | POPTR_0014s17580.1 | 55.6/5.4 | 7/6   | 60.21  | Serine carboxypeptidase-like 20                                             | 72% | Q8L7B2 | <i>Arabidopsis thaliana</i>           | yes |     |
| 199556 <sup>**</sup>  | gw1.IX.21.1                      | POPTR_0009s00820.1 | 49.0/5.4 | 6/6   | 60.20  | Serine carboxypeptidase-like 51                                             | 67% | Q67Y83 | <i>Arabidopsis thaliana</i>           | no  | yes |

Table S2. continued

|                                  |                                   |                    |           |      |        |                                                                      |      |        |                                                     |     |     |
|----------------------------------|-----------------------------------|--------------------|-----------|------|--------|----------------------------------------------------------------------|------|--------|-----------------------------------------------------|-----|-----|
| 249095 <sup>#*</sup>             | gw1.XIX.1495.1                    | POPTR_0019s08160.1 | 52.4/5.2  | 5/4  | 50.27  | Wound-inducible carboxypeptidase                                     | 64%  | Q9M513 | <i>Solanum lycopersicum</i>                         | no  | yes |
| 751613                           | fgenesH4_pg.C_LG_I001216          | POPTR_0001s22090.1 | 55.8/5.3  | 3/1  | 30.25  | Prolylcarboxypeptidase-like protein                                  | 58%  | Q8LFB7 | <i>Arabidopsis thaliana</i>                         | yes |     |
| 825802*                          | estExt_fgenesH4_pg.C_LG_XVIII0531 | POPTR_0018s03020.1 | 49.9/7.4  | 10/7 | 90.39  | 41 kD chloroplast nucleoid DNA binding protein                       | 45%  | Q8H9F4 | <i>Nicotiana glauca</i>                             | yes |     |
| 571847                           | eugene3.00131211                  | POPTR_0013s14800.1 | 90.4/6.2  | 1/1  | 8.19   | Cell survival CED-4-interacting protein MAC-1                        | 61%  | Q5VRN1 | <i>Oryza sativa subsp. japonica</i>                 | no  | no  |
| <b>Carbohydrate metabolism</b>   |                                   |                    |           |      |        |                                                                      |      |        |                                                     |     |     |
| 575698*                          | eugene3.00151093                  | POPTR_0015s14380.1 | 47.9/5.7  | 3/3  | 20.16  | Enolase                                                              | 100% | A9PD49 | <i>Populus trichocarpa</i>                          | no  | yes |
| 772214*                          | fgenesH4_pg.C_LG_XI001367         | POPTR_0011s16170.1 | 59.6/6.1  | 9/8  | 60.23  | Carbohydrate oxidase                                                 | 59%  | Q8SA59 | <i>Helianthus annuus</i>                            | yes |     |
| 286987 <sup>#*</sup>             | gw1.40.747.1                      | POPTR_0014s02940.1 | 43.7/4.8  | 5/1  | 50.27  | Alpha-amylase                                                        | 77%  | Q7X9T1 | <i>Phaseolus angularis</i>                          | no  | yes |
| 644125*                          | grail3.0033012902                 | POPTR_0515s00220.2 | 44.1/5.1  | 15/5 | 120.27 | Alpha-amylase                                                        | 78%  | Q7X9T1 | <i>Phaseolus angularis</i>                          | no  | yes |
| <b>Other metabolic processes</b> |                                   |                    |           |      |        |                                                                      |      |        |                                                     |     |     |
| 816232*                          | estExt_fgenesH4_pg.C_LG_II0662    | POPTR_0002s07290.1 | 41.1/6.3  | 4/3  | 40.35  | Alcohol dehydrogenase 2                                              | 87%  | Q9FZ01 | <i>Vitis vinifera</i>                               | no  | no  |
| 828210                           | estExt_fgenesH4_pg.C_1450022      | POPTR_0018s07000.1 | 53.5/5.8  | 3/3  | 20.14  | Nucleotide pyrophosphatase-like protein                              | 70%  | Q9FS13 | <i>Spinacia oleracea</i>                            | SA  | yes |
| 652386                           | grail3.0024007102                 | POPTR_0006s01080.1 | 45.6/5.3  | 1/1  | 8.14   | Fumarylacetoacetase                                                  | 77%  | Q2HT34 | <i>Medicago truncatula</i>                          | no  | yes |
| 755459                           | fgenesH4_pg.C_LG_II001639         | POPTR_0002s17860.1 | 58.8/9.0  | 1/1  | 8.14   | 3-ketoacyl-CoA synthase 10                                           | 82%  | A9XU46 | <i>Gossypium hirsutum</i>                           | SA  | no  |
| 580100                           | eugene3.01180035                  | POPTR_0003s08760.1 | 17.8/5.1  | 2/2  | 10.21  | Mitochondrial glycine decarboxylase complex H-protein                | 98%  | Q6UJ35 | <i>Populus tremuloides</i>                          | yes |     |
| 204539 <sup>#</sup>              | gw1.IX.5004.1                     | POPTR_0009s01140.1 | 74.6/7.3  | 1/1  | 8.16   | DNA ligase                                                           | 81%  | A7PQQ0 | <i>Vitis vinifera</i>                               | no  | no  |
| 418463 <sup>#</sup>              | gw1.VI.2836.1                     | POPTR_0006s01000.1 | 25.9/4.8  | 1/1  | 10.14  | ABC transporter                                                      | 73%  | Q65CB1 | <i>Populus tremula</i> x <i>Populus tremuloides</i> | no  | yes |
| 821987                           | estExt_fgenesH4_pg.C_LG_X0820     | POPTR_0010s10020.1 | 20.0/9.4  | 1/1  | 10.24  | F9D12.16 protein (Copper binding protein-like, GPI-anchored protein) | 53%  | O81500 | <i>Arabidopsis thaliana</i>                         | yes |     |
| 419378 <sup>#</sup>              | gw1.VIII.806.1                    | POPTR_0008s15040.1 | 16.8/9.0  | 2/2  | 28.27  | F9D12.16 protein (Copper binding protein-like, GPI-anchored protein) | 60%  | O81500 | <i>Arabidopsis thaliana</i>                         | yes |     |
| 417410 <sup>#</sup>              | gw1.VI.1783.1                     | POPTR_0006s06650.1 | 31.6/5.2  | 1/1  | 10.26  | Dicyanin                                                             | 44%  | Q9M510 | <i>Solanum lycopersicum</i>                         | yes |     |
| 652151*                          | grail3.0002074001                 | POPTR_0005s26740.1 | 17.0/5.1  | 4/3  | 40.27  | Plastocyanin A                                                       | 100% | P00299 | <i>Populus nigra</i>                                | no  | yes |
| 813630                           | estExt_fgenesH4_kg.C_LG_II0003    | POPTR_0002s01740.1 | 17.0/4.9  | 5/4  | 40.23  | Plastocyanin B                                                       | 98%  | P11970 | <i>Populus nigra</i>                                | yes |     |
| 574226                           | eugene3.00190700                  | POPTR_0019s10720.1 | 108.0/5.5 | 1/1  | 10.13  | Leucine-rich receptor-like protein kinase                            | 59%  | Q9C7T7 | <i>Arabidopsis thaliana</i>                         | yes |     |
| 294068 <sup>#</sup>              | gw1.66.741.1                      | POPTR_0004s21990.1 | 70.2/5.2  | 1/1  | 8.15   | E3 SUMO-protein ligase SIZ1                                          | 68%  | Q680Q4 | <i>Arabidopsis thaliana</i>                         | no  | no  |
| 802937                           | fgenesH4_pm.C_LG_VII000423        | POPTR_0007s13010.2 | 83.3/6.0  | 1/1  | 8.14   | Bg55 protein                                                         | 60%  | Q93XR9 | <i>Bruguiera gymnorhiza</i>                         | no  | no  |
| 177387 <sup>#</sup>              | gw1.I.5987.1                      | POPTR_0001s46710.1 | 56.8/6.0  | 8/5  | 50.26  | At1g30760/T5I8_22                                                    | 66%  | Q93ZA3 | <i>Arabidopsis thaliana</i>                         | no  | no  |
| <b>Nutrient assimilation</b>     |                                   |                    |           |      |        |                                                                      |      |        |                                                     |     |     |
| 566952                           | eugene3.00101510                  | POPTR_0010s16790.1 | 72.5/5.8  | 4/4  | 40.19  | Purple acid phosphatase                                              | 67%  | Q5MAU7 | <i>Arabidopsis thaliana</i>                         | yes |     |
| 414694 <sup>#</sup>              | gw1.III.1797.1                    | POPTR_0003s17460.1 | 56.6/5.1  | 4/3  | 26.29  | Purple acid phosphatase                                              | 79%  | Q6TPH1 | <i>Arabidopsis thaliana</i>                         | no  | yes |
| 820480                           | estExt_fgenesH4_pg.C_LG_VIII0748  | POPTR_0008s08640.1 | 25.1/5.8  | 5/5  | 40.29  | S-like ribonuclease                                                  | 76%  | Q9LLS1 | <i>Prunus dulcis</i>                                | yes |     |
| <b>Unclassified</b>              |                                   |                    |           |      |        |                                                                      |      |        |                                                     |     |     |
| 216788 <sup>#</sup>              | gw1.VII.1093.1                    | POPTR_0421s00220.1 | 19.2/9.1  | 9/2  | 94.22  | Cysteine-rich repeat secretory protein 38                            | 56%  | Q9LRJ9 | <i>Arabidopsis thaliana</i>                         | no  | no  |
| 292397 <sup>#</sup>              | gw1.64.49.1                       | POPTR_0017s06760.1 | 23.8/6.9  | 1/1  | 10.12  | Cysteine-rich repeat secretory protein 38                            | 53%  | Q9LRJ9 | <i>Arabidopsis thaliana</i>                         | no  | no  |
| 640081 <sup>#*</sup>             | grail3.0008013701                 | POPTR_0001s13320.1 | 17.4/9.6  | 3/3  | 30.26  | Leucine-rich repeat protein                                          | 67%  | A5HKK5 | <i>Nicotiana tabacum</i>                            | no  | yes |
| 293740 <sup>#</sup>              | gw1.66.413.1                      | POPTR_0004s20970.1 | 57.9/8.7  | 1/1  | 8.13   | AT3g11590/F24K9_26                                                   | 51%  | Q945L6 | <i>Arabidopsis thaliana</i>                         | no  | yes |
| 832859                           | estExt_fgenesH4_pm.C_LG_VIII0763  | POPTR_0008s18160.1 | 29.4/6.7  | 1/1  | 8.15   | F21J9.10                                                             | 67%  | Q9FYL9 | <i>Arabidopsis thaliana</i>                         | no  | yes |

Table S2. continued

|                     |                                  |                    |           |       |        |                                                   |     |        |                                     |     |     |
|---------------------|----------------------------------|--------------------|-----------|-------|--------|---------------------------------------------------|-----|--------|-------------------------------------|-----|-----|
| 553942              | eugene3.00030575                 | POPTR_0007s10160.1 | 69.4/9.0  | 1/1   | 8.13   | Tetratricopeptide repeat (TPR)-containing protein | 48% | Q6L4Y6 | <i>Oryza sativa subsp. japonica</i> | no  | yes |
| 252587 <sup>#</sup> | gw1.XV.2023.1                    | POPTR_0015s10470.1 | 46.6/9.8  | 1/1   | 8.14   | Auxin-independent growth promoter-like protein    | 74% | Q9FMW3 | <i>Arabidopsis thaliana</i>         | no  | no  |
| 549865*             | eugene3.00012306                 | POPTR_0001s31740.1 | 20.9/8.7  | 2/2   | 20.26  | Tumor-related protein                             | 37% | P93378 | <i>Nicotiana tabacum</i>            | yes |     |
| 814847*             | estExt_fgenes4_pg.C_LG_I0347     | POPTR_0001s05560.1 | 95.2/5.5  | 34/24 | 280.34 | no sequence similarity to a known protein         |     |        |                                     | yes |     |
| 413168 <sup>#</sup> | gw1.III.271.1                    | POPTR_0003s20500.1 | 95.2/6.4  | 12/2  | 98.34  | no sequence similarity to a known protein         |     |        |                                     | yes |     |
| 588847              | eugene3.26820002                 |                    | 71.0/10.9 | 2/2   | 8.12   | no sequence similarity to a known protein         |     |        |                                     | yes |     |
| 791899              | fgenes4_pg.C_scaffold_3039000001 |                    | 88.5/11.6 | 1/1   | 6.18   | no sequence similarity to a known protein         |     |        |                                     | no  | no  |

<sup>#</sup> protein sequence in JGI database is incomplete

\* protein was also identified via 2D-PAGE MSMS

SA - protein is predicted to serve as signal anchor