

## Supplementary information

**Table S9 The DEPs function as photosynthesis in the infected poplars with *Alternaria alternata***

| Protein name                                | Accession | FC-FI  | MC-MI  | FC-MC  | FI-MI  | KEGG (ko id   ko definition)                                    |
|---------------------------------------------|-----------|--------|--------|--------|--------|-----------------------------------------------------------------|
| ATP synthase subunit b                      | A9PJR0    | 1.104* | 0.781  | 1.021  | 0.779* | K02109 F-type H <sup>+</sup> -transporting ATPase subunit b     |
| ATP synthase subunit b'                     | A9PE72    | 1.062* | 0.839* | 0.913* | 0.691* | K02109 F-type H <sup>+</sup> -transporting ATPase subunit b     |
| ATP synthase subunit b'                     | B9HAF4    | 1.026  | 0.947  | 0.84   | 0.763* | K02109 F-type H <sup>+</sup> -transporting ATPase subunit b     |
| ATP synthase delta chain                    | B9IQM7    | 1.071  | 0.871  | 0.787* | 0.765* | K02113 F-type H <sup>+</sup> -transporting ATPase subunit delta |
| Cytochrome b6-f complex iron-sulfur subunit | B9I6H7    | 1.215* | 1.151* | 0.909  | 0.831  | K02636 cytochrome b6-f complex iron-sulfur subunit, PetC        |
| Cytochrome b6-f complex subunit 4           | B9NJ16    | 1.535* | 0.497* | 1.213* | 0.428* | K02637 cytochrome b6-f complex subunit 4, PetD                  |
| Ferredoxin--NADP reductase                  | B9MXF5    | 1.079  | 1.246* | 0.916  | 1.152* | K02641 ferredoxin--NADP <sup>+</sup> reductase, PetH            |

|                                            |        |        |        |        |        |                                                                |
|--------------------------------------------|--------|--------|--------|--------|--------|----------------------------------------------------------------|
| Photosystem I reaction center subunit VI   | A9PG57 | 0.778* | 0.915  | 0.949  | 1.134  | K02695 photosystem I subunit VI, PsaH                          |
| Photosystem I reaction center subunit N    | B9HES1 | 0.901* | 0.793* | 0.998  | 0.865* | K02701 photosystem I subunit PsaN                              |
| Photosystem II CP43 chlorophyll apoprotein | B9NAT1 | 1.183  | 1.306* | 1.003  | 1.127  | K02705 photosystem II CP43 chlorophyll apoprotein,PsbC         |
| Photosystem II reaction center protein H   | A4GYU0 | 1.147  | 0.686* | 1.124  | 0.671* | K02709 photosystem II PsbH protein, PsbH                       |
| Oxygen-evolving enhancer protein 1         | A9PHA9 | 1.11   | 0.911* | 0.976  | 0.767* | K02716 photosystem II oxygen-evolving enhancer protein 1, PsbO |
| Oxygen-evolving enhancer protein 1         | A9PHI5 | 0.783  | 0.831* | 1.017  | 1.018  | K02716 photosystem II oxygen-evolving enhancer protein 1, PsbO |
| PsbP-like protein 2                        | B9HTN1 | 0.926  | 1.435* | 0.696  | 1.097  | K02717 photosystem II oxygen-evolving enhancer protein 2, PsbP |
| Photosystem II 10 kDa polypeptide          | A9PHU8 | 0.666* | 1.046  | 0.859* | 1.283* | K03541 photosystem II 10kDa protein, PsbR                      |

|                                                 |        |        |        |        |        |                                                                             |
|-------------------------------------------------|--------|--------|--------|--------|--------|-----------------------------------------------------------------------------|
| Oxygen-evolving enhancer protein 3              | A9PFR3 | 1.102  | 0.816* | 0.852* | 0.669* | K08901 photosystem II oxygen-evolving enhancer protein 3, PsbQ              |
| Oxygen-evolving enhancer protein 3              | A9PF82 | 1.254* | 0.924* | 0.963  | 0.736* | K08901 photosystem II oxygen-evolving enhancer protein 3, PsbQ              |
| Thylakoid lumenal protein At1g03610             | A9PK58 | 0.787  | 1.145  | 0.967  | 1.43*  | K08902 photosystem II Psb27 protein, Psb27                                  |
| Chlorophyll a-b binding protein 3               | A9PE75 | 1.104  | 0.81*  | 1.103  | 0.925  | K08909 light-harvesting complex I chlorophyll a/b binding protein 3, Lhca3  |
| Chlorophyll a-b binding protein P4              | B9N4C4 | 1.14   | 0.813  | 0.938  | 0.682* | K08910 light-harvesting complex I chlorophyll a/b binding protein 4, Lhca4  |
| Chlorophyll a-b binding protein of LHCII type 1 | B9I107 | 1      | 0.597* | 1.085  | 0.585* | K08912 light-harvesting complex II chlorophyll a/b binding protein 1, Lhcb1 |
| Chlorophyll a-b binding protein of LHCII type 1 | A9PEI5 | 1.342  | 0.643* | 1.195  | 0.51*  | K08912 light-harvesting complex II chlorophyll a/b binding protein 1, Lhcb1 |

---

|                                          |        |        |        |        |        |                                                                             |
|------------------------------------------|--------|--------|--------|--------|--------|-----------------------------------------------------------------------------|
| Chlorophyll a-b binding protein 5        | A9PFW7 | 1.081  | 0.602* | 1.169* | 0.644* | K08913 light-harvesting complex II chlorophyll a/b binding protein 2, Lhcb2 |
| Chlorophyll a-b binding protein 13       | B9N576 | 1.006  | 0.505* | 1.104  | 0.584* | K08914 light-harvesting complex II chlorophyll a/b binding protein 3, Lhcb3 |
| Chlorophyll a-b binding protein CP29.3   | B9HHN0 | 1.358  | 1.213* | 0.953  | 0.875* | K08915 light-harvesting complex II chlorophyll a/b binding protein 4, Lhcb4 |
| Chlorophyll a-b binding protein CP29.2   | B9HCM1 | 0.942  | 0.626* | 1.226* | 0.786* | K08915 light-harvesting complex II chlorophyll a/b binding protein 4, Lhcb4 |
| Chlorophyll a-b binding protein CP29.2   | B9IG87 | 1.207  | 0.955  | 1.042  | 0.784* | K08915 light-harvesting complex II chlorophyll a/b binding protein 4, Lhcb4 |
| Chlorophyll a-b binding protein CP26     | A9PGZ3 | 1.049  | 0.821* | 1.012  | 0.694  | K08916 light-harvesting complex II chlorophyll a/b binding protein 5, Lhcb5 |
| Chlorophyll a-b binding protein CP24 10A | A9PFP4 | 1.413* | 0.848* | 1.075  | 0.644* | K08917 light-harvesting complex II chlorophyll a/b binding protein 6, Lhcb6 |

---

FC, control female; MC, control male; FI, infected female; MI, infected male. FC-MC: comparison group between control female and control male, FC-FI: comparison group between control female and infected female, MC-MI: comparison group between control male and infected male, FI-MI: comparison group between infected female and infected male. \*:  $P < 0.05$ .

**Table S10 The DEPs function as antioxidant system in the infected poplars with *Alternaria alternata***

| Protein name                        | Accession | FC-FI  | MC-MI  | FC-MC  | FI-MI  | KEGG (ko id   ko definition)                            |
|-------------------------------------|-----------|--------|--------|--------|--------|---------------------------------------------------------|
| <b>Superoxide dismutase in DEPs</b> |           |        |        |        |        |                                                         |
| Superoxide dismutase [Cu-Zn]        | A9PHV3    | 1.028  | 1.166  | 0.714* | 0.918  | K04565 Cu/Zn superoxide dismutase [EC:1.15.1.1]         |
| Superoxide dismutase [Mn]           | B9I887    | 1.258* | 0.948  | 0.813  | 0.756* | K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1] |
| Superoxide dismutase [Mn]           | A9PCP4    | 1.36   | 1.085  | 0.949  | 0.77*  | K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1] |
| <b>Peroxidase in DEPs</b>           |           |        |        |        |        |                                                         |
| Peroxidase 52                       | B9N128    | 2.454* | 2.153* | 0.75*  | 0.669* | K00430 peroxidase [EC:1.11.1.7]                         |
| Peroxidase 51                       | B9GYX4    | 0.803  | 1.155  | 1.23   | 1.663* | K00430 peroxidase [EC:1.11.1.7]                         |
| Peroxidase 4                        | B9I6X1    | 1.399  | 1.404  | 0.712  | 0.726* | K00430 peroxidase [EC:1.11.1.7]                         |
| Peroxidase 4                        | B9I6X2    | 1.385* | 1.561* | 0.768* | 0.903  | K00430 peroxidase [EC:1.11.1.7]                         |

|                                       |        |        |        |        |        |                                                   |
|---------------------------------------|--------|--------|--------|--------|--------|---------------------------------------------------|
| Peroxidase 3                          | B9HHF1 | 0.856* | 1.239* | 0.981  | 1.439* | K00430 peroxidase [EC:1.11.1.7]                   |
| Peroxidase                            | B9IGP7 | 1.457  | 1.653* | 0.801  | 0.977  | K00430 peroxidase [EC:1.11.1.7]                   |
| <b>DEPs in glutathione metabolism</b> |        |        |        |        |        |                                                   |
| Glutamate--cysteine ligase            | B9GWI2 | 1.329* | 0.947  | 1.183* | 0.857  | K01919 glutamate--cysteine ligase<br>[EC:6.3.2.2] |
| Glutathione S-transferase DHAR2       | B9HM36 | 1.035  | 1.337* | 0.755  | 0.991  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Probable glutathione S-transferase    | B9I0G5 | 1.409* | 1.632  | 0.889* | 0.954  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Glutathione S-transferase             | A9PBD6 | 1.223  | 1.226* | 0.767  | 0.754* | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Glutathione S-transferase F11         | A9PHH6 | 0.472  | 0.62*  | 0.907  | 1.241  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Glutathione S-transferase             | A9PFC2 | 1.332* | 1.046  | 0.674  | 0.651* | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |

|                                         |        |        |        |       |        |                                                   |
|-----------------------------------------|--------|--------|--------|-------|--------|---------------------------------------------------|
| Glutathione S-transferase DHAR2         | A9P9R8 | 0.721* | 0.743* | 1.047 | 1.035  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Probable glutathione S-transferase      | B9PAW7 | 0.69*  | 1.031  | 1.056 | 1.494* | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Glutathione S-transferase U17           | A9PGB4 | 1.419* | 1.453* | 1.14  | 1.102  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Glutathione S-transferase L3            | B9MT66 | 1.556* | 1.289  | 0.936 | 0.8*   | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Probable glutathione S-transferase      | B9IHF7 | 1.119  | 1.448* | 0.951 | 1.202  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Probable glutathione S-transferase parC | B9PA81 | 2.647  | 1.845  | 0.927 | 0.657* | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| Glutathione S-transferase F11           | B9MWW0 | 1.916  | 1.705* | 1.221 | 1.104  | K00799 glutathione S-transferase<br>[EC:2.5.1.18] |
| L-ascorbate peroxidase 2                | Q6ZXH7 | 1.537* | 1.155* | 1.087 | 0.818* | K00434 L-ascorbate peroxidase [EC:1.11.1.11]      |

|                                                            |        |        |        |        |        |                                                       |
|------------------------------------------------------------|--------|--------|--------|--------|--------|-------------------------------------------------------|
| Probable L-ascorbate peroxidase 6                          | B9H7G1 | 1.416* | 1.288* | 0.877  | 0.823* | K00434 L-ascorbate peroxidase [EC:1.11.1.11]          |
| Probable L-ascorbate peroxidase 8                          | B9GU24 | 1.186* | 1.217* | 0.982  | 1.045  | K00434 L-ascorbate peroxidase [EC:1.11.1.11]          |
| L-ascorbate peroxidase 3                                   | B9H192 | 1.135  | 0.866* | 1.282* | 0.977  | K00434 L-ascorbate peroxidase [EC:1.11.1.11]          |
| Phospholipid hydroperoxide glutathione peroxidase 1        | A9PK73 | 0.763* | 0.738* | 1.001  | 0.871  | K00432 glutathione peroxidase [EC:1.11.1.9]           |
| Probable phospholipid hydroperoxide glutathione peroxidase | A9PI44 | 1.142  | 1.036  | 0.89   | 0.821* | K00432 glutathione peroxidase [EC:1.11.1.9]           |
| Glutathione reductase                                      | A9PHY8 | 1.719  | 1.503* | 1.013  | 0.849* | K00383 glutathione reductase (NADPH) [EC:1.8.1.7]     |
| 6-phosphogluconate dehydrogenase                           | B9H3V6 | 1.278* | 0.921  | 1.169  | 0.869  | K00033 6-phosphogluconate dehydrogenase [EC:1.1.1.44] |
| 6-phosphogluconate dehydrogenase                           | B9N1W3 | 1.67   | 0.975  | 1.419* | 0.843  | K00033 6-phosphogluconate dehydrogenase [EC:1.1.1.44] |

FC, control female; MC, control male; FI, infected female; MI, infected male. FC-MC: comparison group between control female and control male, FC-FI: comparison group between control female and infected female, MC-MI: comparison group between control male and infected male, FI-MI: comparison group between infected female and infected male. \*:  $P < 0.05$ .

**Table S11 The DEPs function as phenylpropanoid biosynthesis in the infected poplars with *Alternaria alternata***

| Protein name                                | Accession | FC-FI  | MC-MI  | FC-MC  | FI-MI  | KEGG (ko id   ko definition)                                      |
|---------------------------------------------|-----------|--------|--------|--------|--------|-------------------------------------------------------------------|
| Caffeic acid 3-O-methyltransferase 1        | F1CYW2    | 1.589* | 1.679* | 0.736* | 0.792* | K13066 caffeic acid 3-O-methyltransferase<br>[EC:2.1.1.68]        |
| Caffeic acid 3-O-methyltransferase          | B9MTJ6    | 1.178  | 0.791  | 1.12   | 0.773* | K13066 caffeic acid 3-O-methyltransferase<br>[EC:2.1.1.68]        |
| Uncharacterized acetyltransferase At3g50280 | B9GWR1    | 0.663* | 0.856  | 1.069  | 1.403* | K13065 shikimate O-hydroxycinnamoyl transferase<br>[EC:2.3.1.133] |
| Acetyl-CoA-benzylalcohol acetyltransferase  | B9N4F7    | 1.161  | 1.065  | 1.436* | 1.338  | K13065 shikimate O-hydroxycinnamoyl transferase<br>[EC:2.3.1.133] |
| BAHD acyltransferase DCR                    | B9IDB6    | 0.922  | 0.694* | 1.413* | 1.131  | K13065 shikimate O-hydroxycinnamoyl transferase<br>[EC:2.3.1.133] |
| Aldehyde dehydrogenase family 2 member C4   | B9ILK3    | 1.224  | 1.468* | 0.922  | 1.124  | K12355 coniferyl-aldehyde dehydrogenase<br>[EC:1.2.1.68]          |

|                                    |        |        |        |        |        |                                                           |
|------------------------------------|--------|--------|--------|--------|--------|-----------------------------------------------------------|
| Phenylalanine ammonia-lyase        | B2Z6R1 | 1.229* | 0.987  | 1.181  | 0.987  | K10775 phenylalanine ammonia-lyase [EC:4.3.1.24]          |
| Phenylalanine ammonia-lyase G4     | B2Z6R3 | 1.28*  | 1.705* | 0.896  | 1.075  | K10775 phenylalanine ammonia-lyase [EC:4.3.1.24]          |
| Cytochrome P450 71A1               | B9GW08 | 0.705* | 0.564* | 1.309* | 1.07   | K09755 ferulate-5-hydroxylase [EC:1.14.-.-]               |
| Flavonoid 3'-monooxygenase         | B9GW07 | 0.637* | 0.611* | 1.197* | 1.115* | K09755 ferulate-5-hydroxylase [EC:1.14.-.-]               |
| Cinnamoyl-CoA reductase 1          | B9HNY0 | 1.243* | 1.095  | 1.494  | 1.237  | K09753 cinnamoyl-CoA reductase [EC:1.2.1.44]              |
| Cinnamoyl-CoA reductase 1          | B2Z6Q2 | 1.364  | 1.503* | 0.888  | 0.934  | K09753 cinnamoyl-CoA reductase [EC:1.2.1.44]              |
| Beta-glucosidase 44                | B9IE97 | 0.699  | 0.65*  | 1.225  | 1.127  | K05350 beta-glucosidase [EC:3.2.1.21]                     |
| Putative beta-glucosidase 9        | B9MZ87 | 1.217  | 1.623* | 1.321* | 1.966* | K01188 beta-glucosidase [EC:3.2.1.21]                     |
| Cyanogenic beta-glucosidase        | B9GEP0 | 1.276* | 2.018* | 0.845* | 1.268* | K01188 beta-glucosidase [EC:3.2.1.21]                     |
| Caffeoyl-CoA O-methyltransferase 2 | Q8GV07 | 1.703* | 2.013* | 0.781* | 0.944  | K00588 caffeoyl-CoA O-methyltransferase<br>[EC:2.1.1.104] |

|                                           |        |        |        |        |        |                                                           |
|-------------------------------------------|--------|--------|--------|--------|--------|-----------------------------------------------------------|
| Trans-cinnamate 4-monooxygenase           | A9PBZ7 | 1.286  | 1.49*  | 0.865* | 1.114  | K00487 trans-cinnamate 4-monooxygenase<br>[EC:1.14.13.11] |
| Peroxidase 4                              | B9I6X2 | 1.385* | 1.561* | 0.768* | 0.903  | K00430 peroxidase [EC:1.11.1.7]                           |
| Peroxidase 52                             | B9N128 | 2.454* | 2.153* | 0.75*  | 0.669* | K00430 peroxidase [EC:1.11.1.7]                           |
| Peroxidase 3                              | B9HHF1 | 0.856* | 1.239* | 0.981  | 1.439* | K00430 peroxidase [EC:1.11.1.7]                           |
| Peroxidase 51                             | B9GYX4 | 0.803  | 1.155  | 1.23   | 1.663* | K00430 peroxidase [EC:1.11.1.7]                           |
| Peroxidase 4                              | B9I6X1 | 1.399  | 1.404  | 0.712  | 0.726* | K00430 peroxidase [EC:1.11.1.7]                           |
| Peroxidase                                | B9IGP7 | 1.457  | 1.653* | 0.801  | 0.977  | K00430 peroxidase [EC:1.11.1.7]                           |
| Probable cinnamyl alcohol dehydrogenase 6 | A9PHZ1 | 0.769* | 0.664* | 1.305* | 1.294  | K00083 cinnamyl-alcohol dehydrogenase<br>[EC:1.1.1.195]   |
| Probable cinnamyl alcohol dehydrogenase 9 | B9GGU3 | 1.103  | 1.192  | 1.174  | 1.294* | K00083 cinnamyl-alcohol dehydrogenase<br>[EC:1.1.1.195]   |

|                                         |        |        |        |       |        |                                                         |
|-----------------------------------------|--------|--------|--------|-------|--------|---------------------------------------------------------|
| Probable cinnamyl alcohol dehydrogenase | Q9FSC7 | 2.057* | 2.022* | 0.897 | 0.796* | K00083 cinnamyl-alcohol dehydrogenase<br>[EC:1.1.1.195] |
|-----------------------------------------|--------|--------|--------|-------|--------|---------------------------------------------------------|

FC, control female; MC, control male; FI, infected female; MI, infected male. FC-MC: comparison group between control female and control male, FC-FI: comparison group between control female and infected female, MC-MI: comparison group between control male and infected male, FI-MI: comparison group between infected female and infected male. \*:  $P < 0.05$ .

**Table S12. The interaction network of DEPs in the phenylpropanoid pathway.**

| Node 1 | Node 2 | Node 1<br>string id | Node 2<br>string id | Neighborhood<br>on chromosome | Phylogenetic<br>cooccurrence | homology | coexpression | Experimentally<br>determined<br>interaction | Database<br>annotated | Automated<br>textmining | Combined<br>score |
|--------|--------|---------------------|---------------------|-------------------------------|------------------------------|----------|--------------|---------------------------------------------|-----------------------|-------------------------|-------------------|
| A9PBZ7 | B9GPN4 | A0A4U5<br>QF09      | A0A4U5<br>MZC0      | 0                             | 0                            | 0        | 0.056        | 0.129                                       | 0.291                 | 0.184                   | 0.46              |
| A9PBZ7 | Q8GV07 | A0A4U5<br>QF09      | A0A4U5<br>QDI9      | 0                             | 0                            | 0        | 0.219        | 0                                           | 0.052                 | 0.471                   | 0.574             |
| A9PBZ7 | B9ILK3 | A0A4U5<br>QF09      | A0A4U5<br>QFX0      | 0                             | 0                            | 0        | 0.049        | 0                                           | 0.222                 | 0.259                   | 0.403             |
| A9PBZ7 | B2Z6Q2 | A0A4U5<br>QF09      | A0A4U5<br>QFE1      | 0                             | 0                            | 0        | 0.064        | 0.129                                       | 0.53                  | 0.215                   | 0.658             |
| A9PBZ7 | B2Z6R1 | A0A4U5<br>QF09      | A0A4U5<br>QRX1      | 0                             | 0                            | 0        | 0.085        | 0                                           | 0.857                 | 0.22                    | 0.889             |
| A9PBZ7 | B2Z6R3 | A0A4U5<br>QF09      | A0A4U5<br>R2N1      | 0                             | 0                            | 0        | 0.085        | 0                                           | 0.881                 | 0.471                   | 0.937             |
| A9PHZ1 | B9N128 | A0A4U5<br>QHC5      | A0A4U5<br>N728      | 0                             | 0                            | 0        | 0            | 0.049                                       | 0.906                 | 0.235                   | 0.925             |
| A9PHZ1 | Q9FSC7 | A0A4U5<br>QHC5      | A0A4U5<br>Q646      | 0                             | 0.072                        | 0.938    | 0            | 0                                           | 0.906                 | 0                       | 0.909             |
| A9PHZ1 | B9GGU3 | A0A4U5<br>QHC5      | A0A4U5<br>QCY1      | 0                             | 0.061                        | 0.959    | 0            | 0                                           | 0.906                 | 0                       | 0.908             |
| A9PHZ1 | B9I6X2 | A0A4U5<br>QHC5      | A0A4U5<br>QF74      | 0                             | 0                            | 0        | 0            | 0.049                                       | 0.824                 | 0.049                   | 0.826             |

|        |        |                |                |       |      |       |       |       |       |       |       |
|--------|--------|----------------|----------------|-------|------|-------|-------|-------|-------|-------|-------|
| A9PHZ1 | B2Z6Q2 | A0A4U5<br>QHC5 | A0A4U5<br>QFE1 | 0     | 0    | 0     | 0.076 | 0     | 0.714 | 0.045 | 0.725 |
| A9PHZ1 | B9ILK3 | A0A4U5<br>QHC5 | A0A4U5<br>QFX0 | 0.071 | 0    | 0     | 0.093 | 0     | 0.906 | 0.091 | 0.918 |
| A9PHZ1 | B9IGP7 | A0A4U5<br>QHC5 | A0A4U5<br>QWT6 | 0     | 0    | 0     | 0     | 0.049 | 0.503 | 0.043 | 0.508 |
| A9PHZ1 | B9GYX4 | A0A4U5<br>QHC5 | A0A4U5<br>QTF4 | 0     | 0    | 0     | 0     | 0.049 | 0.906 | 0     | 0.906 |
| B2Z6Q2 | Q9FSC7 | A0A4U5<br>QFE1 | A0A4U5<br>Q646 | 0     | 0    | 0     | 0.076 | 0     | 0.714 | 0.183 | 0.765 |
| B2Z6Q2 | B9GGU3 | A0A4U5<br>QFE1 | A0A4U5<br>QCY1 | 0     | 0    | 0     | 0.076 | 0     | 0.714 | 0.153 | 0.756 |
| B2Z6Q2 | Q8GV07 | A0A4U5<br>QFE1 | A0A4U5<br>QDI9 | 0.069 | 0    | 0     | 0.078 | 0     | 0.53  | 0.227 | 0.646 |
| B2Z6Q2 | B2Z6R3 | A0A4U5<br>QFE1 | A0A4U5<br>R2N1 | 0     | 0    | 0     | 0     | 0     | 0.053 | 0.474 | 0.48  |
| B2Z6Q2 | B9ILK3 | A0A4U5<br>QFE1 | A0A4U5<br>QFX0 | 0     | 0    | 0     | 0.053 | 0     | 0.714 | 0.127 | 0.742 |
| B2Z6R1 | Q8GV07 | A0A4U5<br>QRX1 | A0A4U5<br>QDI9 | 0     | 0    | 0     | 0.082 | 0     | 0     | 0.476 | 0.499 |
| B2Z6R1 | B9ILK3 | A0A4U5<br>QRX1 | A0A4U5<br>QFX0 | 0.08  | 0    | 0     | 0.141 | 0     | 0     | 0.406 | 0.489 |
| B2Z6R1 | B2Z6R3 | A0A4U5<br>QRX1 | A0A4U5<br>R2N1 | 0     | 0.05 | 0.982 | 0     | 0     | 0.881 | 0     | 0.882 |
| B2Z6R3 | Q8GV07 | A0A4U5<br>R2N1 | A0A4U5<br>QDI9 | 0     | 0    | 0     | 0.082 | 0     | 0     | 0.582 | 0.599 |

|        |        |                |                |       |       |       |       |       |       |       |       |
|--------|--------|----------------|----------------|-------|-------|-------|-------|-------|-------|-------|-------|
| B2Z6R3 | B9ILK3 | A0A4U5<br>R2N1 | A0A4U5<br>QFX0 | 0.08  | 0     | 0     | 0.141 | 0     | 0     | 0.517 | 0.584 |
| B9GEP0 | B9IE97 | A0A4U5<br>QS94 | A0A4U5<br>QKR0 | 0     | 0.082 | 0.918 | 0     | 0     | 0.485 | 0     | 0.507 |
| B9GGU3 | B9N128 | A0A4U5<br>QCY1 | A0A4U5<br>N728 | 0     | 0     | 0     | 0     | 0.049 | 0.906 | 0.049 | 0.907 |
| B9GGU3 | Q9FSC7 | A0A4U5<br>QCY1 | A0A4U5<br>Q646 | 0     | 0.065 | 0.952 | 0     | 0     | 0.905 | 0     | 0.907 |
| B9GGU3 | B9IGP7 | A0A4U5<br>QCY1 | A0A4U5<br>QWT6 | 0     | 0     | 0     | 0     | 0.049 | 0.503 | 0.043 | 0.508 |
| B9GGU3 | B9I6X2 | A0A4U5<br>QCY1 | A0A4U5<br>QF74 | 0     | 0     | 0     | 0     | 0.049 | 0.821 | 0.049 | 0.823 |
| B9GGU3 | B9GYX4 | A0A4U5<br>QCY1 | A0A4U5<br>QTF4 | 0     | 0     | 0     | 0     | 0.049 | 0.906 | 0     | 0.906 |
| B9GGU3 | B9ILK3 | A0A4U5<br>QCY1 | A0A4U5<br>QFX0 | 0.071 | 0     | 0     | 0.093 | 0     | 0.906 | 0.091 | 0.918 |
| B9GPN4 | Q9FSC7 | A0A4U5<br>MZC0 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0.076 | 0     | 0.37  | 0.057 | 0.403 |
| B9GPN4 | B9ILK3 | A0A4U5<br>MZC0 | A0A4U5<br>QFX0 | 0     | 0     | 0     | 0.053 | 0     | 0.528 | 0.049 | 0.537 |
| B9GPN4 | Q8GV07 | A0A4U5<br>MZC0 | A0A4U5<br>QDI9 | 0.069 | 0     | 0     | 0.078 | 0     | 0.52  | 0.287 | 0.666 |
| B9GYX4 | Q9FSC7 | A0A4U5<br>QTF4 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0     | 0.049 | 0.906 | 0.184 | 0.92  |
| B9HHF1 | Q9FSC7 | A0A4U5<br>NKC1 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0     | 0     | 0.823 | 0.081 | 0.83  |

|        |        |                |                |       |       |       |       |       |       |       |       |
|--------|--------|----------------|----------------|-------|-------|-------|-------|-------|-------|-------|-------|
| B9I6X1 | Q9FSC7 | A0A4U5<br>QFC7 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0     | 0.049 | 0.872 | 0     | 0.873 |
| B9I6X2 | Q9FSC7 | A0A4U5<br>QF74 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0     | 0.049 | 0.872 | 0     | 0.873 |
| B9IE97 | B9MZ87 | A0A4U5<br>QKR0 | A0A4V6<br>A2P9 | 0     | 0.082 | 0.917 | 0     | 0     | 0.485 | 0     | 0.507 |
| B9IGP7 | Q9FSC7 | A0A4U5<br>QWT6 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0     | 0.049 | 0.881 | 0     | 0.881 |
| B9ILK3 | Q9FSC7 | A0A4U5<br>QFX0 | A0A4U5<br>Q646 | 0.071 | 0     | 0     | 0.093 | 0     | 0.906 | 0.091 | 0.918 |
| B9ILK3 | Q8GV07 | A0A4U5<br>QFX0 | A0A4U5<br>QDI9 | 0     | 0     | 0     | 0.063 | 0     | 0.27  | 0.432 | 0.577 |
| B9ILK3 | B9MTJ6 | A0A4U5<br>QFX0 | A0A4U5<br>QS31 | 0     | 0     | 0     | 0     | 0     | 0.18  | 0.379 | 0.469 |
| B9MTJ6 | Q8GV07 | A0A4U5<br>QS31 | A0A4U5<br>QDI9 | 0     | 0     | 0     | 0     | 0     | 0     | 0.52  | 0.52  |
| B9N128 | Q9FSC7 | A0A4U5<br>N728 | A0A4U5<br>Q646 | 0     | 0     | 0     | 0     | 0.049 | 0.906 | 0     | 0.906 |
| Q8GV07 | Q9FSC7 | A0A4U5<br>QDI9 | A0A4U5<br>Q646 | 0.059 | 0     | 0     | 0.113 | 0     | 0.247 | 0.38  | 0.558 |

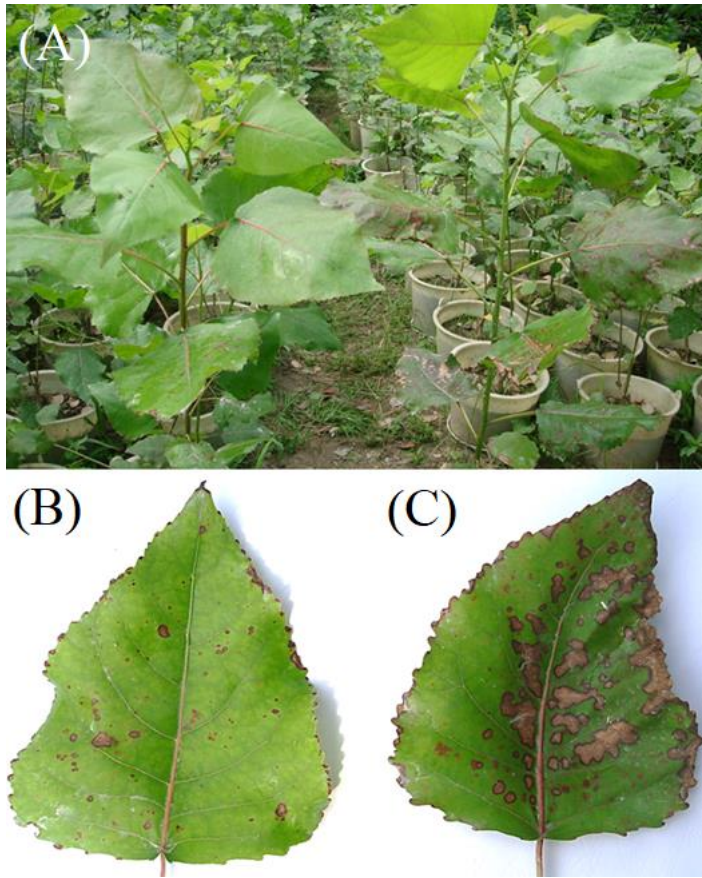


**Figure S1. The symptoms of infected male and female *Populus deltoides* after 5 days of inoculation with *Alternaria alternata*. (A): Infected male plants; (B): Infected female plants. These figures show the condition of a one-year-old cutting that has grown for two months and has been inoculated with the pathogen for 5 days.**

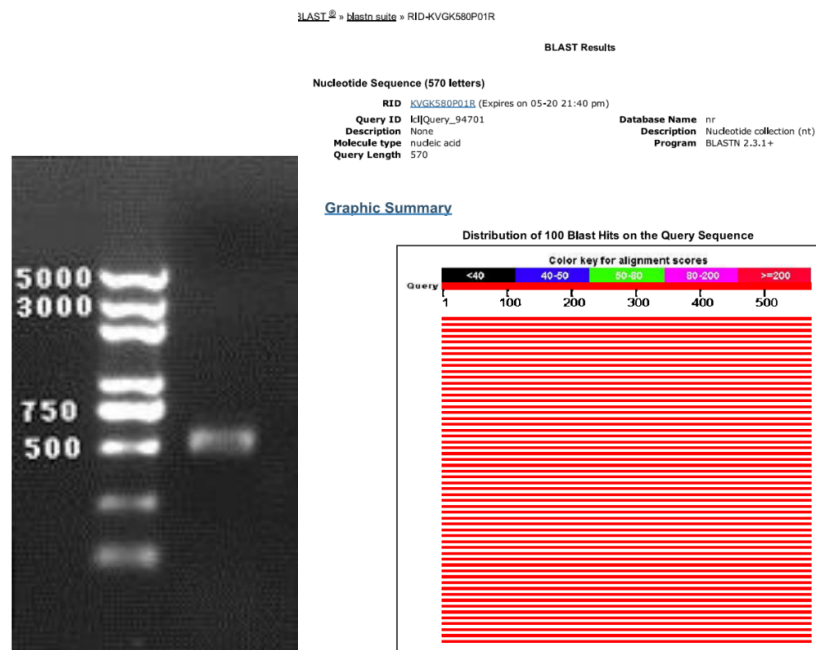


**Figure S2 *Alternaria alternata* ITS sequence amplification plot and sequence alignment result graph.**

ITS sequences: (ITS1 primer) 5' -TCCTCCGCTTATTGATATGCTTAAGTTCAGCGGGTATCCCTACCTGATCCGAGGTCAAAAGTTGAAAAAAGGCTTA  
 ATGGATGCTAGACCTTTGCTGATAGAGAGTGCGACTTGTGCTGCGCTCCGAAACCAGTAGGCCGGCTGCCAATTACTTTAAGGCGAGTCTCCAGCAAA  
 GCTAGAGACAAGACGCCCAACACCAAGCAAAGCTTGAGGGTACAAATGACGCTCGAACAGGCATGCCCTTTGGAATACCAAAGGGCGCAATGTGCGT  
 TCAAAGATTCGATGATTCACTGAATTCTGCAATTCACACTACTTATCGCATTTTCGCTGCGTTCTTCATCGATGCCAGAACCAAGAGATCCGTTGTTGAAA  
 GTTGTAATTATTAATTTGTTACTGACGCTGATTGCAATTACAAAAGGTTTATGTTTGTCTAGTGGTGGGCGAACCCACCAAGGAAACAAGAAGTACGC  
 AAAAGACAAGGGTGAATAATTCAGCAAGGCTGTAACCCCGAGAGGTTCCAGCCCGCCTTCATATTTGTGTAATGATCCCTCCGCAGGTTCACCTACGGA  
 -3' (ITS4 primer)