

SUPPORTING INFORMATION

Table S3: *Primers used for qRT-PCR.*

| Gene name | #ID | Primers (5'-3') | |
|--|--------------------|-----------------|----------------------------|
| calcium-dependent protein kinase (CPK) | BMK_Unigene_089127 | Forward | GCC GAC GCA GTT GTT TCC |
| | | Reverse | TCC ACC GCT CGT CTC CAA TG |
| | BMK_Unigene_101535 | Forward | CTC TGC GTA CCG TGT GAT GT |
| | | Reverse | CAG CAC CAT TTG GGC CTT TC |
| pathogenesis-related protein 1 (PR1) | BMK_Unigene_005746 | Forward | TCA GAC TTG TCT CCC GTG GT |
| | | Reverse | ACC CGG AGT CTT TTC ATG GG |
| respiratory burst oxidase homolog protein B (RBOH) | BMK_Unigene_108053 | Forward | AAC TGT CGA TCC ACT CCA CC |
| | | Reverse | GCT TGG GGT TTT TCG CCT TG |
| jasmonate ZIM domain-containing protein (JAZ) | BMK_Unigene_089170 | Forward | GTG AGT ACG CAC TAA CCA CG |
| | | Reverse | GCA AAG GCT TGT ACA GGG GA |
| ethylene-insensitive protein 3 (EIN3) | BMK_Unigene_009272 | Forward | GCA CCA GTC GTA CCA GAA GG |
| | | Reverse | GAG CGA CGC TAA CCT ATC CC |
| auxin responsive GH3 gene family (GH3) | BMK_Unigene_104945 | Forward | GGT TCT TGA ACT GCT CGC TC |
| | | Reverse | GGG GCT CTA CTT CCT GTT CG |
| nitric-oxide synthase (NOS) | BMK_Unigene_010760 | Forward | GCC ACC TAC GAC CTG AAG AA |
| | | Reverse | CGA CAA CAG CTT GCA CCT TC |
| disease resistance protein RPP13-like (PRM1) | BMK_Unigene_071076 | Forward | GTC AGC CAG TCG TTG CTT TG |
| | | Reverse | GCG ACG TCT CCT ACG ACA TT |

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|---|--------------------|---------|-----------------------------|
| probable WRKY transcription factor 2 (WRKY 1/2) | BMK_Unigene_086590 | Forward | AGC AAC AAG GTA AGG GGT GT |
| | | Reverse | GGA CGG ACA GAC ATA CAA CCT |
| | BMK_Unigene_066637 | Forward | TTC TTT CCC TCC GGC GAA C |
| | | Reverse | TCT TCG CCG TTC GTT CGT T |
| SAUR family protein (SAUR) | BMK_Unigene_085384 | Forward | CAT GGC CCG GCT TAG TTC TT |
| | | Reverse | AGT CAG CAA GCC GTT TCA GG |
| | BMK_Unigene_087406 | Forward | GAT CAG TTC TTG GAG AGG CGG |
| | | Reverse | GGA GTT CGG GTA CAA GCA GG |
| two-component response regulator ARR-A family (A-ARR) | BMK_Unigene_095193 | Forward | CAC CTT CCT GTC GCT CTT CG |
| | | Reverse | TTC GTC TCG TTG TTT GGG CT |
| phytochrome-interacting factor 4 (PIF4) | BMK_Unigene_104592 | Forward | GGT GAT GCA TCC GTT CCT CT |
| | | Reverse | CGT CCA TCG TTG TCG GAT CT |
| auxin-responsive protein IAA (AUX/IAA) | BMK_Unigene_094098 | Forward | ACA TGC GCC ACC GTT TAA AAT |
| | | Reverse | GCT GTT TGT TGT GTG GAG CA |
| Nonexpressor of PR genes 1 (NPR1) | BMK_Unigene_092391 | Forward | AAC GGT TGC CCG TTG TAT CT |
| | | Reverse | ACC TCG AAA ACC GAG TTG CT |
| TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA) | BMK_Unigene_102036 | Forward | TTC CTG CTG CAA AGA GTG GT |
| | | Reverse | TTC TGG CCT GCA GTA CCT TG |
| serine/threonine-protein kinase SRK2 (SnRK2) | BMK_Unigene_103278 | Forward | AAG AAC TTC CGG CGC TAT GT |
| | | Reverse | GGG TCA GCT ACT GCC ATT CC |
| | BMK_Unigene_091577 | Forward | GCA GTC TTG GGA TAC GTG GA |
| | | Reverse | CTG GTC GGT GGT TAC CCT TT |

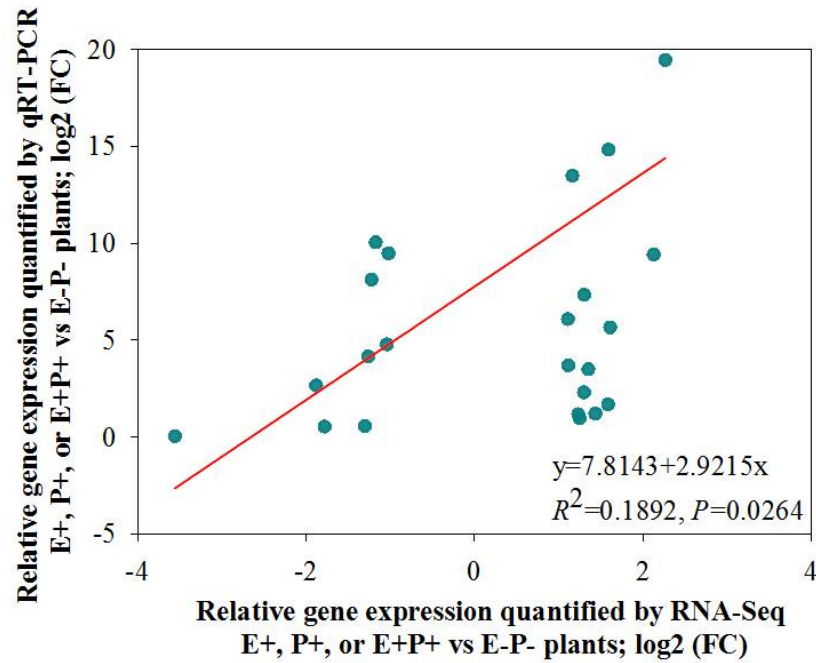
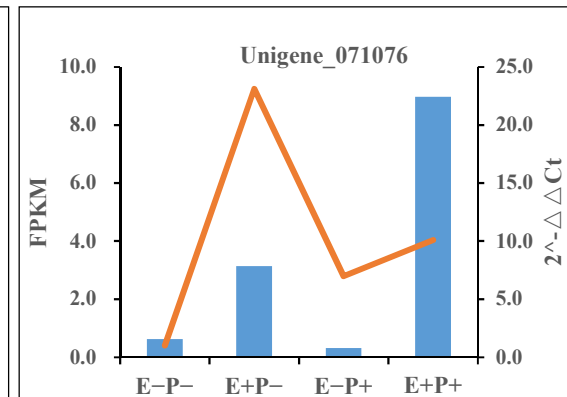
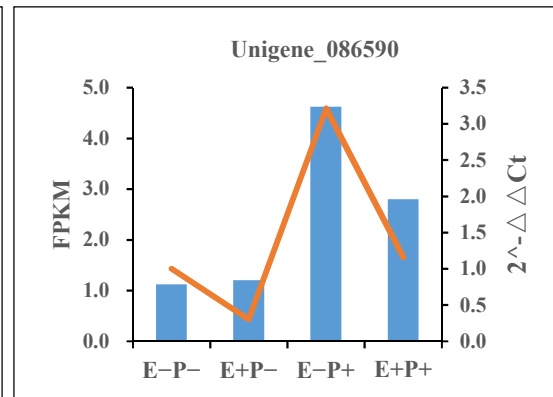
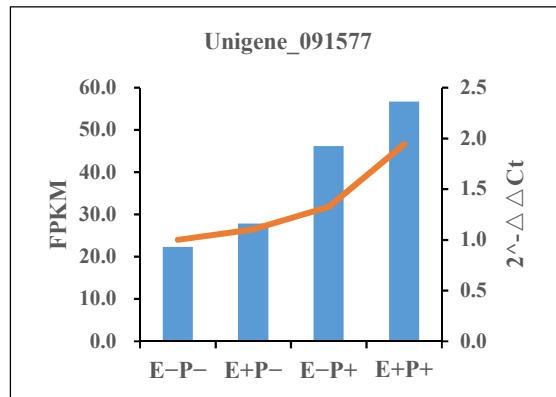
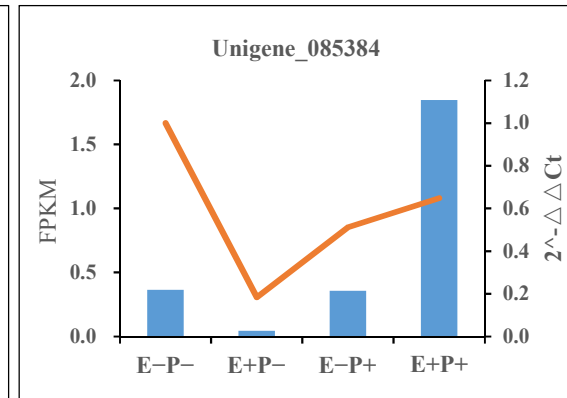
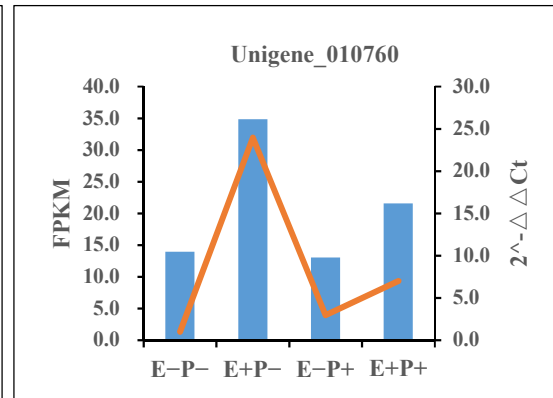
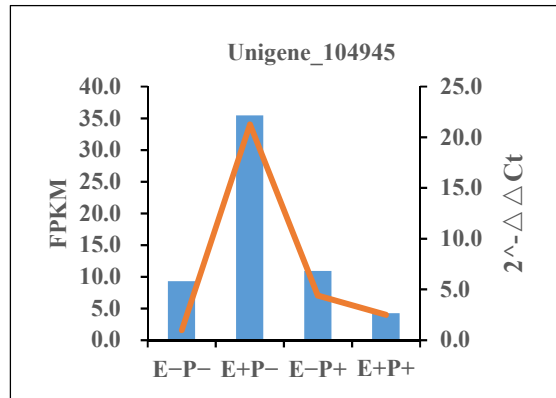


Figure S1: Relationship between expression values of genes quantified by qRT-PCR and RNA-Seq from *Achnatherum inebrians* plants associated with the endophyte *Epichloë gansuensis* (E+), the pathogen *Blumeria graminis* (P+), and both microorganisms (E+P+). The gene expression levels were measured 31/2 weeks after the pathogen inoculation on plants. The complete list of genes is described on Table S3. Relative gene expression values were referred to the E–P– condition (i.e. plants free of endophytes and pathogens) and expressed as log2 fold changes (FC) ($n = 3$).



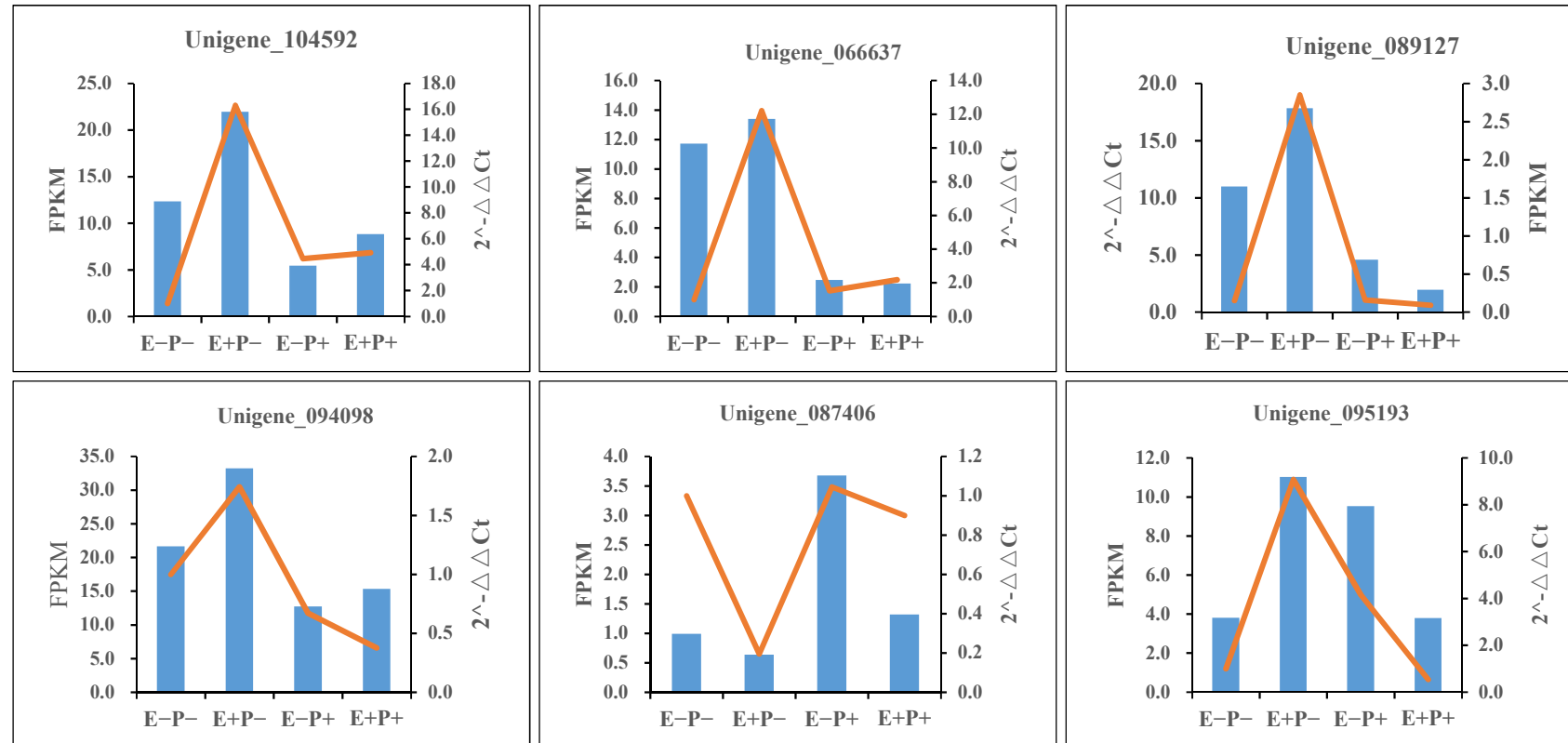


Figure S2: DEGs (differently expressed genes) identified by RNA-Seq were validated by quantitative qRT-PCR analyses. Histograms indicate the relative expression level determined by qRT-PCR of each gene using the $2^{-\Delta\Delta Ct}$ (cycle threshold) method (left y-axis). Lines represent FPKM

(frag-ments per kilobase of exon model per million mapped fragments) of the differently expressed genes according to RNA-Seq (right y-axis). *E+* and *E−* indicate *Achnatherum inebrians* plants with and without the fungal endophyte *Epichloë gansuensis*, respectively. *P+* and *P−* mean *A. inebrians* plants inoculated and non-inoculated with the pathogen *Blumeria graminis*, respectively. The complete list of genes is described on Table S3.