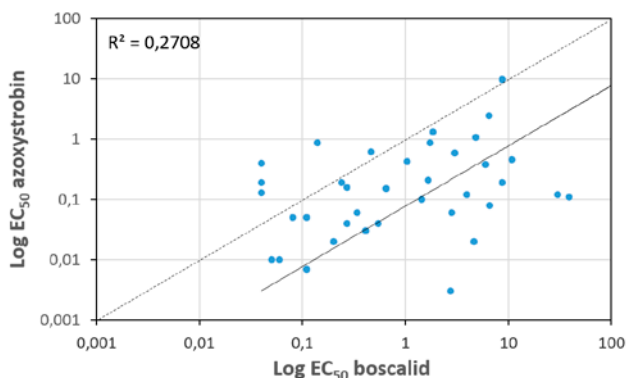
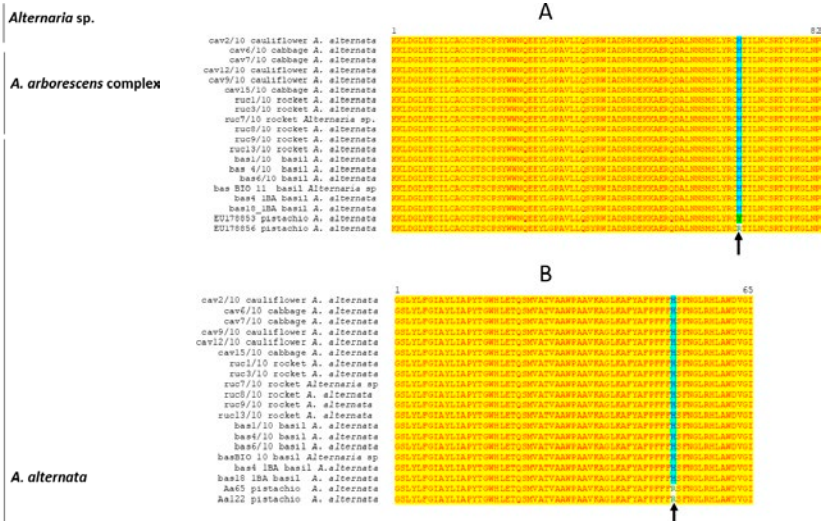


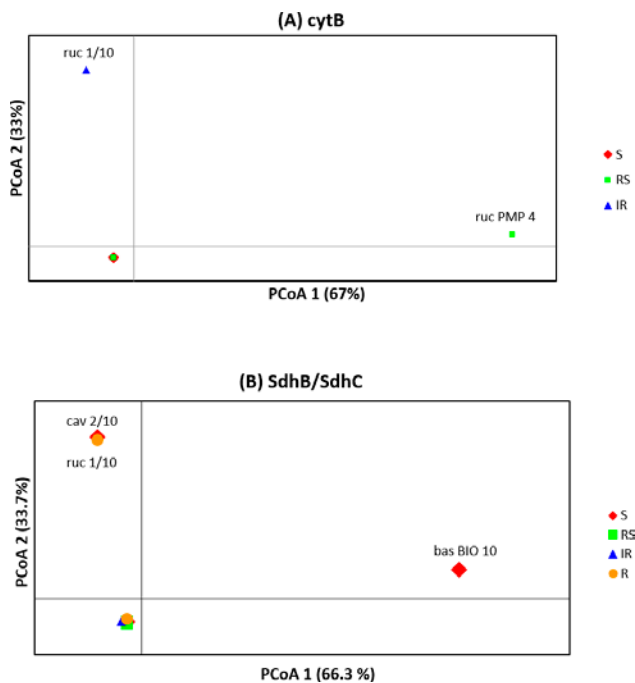
**Supplementary Figure 1.** Phylogenetic relationships of *Alternaria* spp. based on ITS, *tub2*, *endoPG* and *H3* sequences. The concatenated phylogenetic tree was obtained from a Bayesian analysis using a K81+I+G model. The name and host affiliation are indicated for each strain. Reference isolates of *A. alternata* and *A. arborescens* (Woudenberg *et al.*, 2015) are shown in bold.



**Supplementary Figure 2.** Cross-resistance (correlation among EC<sub>50</sub> values) between azoxystrobin and boscalid in 36 *Alternaria* spp. isolates from leafy vegetable crops.



**Supplementary Figure 3.** Amino acid alignment of the partial SdhB and SdhC coding regions. The 18 studied and two reference *A. alternata* strains are shown. (A) SdhB amino acid position 277, where histidine (CAC) was substituted with tyrosine (TAC) or with arginine (CGC) in the reference resistant strains (Avenot *et al.*, 2008a), is shown by the arrow. (B) SdhC amino acid position 134, where histidine (CAC) was substituted with arginine (CGC) in some previously reported resistant strains (Avenot *et al.*, 2009), is shown by the arrow.



**Supplementary Figure 4.** Principal coordinates analysis (PCoA) among subpopulations of *Alternaria* spp., based on *cytb* (a) and concatenated SdhB/SdhC (b) genes. S = sensitive to fungicides, RS = reduced sensitivity, IR = intermediate resistant, R = resistant.