



Figure S3. Primer design strategies for PCR-based identification of *C. gloeosporioides* s.l.. Primer designs were based on sequence alignment of all 14 known *Colletotrichum* mitogenomes. **a.** P₁/P₂ is expected to produce a ~ 360 bp band for isolates not belonging to *C. gloeosporioides* s.l., and a band larger than 1,500 bp for *C. gloeosporioides* s.l. isolates. **b.** The P₁ primer binding site sequences of the 14 *Colletotrichum* mitogenomes, indicating high-level nucleotide conservation. **c.** Primer locations and expected amplicon sizes for P₃/P₄, P₅/P₆, and P₇/P₈ primer pairs in (LQ22, 1104-7) and out of *C. gloeosporioides* s.l. (*C. actutatum*).