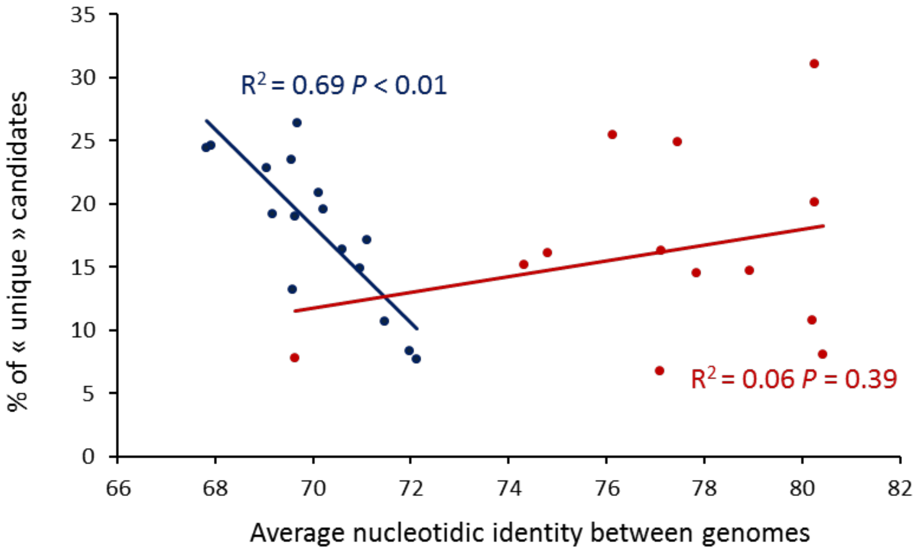
A – Module 2 - orthoMCL search



B – Module 3 - BLASTp and BLASTn filtering

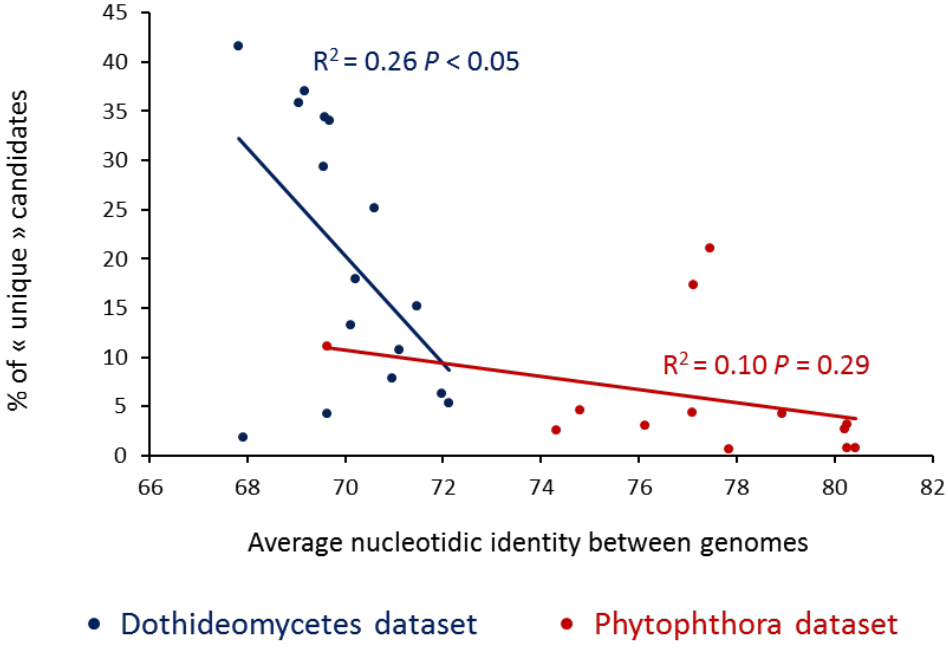


Figure S2. **Relationships between the proportion of "unique" candidates and the average nucleotidic identity between genomes in the Phytophthora and Dothideomycetes datasets.** A) Unique candidates as predicted in Module 2 of the pipeline (OrthoMCL search); B) unique candidates retained after Module 3 (filtering with BLASTp and BLASTn with e-value cutoff of 1e-05).