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2 **Appendix A Strategy for the iTRAQ-based quantitative proteomic analysis.** At
 3 40 hours after inoculation (HAI), mock and *R. solani* -inoculated leaf sheathes were
 4 collected to extract total proteins. Total proteins were digested with trypsin enzyme,
 5 the peptides were labeled with the iTRAQ reagent and pooled. The Pooled peptides
 6 were fractionated using the HPLC system. Then individual fractions were identified and
 7 quantified by LC-MS/MS. Finally, MS raw data were analyzed using bioinformatics
 8 tools. n=number of sampled plants.