## S7 - Gene Ontology analysis of S. scitamineum

## A GO Biological Process GO: 0008152 metabolic process GO: 0005975 carbohydrate metabolic process GO: 0006508 proteolysis GO: 00071554 cell wall organization or biogenesis GO: 0044036 cell wall macromolecule metabolic process GO: 0006950 response to stress GO: 0009607 response to biotic stimulus % Sequences **B** GO Molecular Function GO: 0003824 catalytic activity GO: 0016787 hydrolase activity GO: 0016798 Glycosyl bonds hydrolase activity GO: 0004553 O-glycosyl hydrolase activity GO: 0008233 peptidase activity GO: 0070011 L-amino acids peptides peptidase activity GO: 0070011 exopeptidase activity GO: 0008236 serine-type peptidase activity GO: 0017171 serine hydrolase activity GO: 0004180 carboxypeptidase activity GO: 0004190 aspartic-type endopeptidase activity GO: 0070001 aspartic-type peptidase activity GO: 0046556 alpha-L-arabinofuranosidase activity GO: 0030246 carboydrate binding Carbohydrate metabolism % Sequences Pathogenisis and defense

**Figure A.** Gene Ontologies enriched in the *S. scitamineum* secretome. (A) Biological process and (B) Molecular Function. Graphs represents the percentage of sequences in each GO term enriched in the S. scitamineum secretome (number of proteins with annotation/total number proteins).

Peptides metabolism Oxireduction