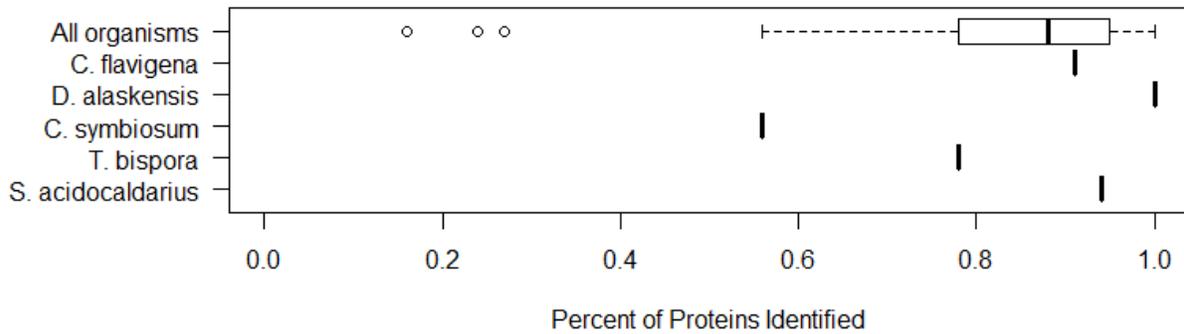




### Cysteine and Methionine Metabolism



This high coverage is typical for amino acid metabolic pathways, and any pathway annotated in KEGG. Thus the Library is both deep in its coverage of annotated protein function and broad in its coverage of taxonomic diversity.

