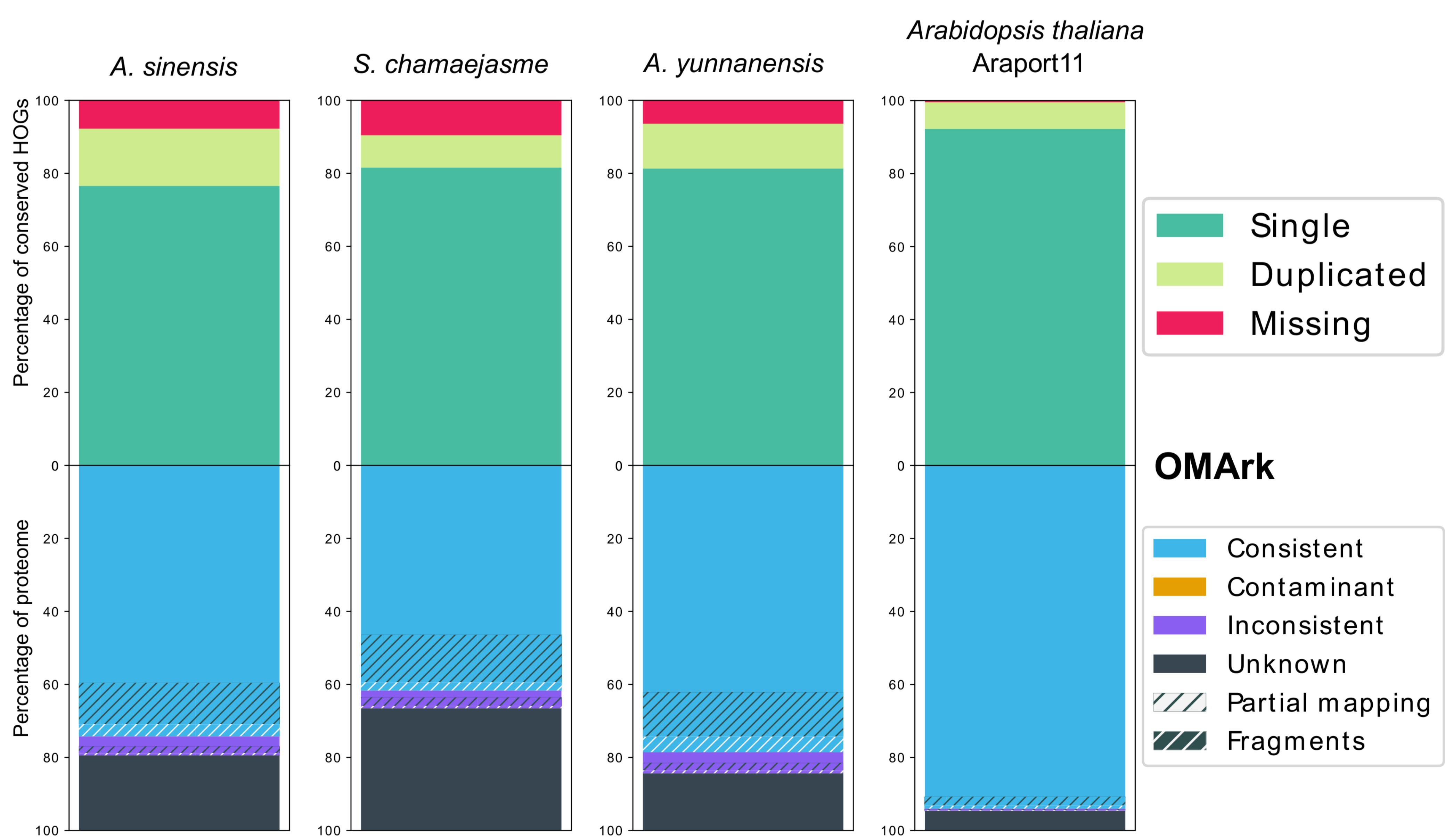


# Thymelaeaceae annotations have issues but most predicted proteins have homologs with transcript evidence

For additional information including methods, references and image attributions, scan this!



**Notes**

**OMArk**

Consistent
Contaminant
Inconsistent
Unknown
Partial mapping
Fragments

0.30      0.42      0.38      0.24      **Mono:multi-exonic genes**

Broken GFF      Methods issues      GFF-FASTA mismatch      -      **Issues**

92      70      89      -      **% proteins with transcript evidence\***

\* in orthogroup with *A. sinensis* protein backed by transcript data