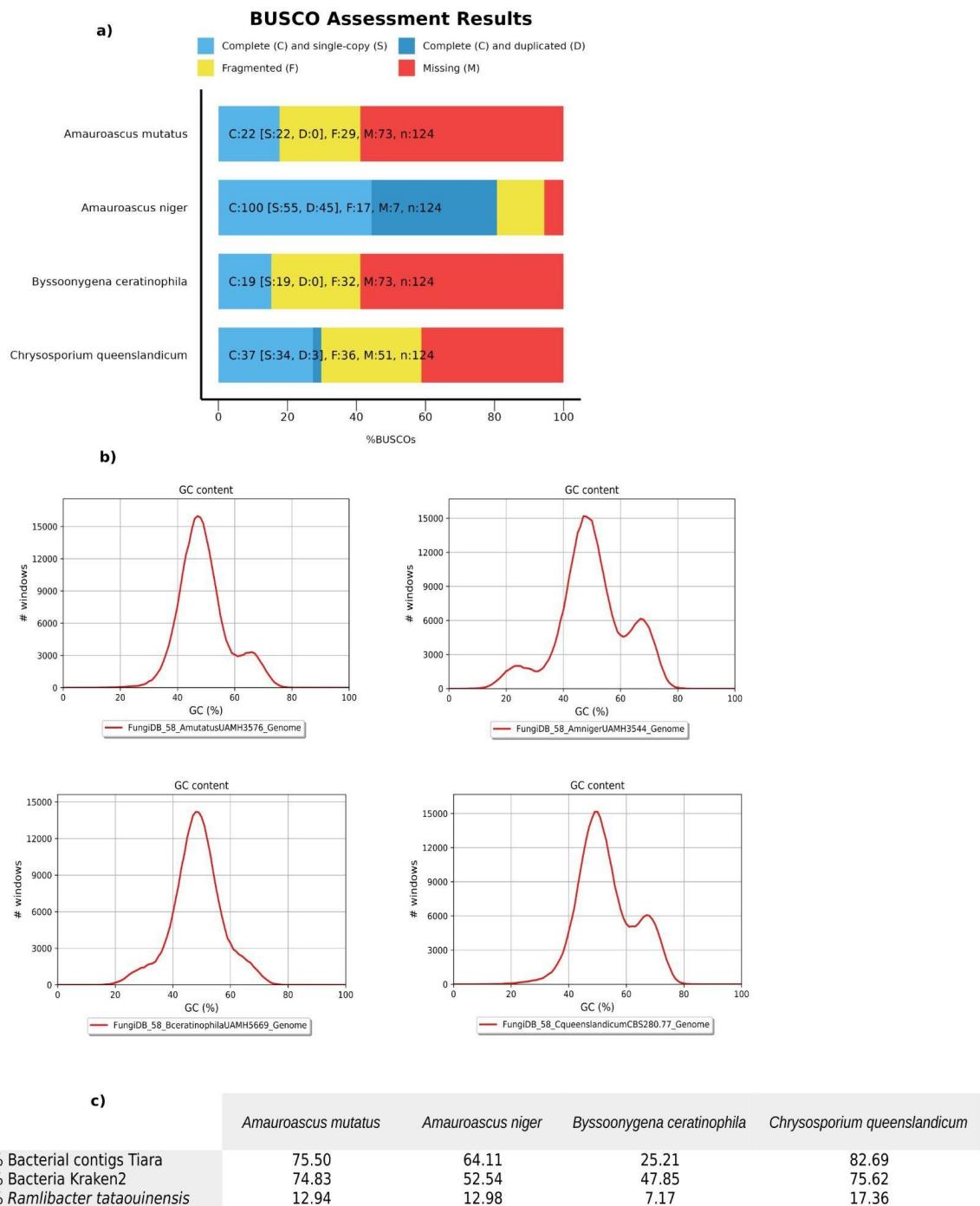
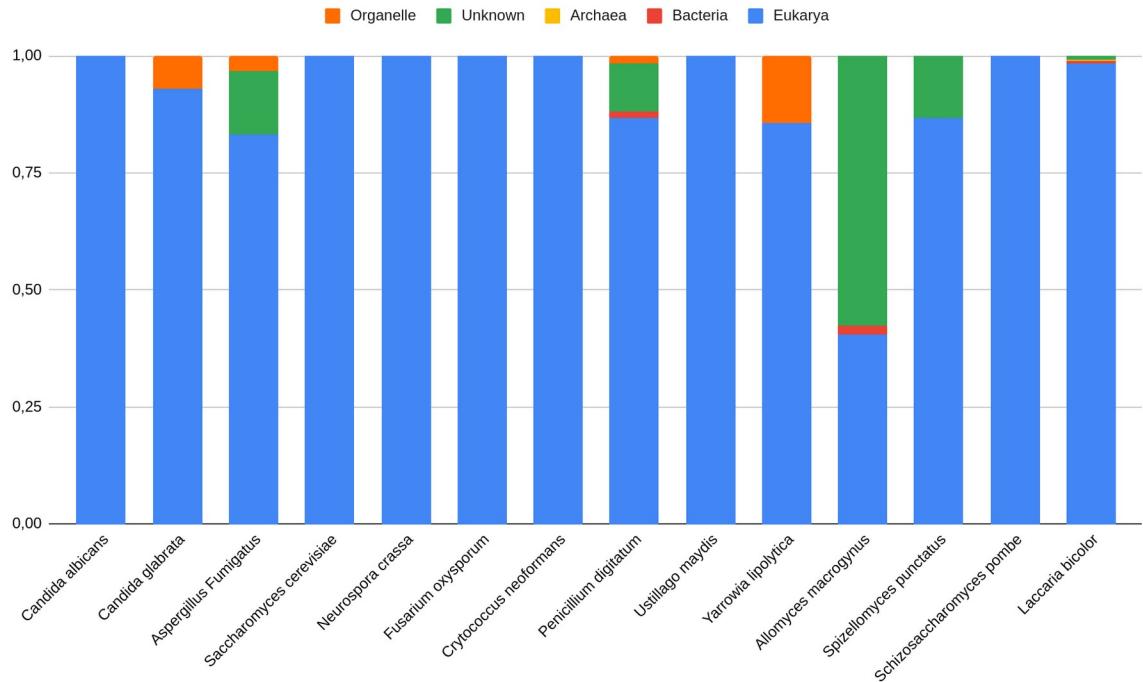


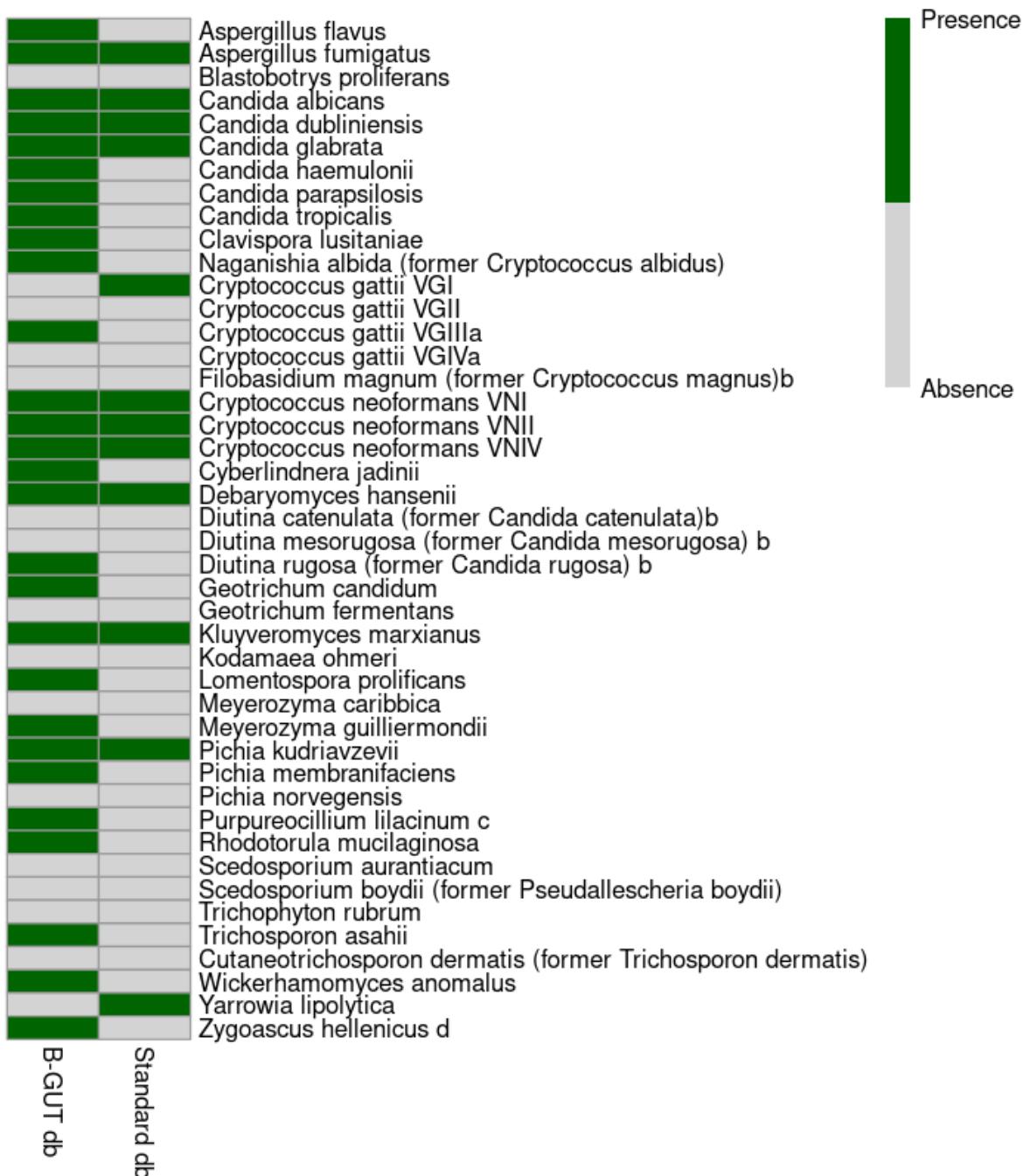
Figure S1. Smoothed version of the histogram representing the % of bacteria according to the different databases.



Supplementary figure S2. Metrics suggesting potential contamination of *Amauroascus mutatus*, *Amauroascus niger*, *Byssomyces ceratinophila* and *Chrysosporium queenslandicum*. A) BUSCO results using the bacterial lineage database. B) GC content distribution. C) Table summarizing the percentage of contigs classified as bacteria using Tiara, and the percentage of Bacteria and of *Ramlibacter tataouinensis* species detected by Kraken2 using the standard database.



Supplementary Figure S3. Tiara classification of 14 fungal models. At the y axis it is represented by the % (At scale from 0 to 1) of contigs classified at each category (Organelle, Unknown, Archaea, Bacteria or Eukarya).



Supplementary Figure S4. Heatmap representing the presence or absence of the fungal species included in the fungal mock. Green indicates correct assignment. Green represents presence and grey absence.

Supplementary Table S1. Assignment by kraken2 of mock communities, using a version of the B-GUT database with hybrids (B-GUT with hybrids) and the Standard kraken2 database.

OUR MOCK (ZymoBIOMICS® Gut Microbiome Standard, reference D6331, ZymoResearch)

	Expected composition (%)	B-GUT with hybrids	Standard db
<i>Candida albicans</i>	1,5	1,38	1,41
<i>Saccharomyces cerevisiae</i>	1,4	0,23	1,05

MOCK from study: <https://PMC7355182/>

	Expected composition (%)	B-GUT with hybrids	Standard db
<i>Saccharomyces cerevisiae</i>	2	0,35	1,95
<i>Cryptococcus neoformans</i>	2	1,41	3,06

Supplementary tables:

<https://docs.google.com/spreadsheets/d/1eYhusAQu3mqA84VL0uiKyFDD5dYiBQm0nO1nL0XVdI/edit?usp=sharing>