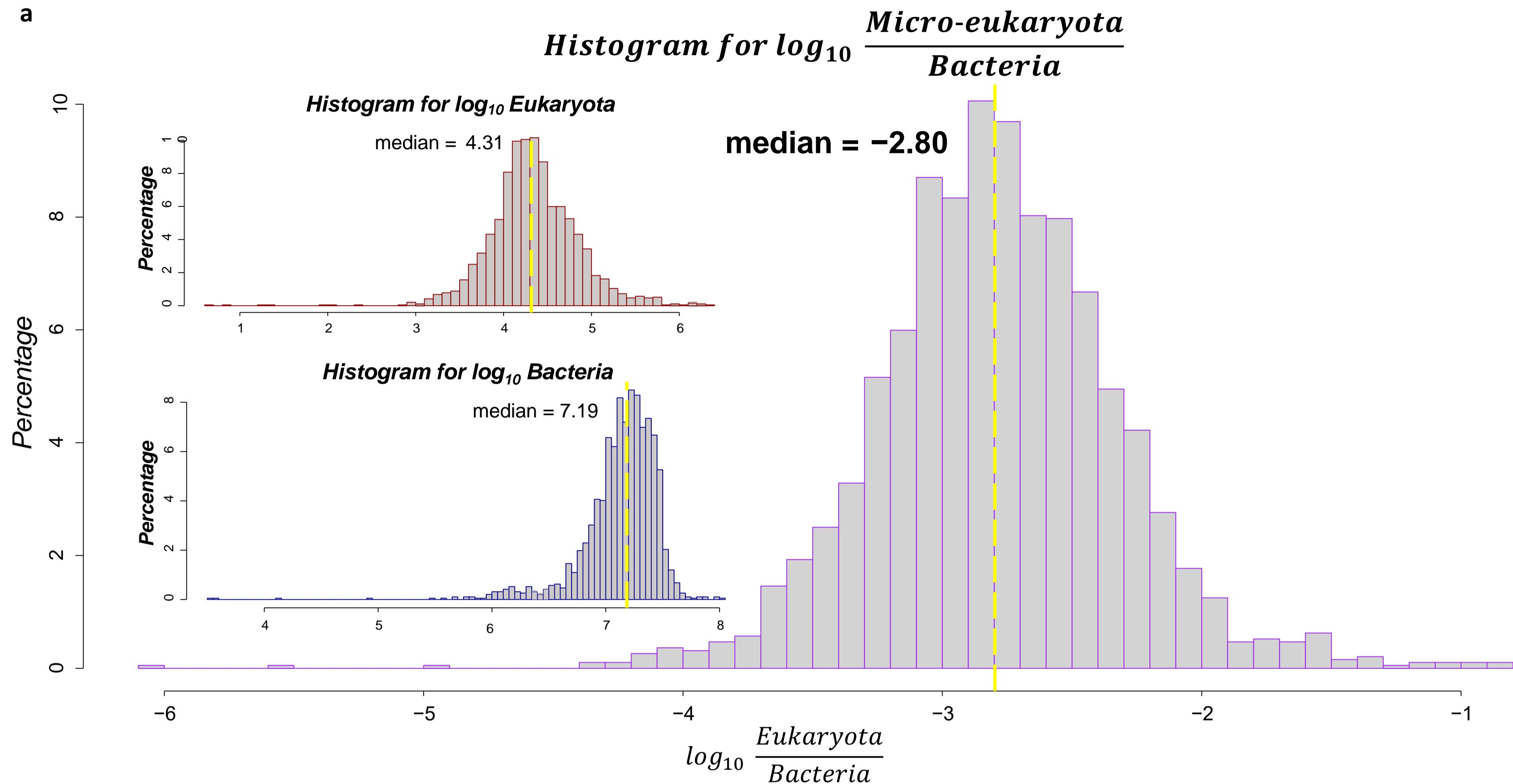
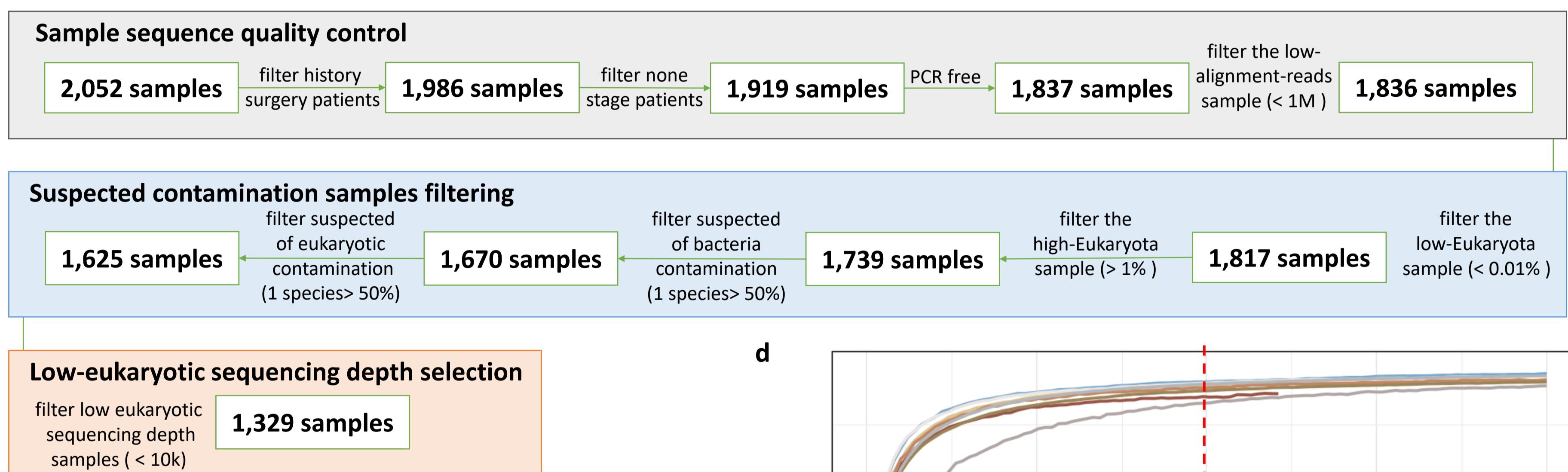


Raw Metagenome Sequencing Data Profile

a



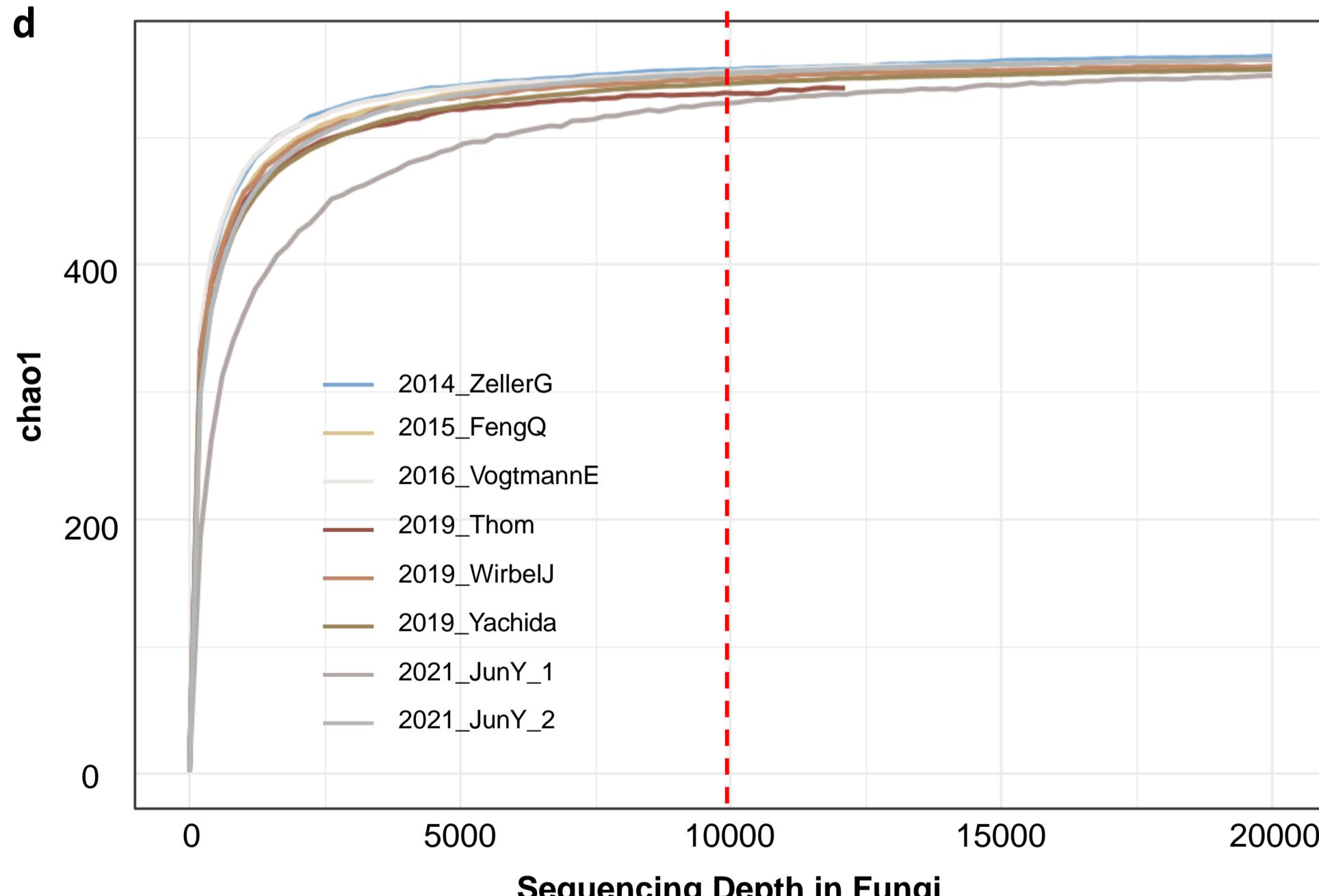
b



c

Items	adenoma	CRC	CTRL	filter	leave
import samples	453	641	743	-	1,837
filter low-align-reads samples	453	641	742	1	1,836
filter low-Eukaryota samples	448	633	736	19	1,817
filter high-Eukaryota samples	435	597	707	78	1,739
filter suspected bacteria contamination samples	418	577	675	69	1,670
filter suspected eukaryotic contamination samples	409	561	655	45	1,625
filter low eukaryotic sequencing depth samples	350	454	525	296	1,329

d

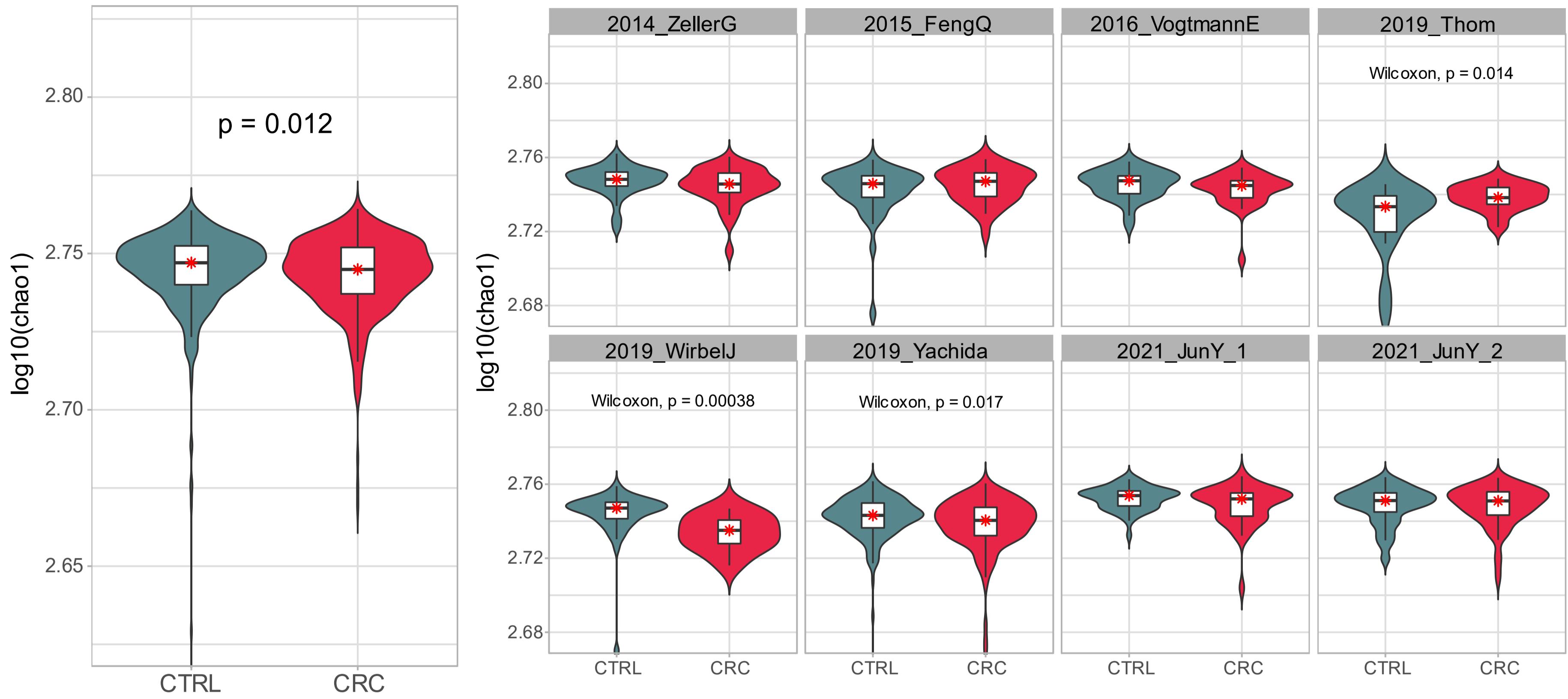


Micro-Eukaryota contains around 0.1% in the gut microbiota, which is consistent with previous research.

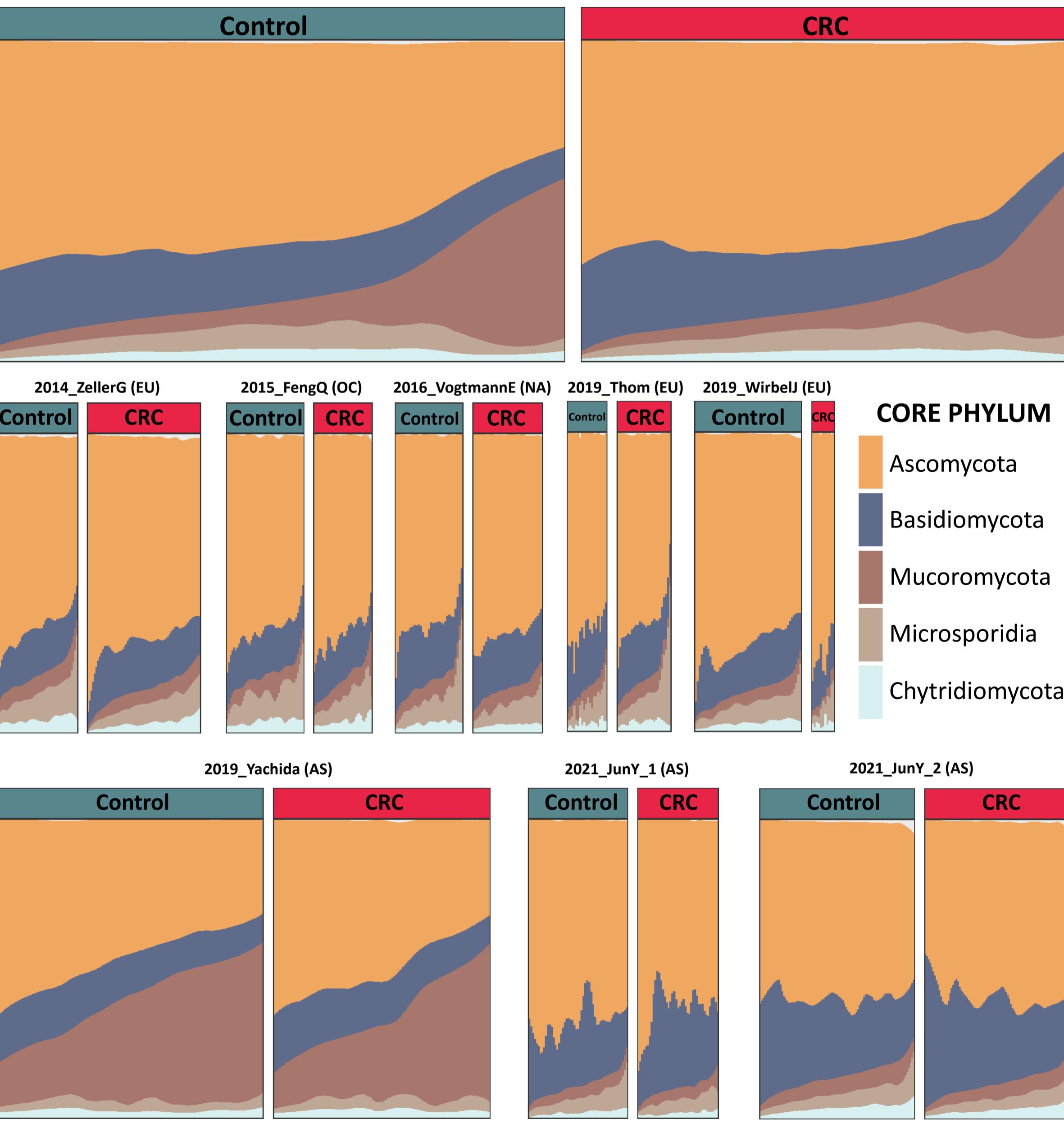
With the strict inclusion criteria, even if the sample size would be drastically reduced, the results would be more credible.

Alpha Diversity in Micro-eukaryotic level

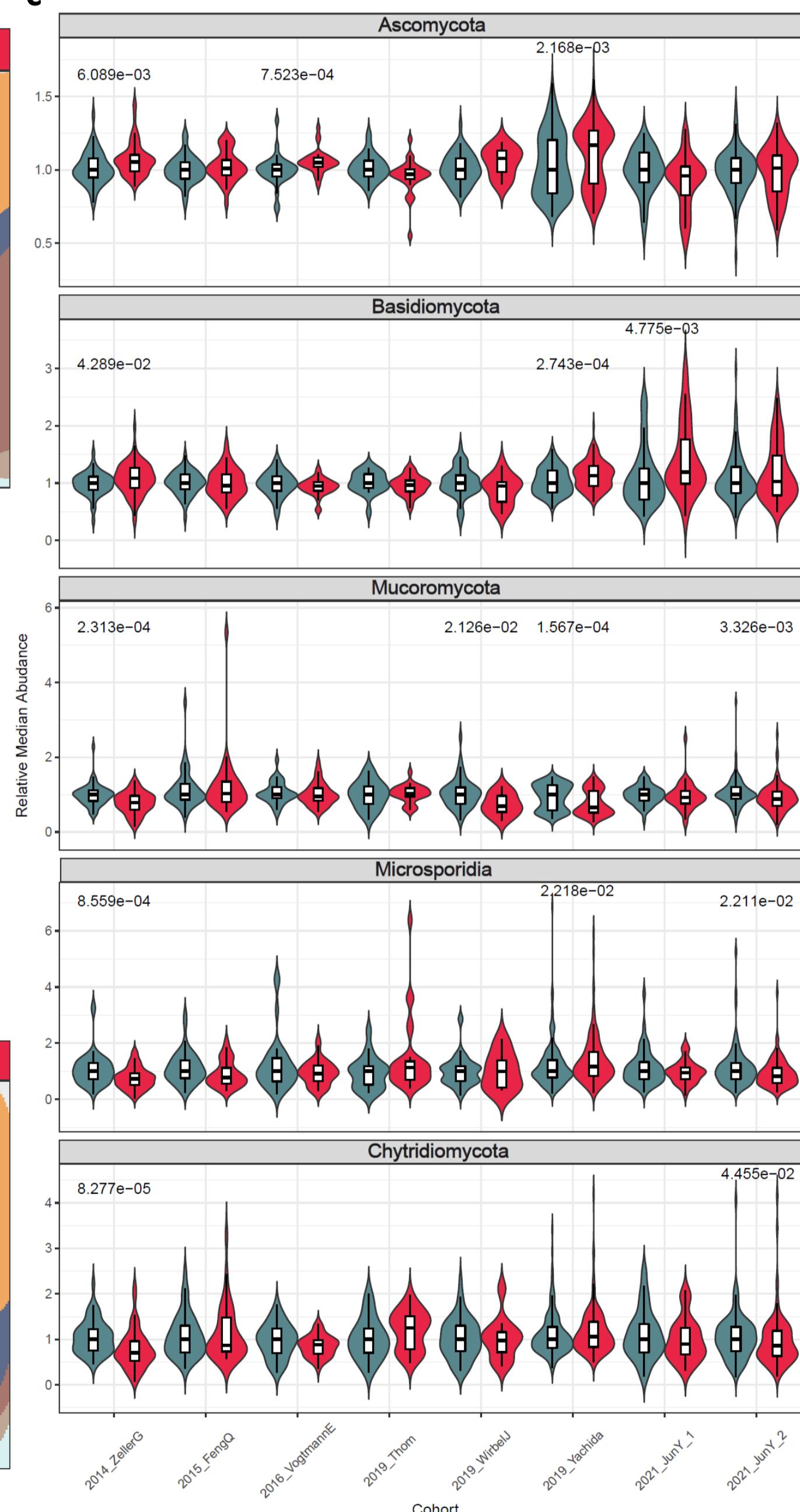
a



b



c



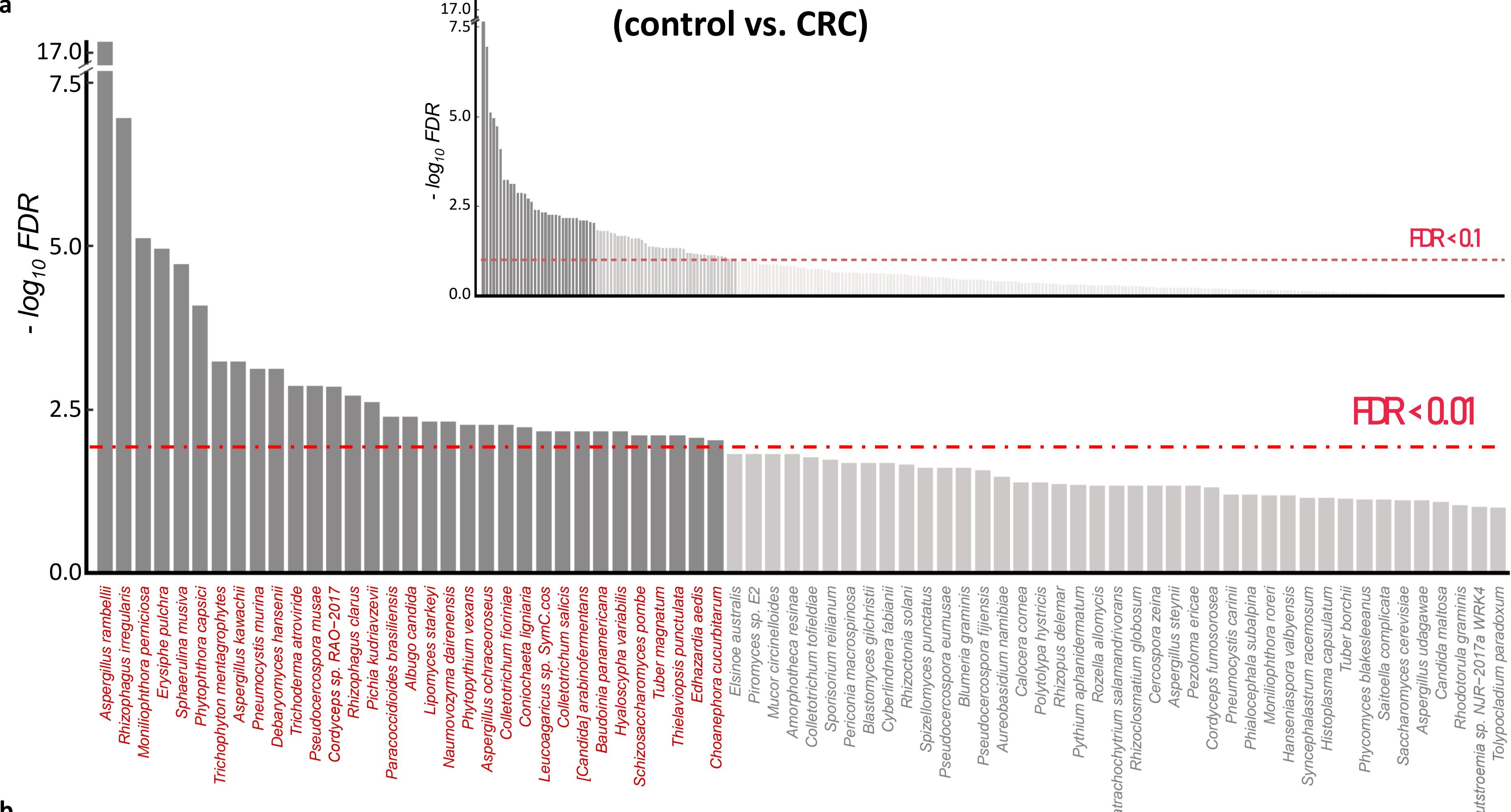
The composition of eukaryotic microorganisms at the phylum level remains consistent overall.

Ascomycota, Basidiomycota, Mucoromycota, Microsporidia and Chytridiomycota are the main phylum in gut microbiota.

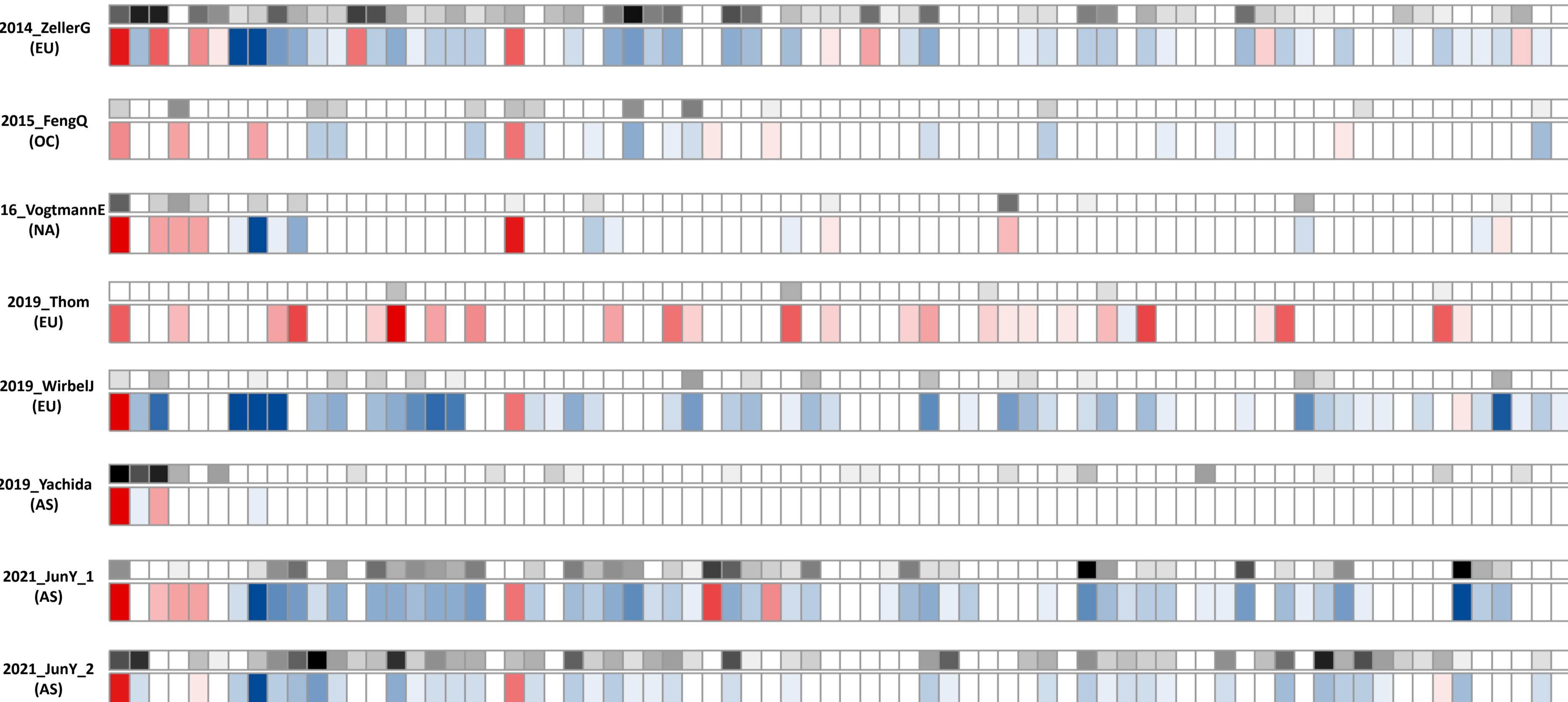
The cohort has an individual difference, such as, Mucoromycota plays higher ratio than other cohorts, Basidiomycota also is higher contribution in our lab datasets.

Micro-eukaryotic features selection (control vs. CRC)

a



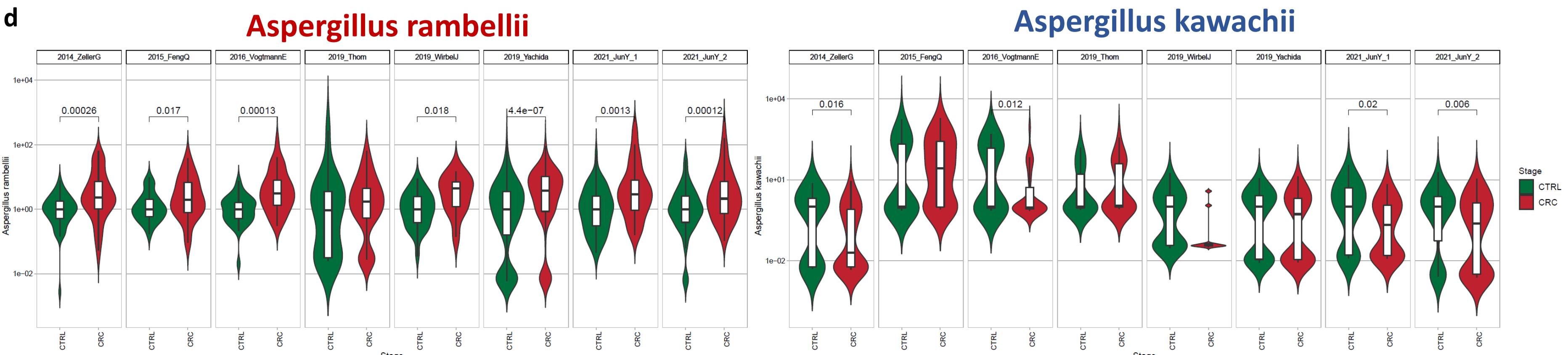
b



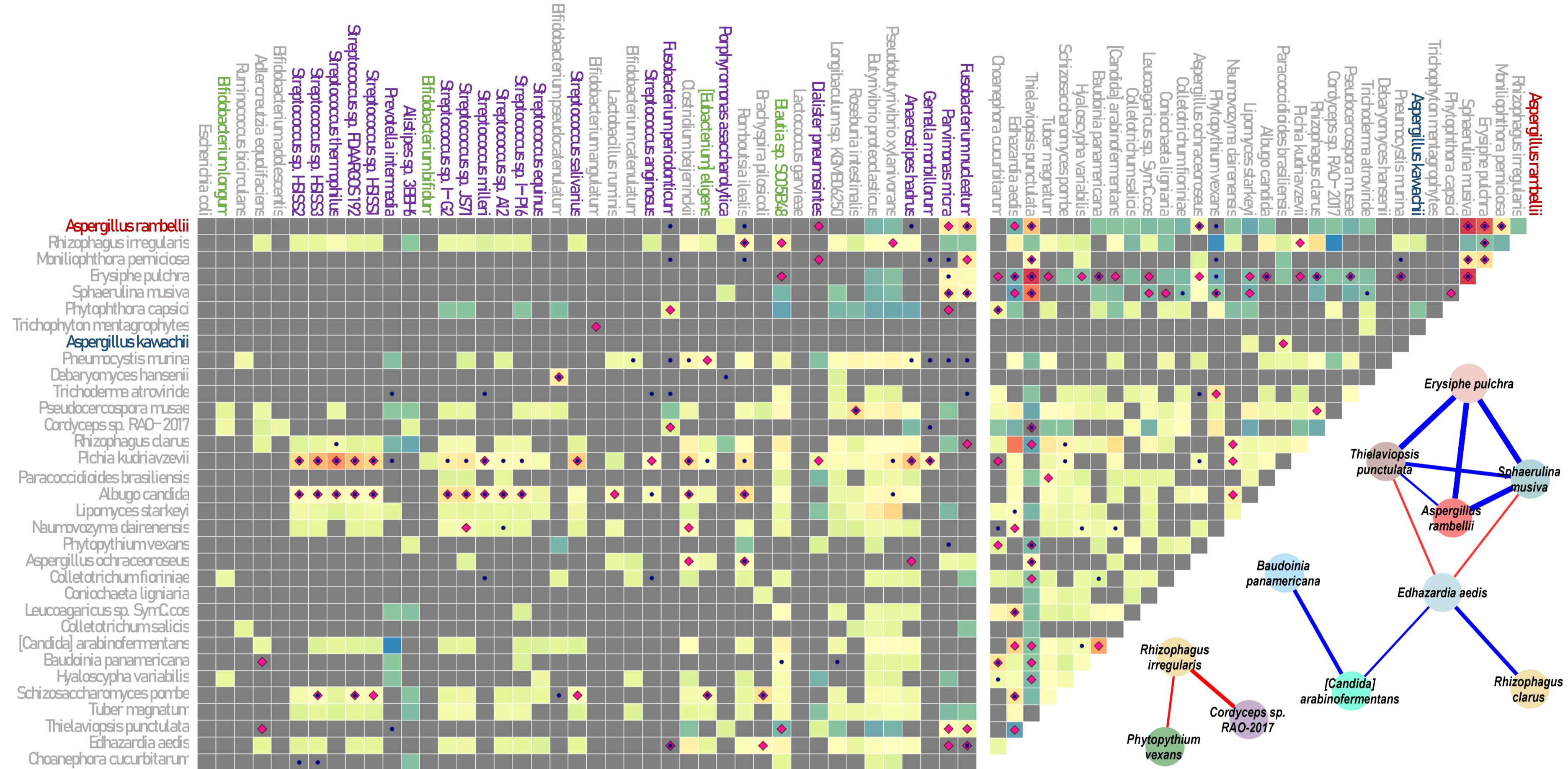
c



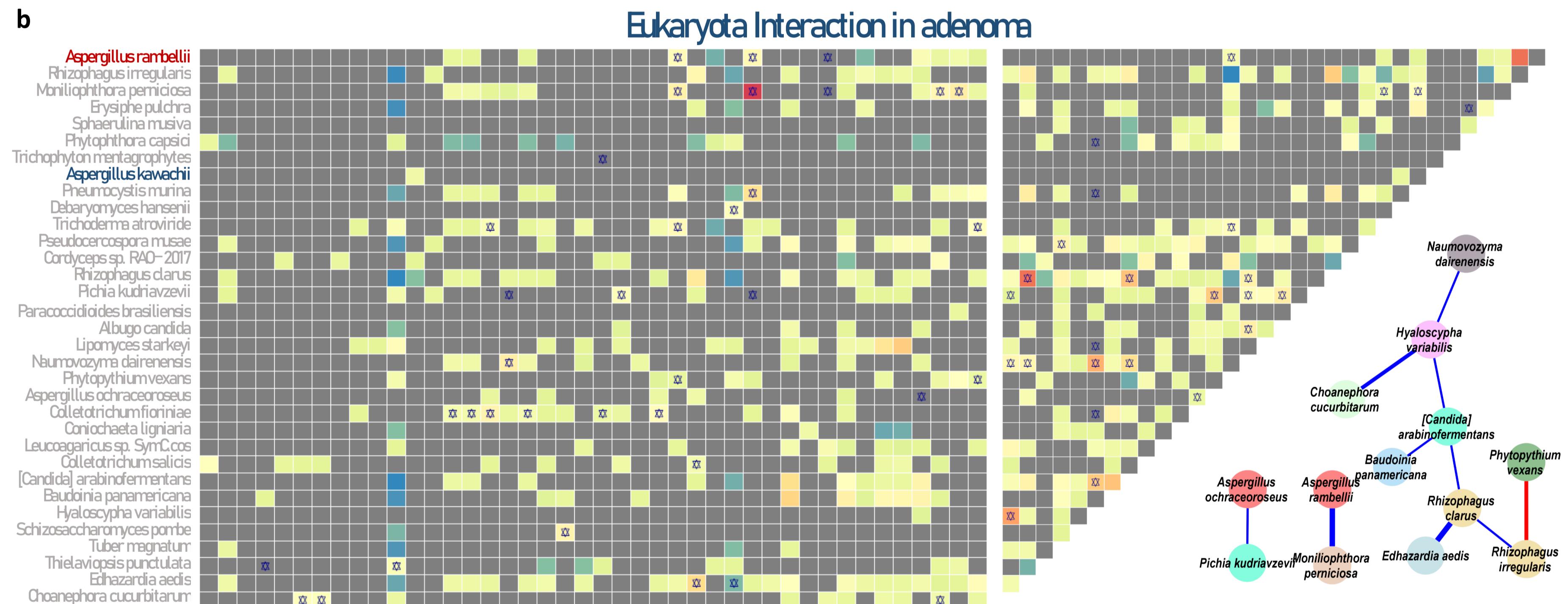
d



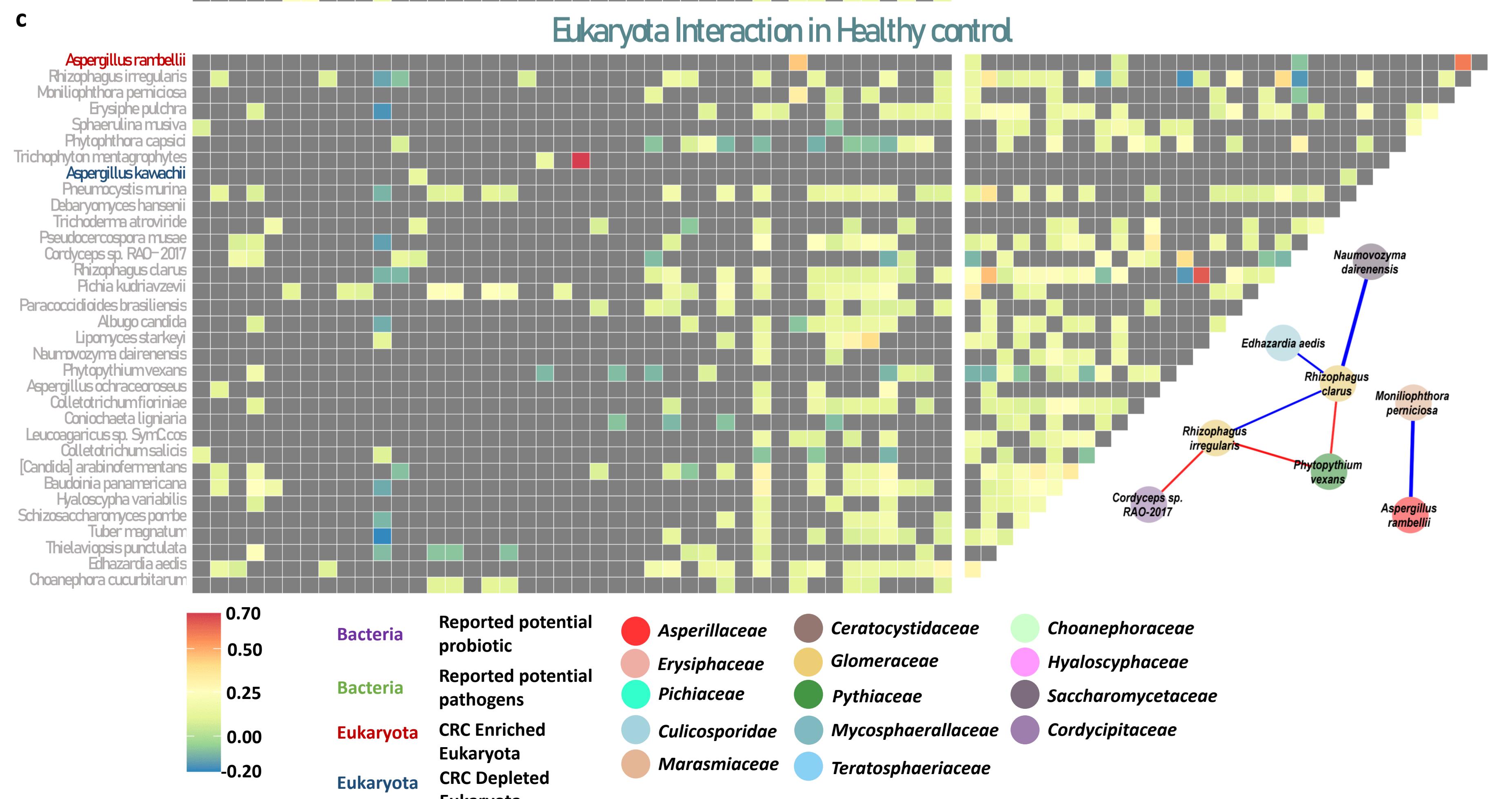
Eukaryota Interaction in CRC group



b

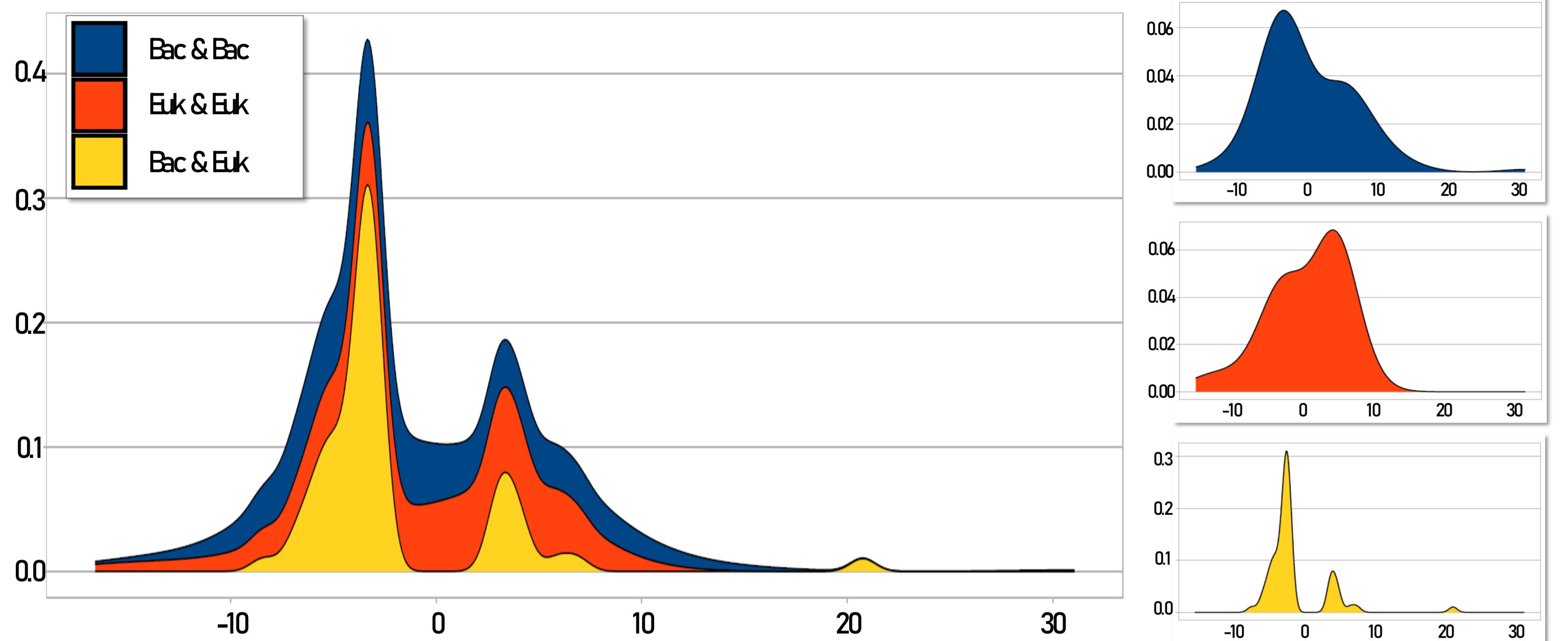


c



Density Plot with z-score in various kingdom features (control vs CRC)

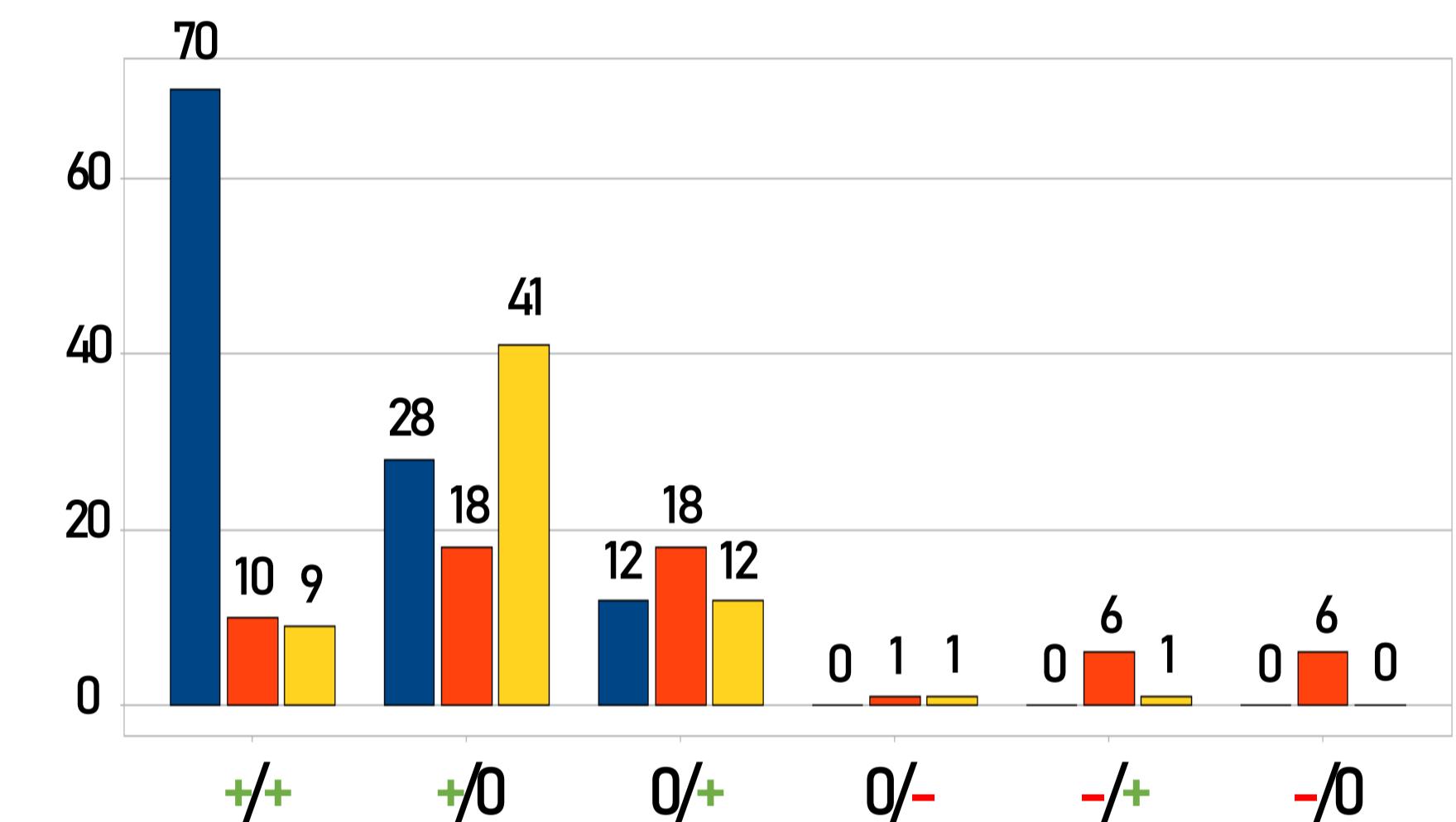
z-score represents the relative strength of differential correlation



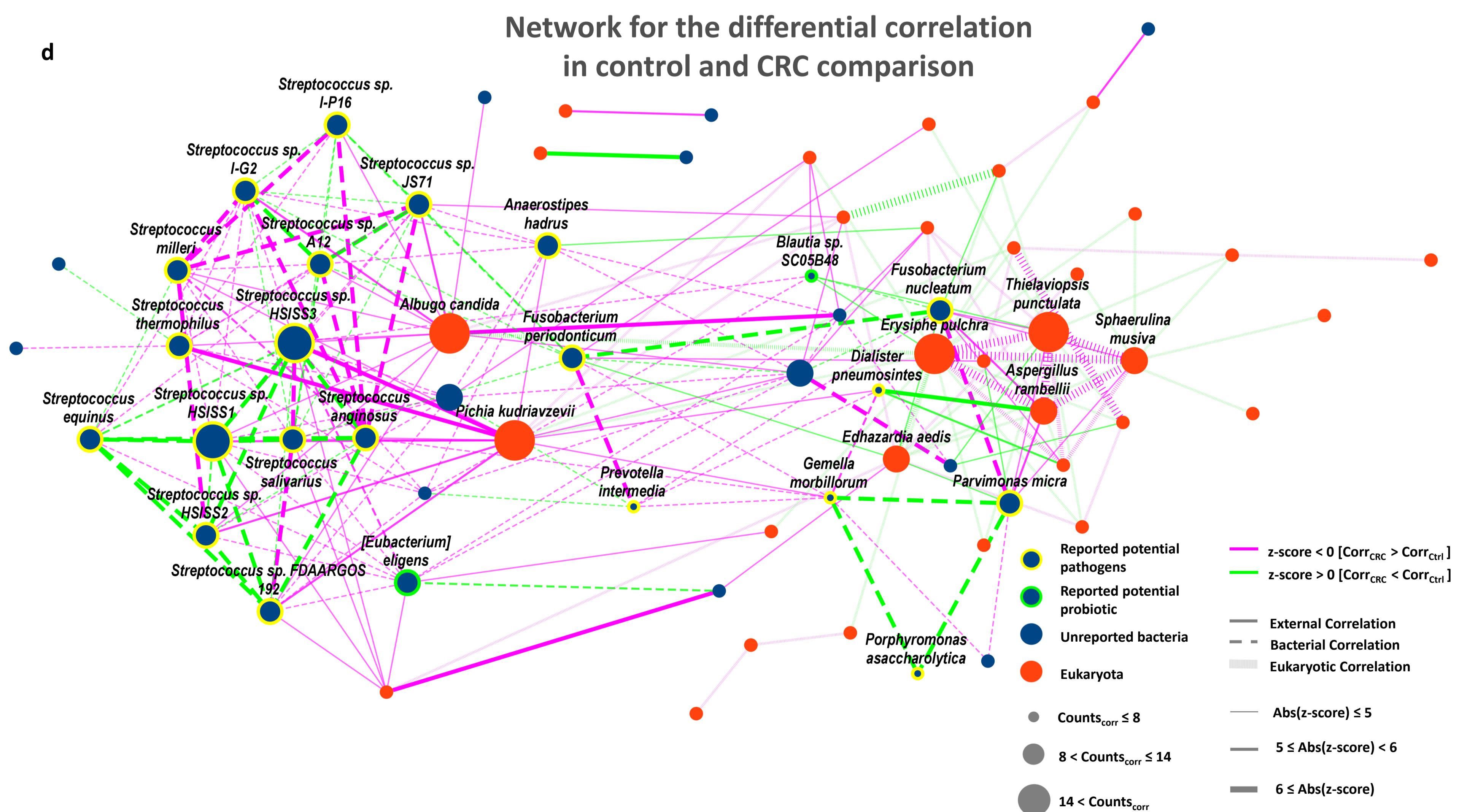
b Definition of differential correlation classes

Feature Pair Correlation in control		
$p > 0$ $p < 0.05$	$p > 0.05$	$p < 0$ $p < 0.05$
+/+ $p < 0.05$	+/0 $p > 0.05$	+/- $p < 0$
<i>z score ∈ (−∞, +∞)</i>	<i>z score ∈ (−∞, 0)</i>	<i>z score ∈ (−∞, 0)</i>
0/+ $p < 0.05$	0/0 <i>z score without meaning</i>	0/- $p < 0$
<i>z score ∈ (0, +∞)</i>	<i>z score ∈ (0, +∞)</i>	<i>z score ∈ (−∞, 0)</i>
-/+ $p < 0.05$	-/0 $p > 0.05$	-/- $p < 0$
<i>z score ∈ (0, +∞)</i>	<i>z score ∈ (0, +∞)</i>	<i>z score ∈ (−∞, +∞)</i>

c Counts of differential correlation classes with various features



d Network for the differential correlation in control and CRC comparison



Future Goals

For this project

1. Paper written
2. Feature further analysis
 - *Aspergillus rambellii*
 - *Aspergillus kawachii*
3. Cell line co-culture
4. Animal experiment validation
 - AEEC (*Animal Experimentation Ethics Committee*) applying
 - Animal License applying
 - APC^{min+} model validation

Another project

1. Lixia's Multifocal-HCC project