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.

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

Ascomycota, Basidiomycota, Mucoromycota, Microsporidia and Chyttridiomycota 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.

With multiple criteria, we obtained 74 significant different features, 33 mainly different features and 2 core features.

We also explored the performance of these 74 features in different cohorts and do some comparison between Control group and CRC group.

To validation our results, we utilized the same method in bacteria selection.

As you can see, the bacterial selection is credible, most of them are the reported potential probiotic or pathogens.

To showing the most importance interaction in micro-Eukaryota, we also plot the network for it in each stage.

As the picture shows, the correlation counts would be increased during the disease development.

To determine the relative strength of differential correlation between control group and CRC group,

We used the DGCA (Differential Gene Correlation Analysis) to show the difference.

As the figure a, we could know that the correlation between bacteria would play much stronger in CRC than control group,

but it plays the opposite in the correlation between Eukaryota.

In addition, the correlation between bacteria and Eukaryota is clear hierarchy in two stages.

The figure b is the definition of differential correlation classes and figure c is the composition of each correlation classes.

At last, figure d shows the network for the differential correlation in these 2 stages.