Colorectal cancer is the third most common non-sex-specific cancer and is responsible for the second-highest mortality rate after lung cancer1. There would be over a quarter of a million patients were diagnosed with colorectal cancer (CRC), and its mortality rate is more than 5% every year worldwide2. More seriously, the annual worldwide occurrence rate of CRC is estimated to increase by approximately 80% to more than two million cases over the next two decades3. As opposed to hereditary CRCs, sporadic CRCs account for about 75% of CRCs and couldn’t be explained through genetic predisposition or family history of CRC4. In the previous studies, several kinds of research5–8 have revealed that the perturbed enteric microbiome was an important risk factor for CRC development. Wirbel9 and Thomas10’s team have also reported the microbial signatures specific for CRC and the association between the gut microbiome and choline degradation, respectively, through the meta-analysis with approximately 1,000 individuals from five cohorts. However, the role of microbial components other than gut bacteria, such as microeukaryotes, is largely unexplored in CRC, partly due to their relatively lower abundance and lack of well-characterized reference genomes. There have been reports exposing that perturbed gut fungi were associated with Inflammatory bowel disease and liver cirrhosis11–13. Except our previous study14 disclosed the fungal biomarker in CRC in the Chinese cohort, no other research reported the related study.

We performed a meta-analysis of eight publicly available datasets and one new cohort from Chinese in this study. After the consistent filtering and pre-processing, we included 525 healthy control, 350 adenoma patients, and 454 CRCs, a total of 1,329 samples from eight cohorts among four continents. First, we discovered altered micro-eukaryotic diversity in CRC compared with healthy control. Second, we revealed a list of microeukaryotes that played a significant difference in CRC. Moreover, we explored the performance of selective candidates in each cohort, and we obtained two outstanding performance microeukaryotes, Aspergillus rambellii and Aspergillus kawachii. Third, the micro-eukaryotic interrelationships and the association between selective micro eukaryotes and bacteria in three stages were exhibited and compared. Interestingly, we identified that *A. rambellii* and two CRC-related pathogens, *F. nucleatum*, and *P. micra*, showed a significant difference between the CRC and healthy control. In the last, we validated the A. rambellii and its conditioned medium promoted the viability of colon cancer cells.