Although fungi are an essential part of the gut microbiome, few studies have investigated how they work in CRC. We conducted a meta-analysis that included 1325 fecal metagenomes from seven publically accessible publications. We found a core group of 33 fungal species that were significantly enriched in CRC (false discovery rate (FDR) < 0.01), which Aspergillus rambellii performed the most significant difference (FDR = 5.13E-18) in CRC comparison. In seven of eight cohorts, the AUC of the classifier with combined fungal and bacterial markers was 1.44% - 10.60% higher than the bacterial classifier. Among 14 features in the combined classifier, *A. rambellii* was the most important fungal feature and ranking 4th. We investigated and compared the relationships of 64 key species (33 fungi and 31 bacteria) and discovered that cross-kingdom interactions are critical for colorectal carcinogenesis. There were strong differential correlations between *A. rambellii* and two CRC-related pathogens, *Fusobacterium* *nucleatum* and *Parvimonas* *micra*. These results showed that *A. rambellii* may play a key role in colorectal carcinogenesis, and we evidenced it could promote the CRC by a list of the colorectal cancer stem cell proliferation experiment.