Supplementary information

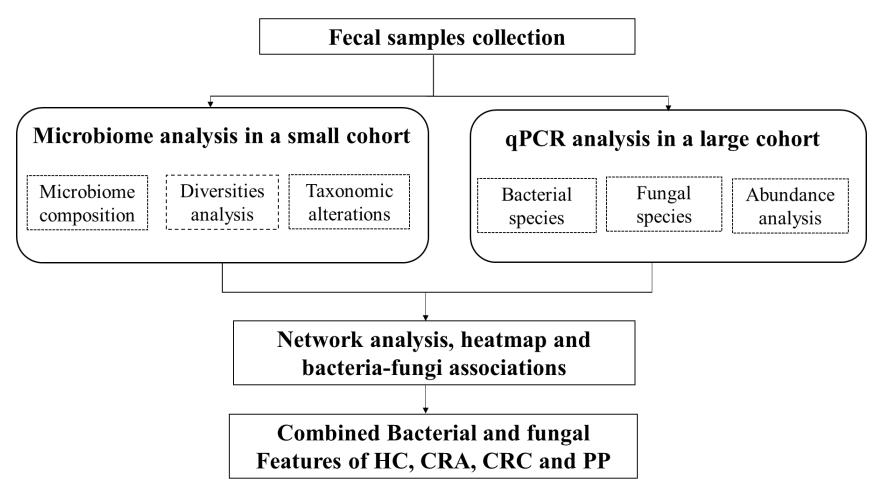
Supplementary Tables

Supplementary Table 1. Demographics of the study participants (Mean \pm Standard Deviation)

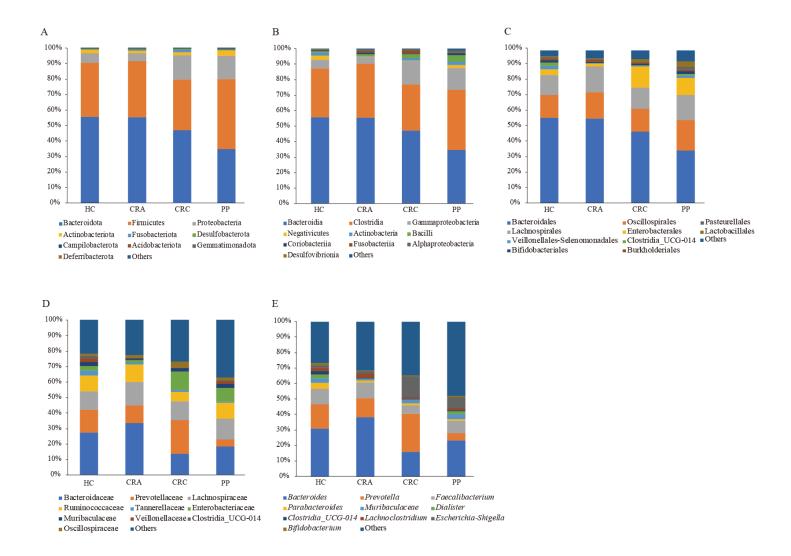
Cohort	Factors	CRC	CRA	PP	НС	<i>p</i> -value	
Cohort 1	Size	15	19	19	18		
	Age	$62.05 \pm$	$55.42 \pm$	55.80 ± 13.4	48.04 ± 5.82	p = 0.09	
		12.58	10.47				
	Gender	Male: 9	Male: 14	Male: 14	Male: 8	p = 0.52	
		Female: 6	Female: 5	Female: 5	Female: 10		
	BMI	23.08 ± 3.42	24.11 ± 4.12	23.87 ± 4.22	24.11 ± 3.02	p = 0.32	
Cohort 2	Size	92	119	95	96		
	Age	62.19 ± 6.21	60.11 ± 4.77	61.11 ± 5.70	62.11 ± 5.32	p = 0.19	
	Gender	Male: 49	Male: 55	Male: 46	Male: 49	0.42	
		Female: 43	Female: 64	Female: 51	Female: 47	p = 0.42	
	BMI	23.81 ± 3.34	23.22 ± 3.16	24.51 ± 3.48	24.11 ± 3.38	p = 0.35	

Supplementary Table 2. qPCR primers and their sequences in this study

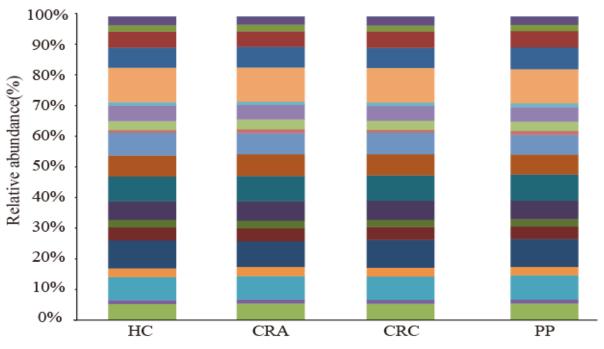
Species	Upper primer sequence (5'-3')	Lower primer sequence (5'-3')		
Fusobacterium	CAACCATTACTTTAACTCTACCAT	GTTGACTTTACAGAAGGAGATTA		
nucleatum	GTTCA	TGTAAAAATC		
Bifidobacterium	CTTACTTCGCCTTCTTTGCTCCGTA	AGAAGTCCAAGACTTTGGCCCTG		
bifidum	C	A		
Candida albicans	TTTATCATCTTGTCACAGCAGA	ATCCCGCCTTGCCACTACCG		
Saccharomyces	AGGAGTGCGGCTCTTAG	TACTTACCGAGGCAAGCTCCA		
cerevisiae	noonorocoociermo			



Supplementary Figure 1. Analysis flowchart of the study



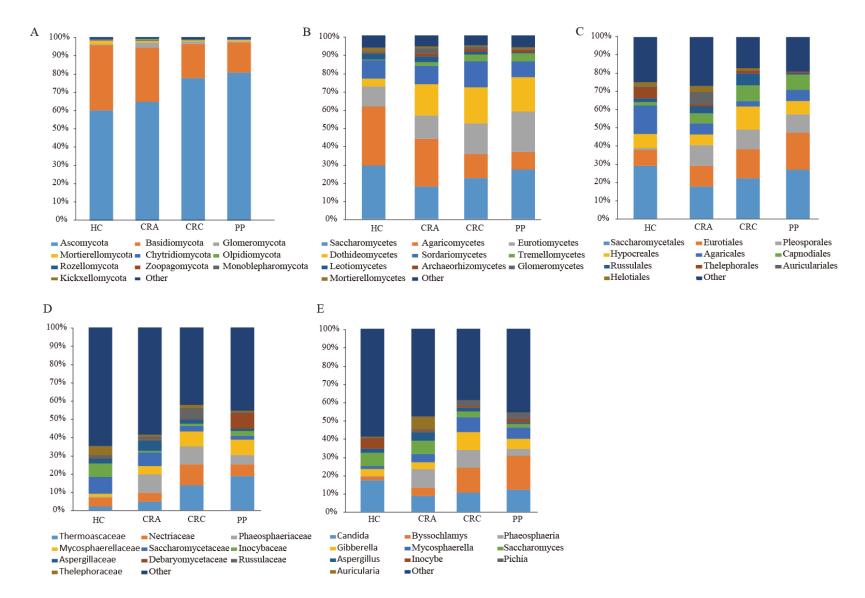
Supplementary Figure 2. Taxonomic analysis of gut bacteria from 16S rRNA sequencing. Compositions of gut bacteria of HC, CRA, CRC, and PP groups at phyla (A), classes (B), orders (C), families (D), and genera (E) levels.



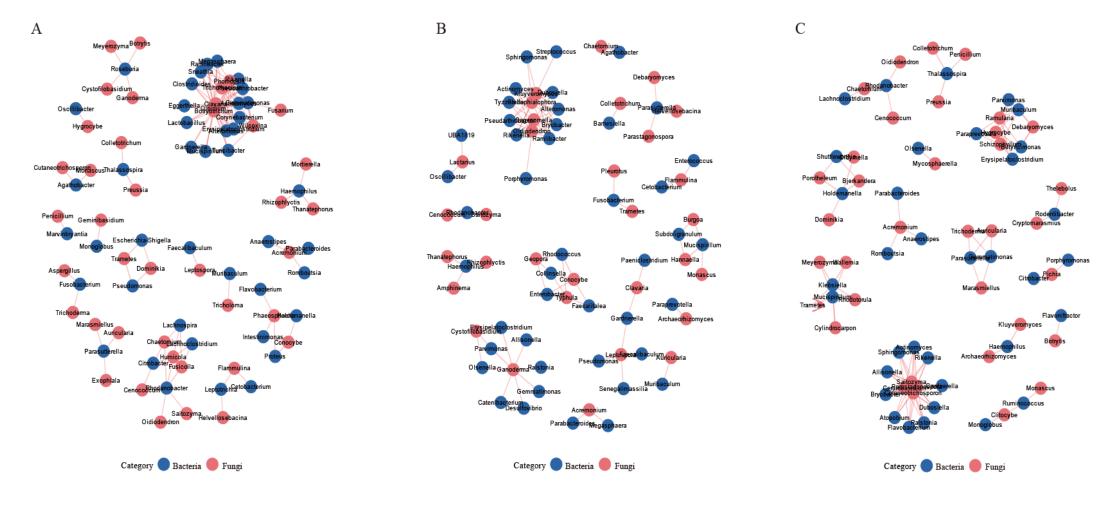
- RNA processing and modification
- Energy production and conversion
- Amino acid transport and metabolism
- Carbohydrate transport and metabolism
- Lipid transport and metabolism
- Transcription
- Cell wall/membrane/envelope biogenesis
- Posttranslational modification, protein turnover, chaperones
- Secondary metabolites biosynthesis, transport and catabolism
- Function unknown
- Intracellular trafficking, secretion, and vesicular transport
- ■Extracellular structures
- Cytoskeleton

- Chromatin structure and dynamics
- ■Cell cycle control, cell division, chromosome partitioning
- Nucleotide transport and metabolism
- ■Coenzyme transport and metabolism
- Translation, ribosomal structure and biogenesis
- Replication, recombination and repair
- Cell motility
- Inorganic ion transport and metabolism
- General function prediction only
- Signal transduction mechanisms
- Defense mechanisms
- Nuclear structure

Supplementary Figure 3. Functional predictions for four groups based on PICRUSt analysis.



Supplementary Figure 4. Taxonomic analysis of gut fungi from ITS sequencing. Compositions of gut fungi of HC, CRA, CRC, and PP groups at phyla (A), classes (B), orders (C), families (D), and genera (E) levels.



Supplementary Figure 5. Correlation network between bacteria and fungi in HC vs. CRC (A), HC vs. CRA (B), and HC vs. PP (C), respectively. Notes: blue circles: bacteria; red circles: fungi.