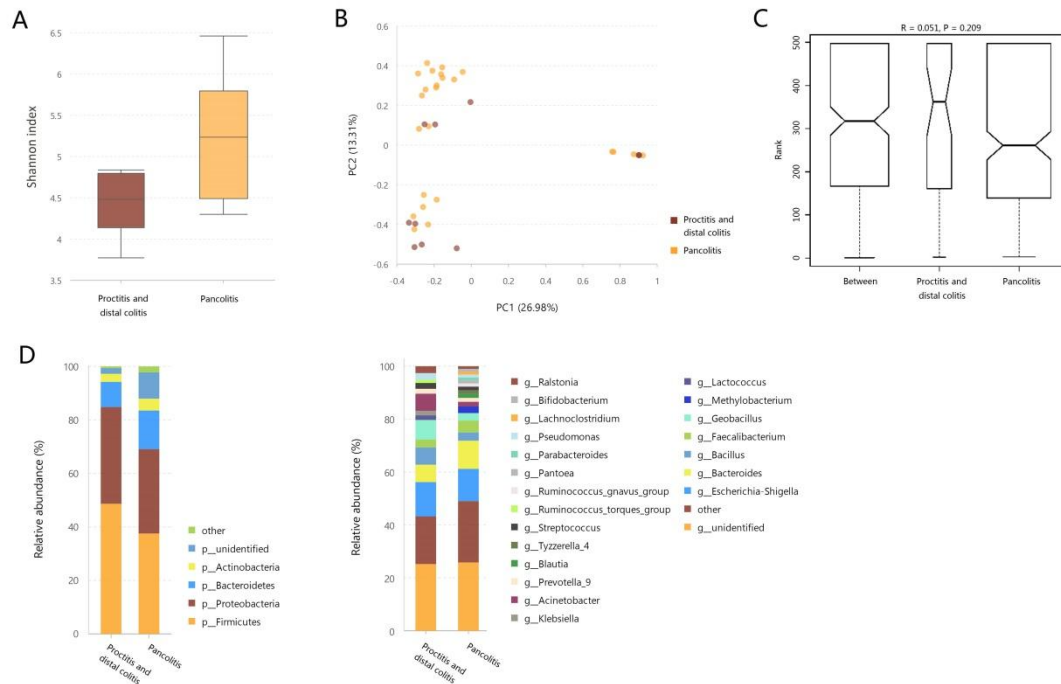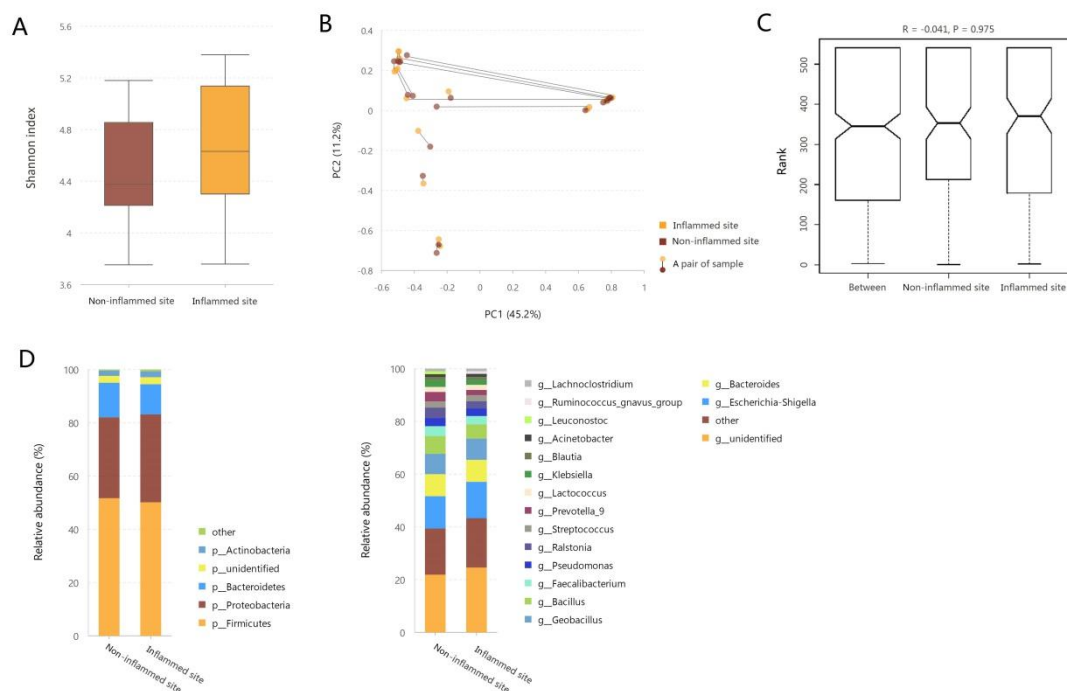**Supplementary Figure 1 The statistical analysis of the sequencing results of the microflora in stool samples from patients with different disease extent.** A: The α-diversity of microbiota evaluated by Shannon index. The ordinate showed the Sharnon index, and the abscissa showed the groups. The α-diversity of fecal bacteria in "partial colitis" group (Shannon index 3.65 ± 1.01) was similar to that in pancolitis group (Shannon index 3.34 ± 1.13, *P* = 0.356); B: Principal component analysis. The flora structure of these two groups showed little difference in principal component analysis rectangular Coordinate; C: The analysis of similarities. The intergroup difference these groups was not significant; D: The relative abundance of the bacteria at the phylum (the left bar graph) and genus (the right bar graph) level. The ordinate showed the relative abundance (%), and the abscissa axis showed the sample sites.
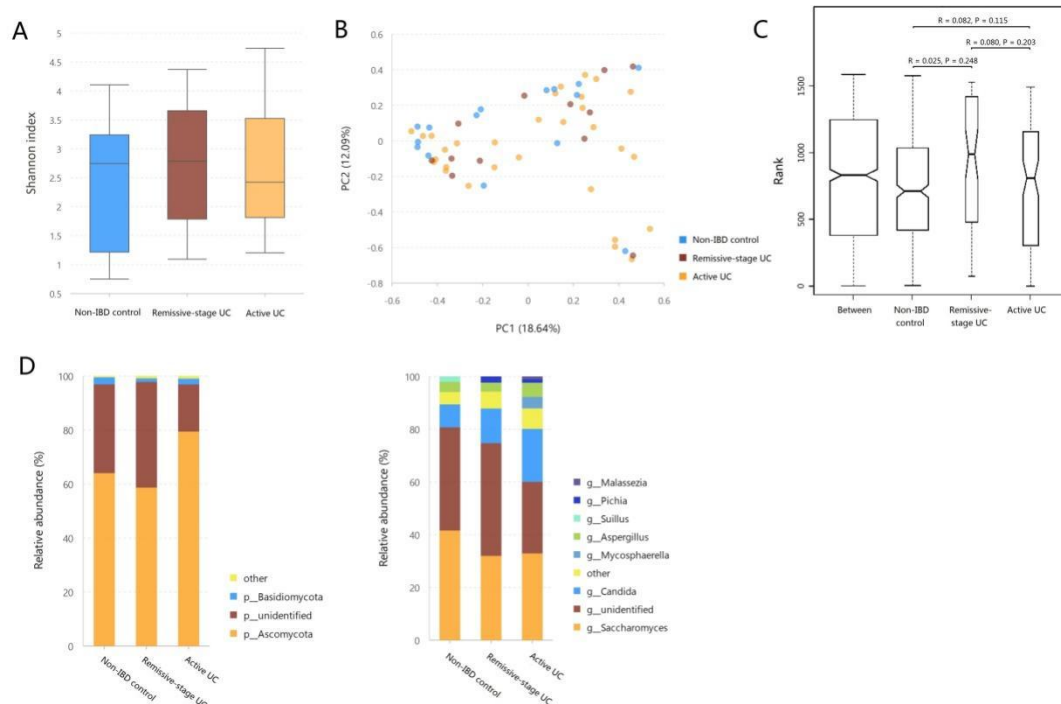
Supplementary Figure 2 The statistical analysis of the sequencing results of the microflora in mucosa samples from patients with different disease extent. A: The α-diversity of microbiota evaluated by Shannon index. The ordinate showed the Sharnon index, and the abscissa showed the groups. The α-diversity of mucosal bacteria in "partial colitis" group (Shannon index 4.33 ± 0.63) was similar to that in pancolitis group (Shannon index 5.29 ± 0.97, *P* = 0.007); B: Principal component analysis. The flora structure of these two groups showed little difference in principal component analysis rectangular Coordinate; C: The analysis of similarities. The intergroup difference of these groups was not significant; D: The relative abundance of the bacteria at the phylum (the left bar graph) and genus (the right bar graph) level. The ordinate showed the relative abundance (%), and the abscissa axis showed the sample sites.
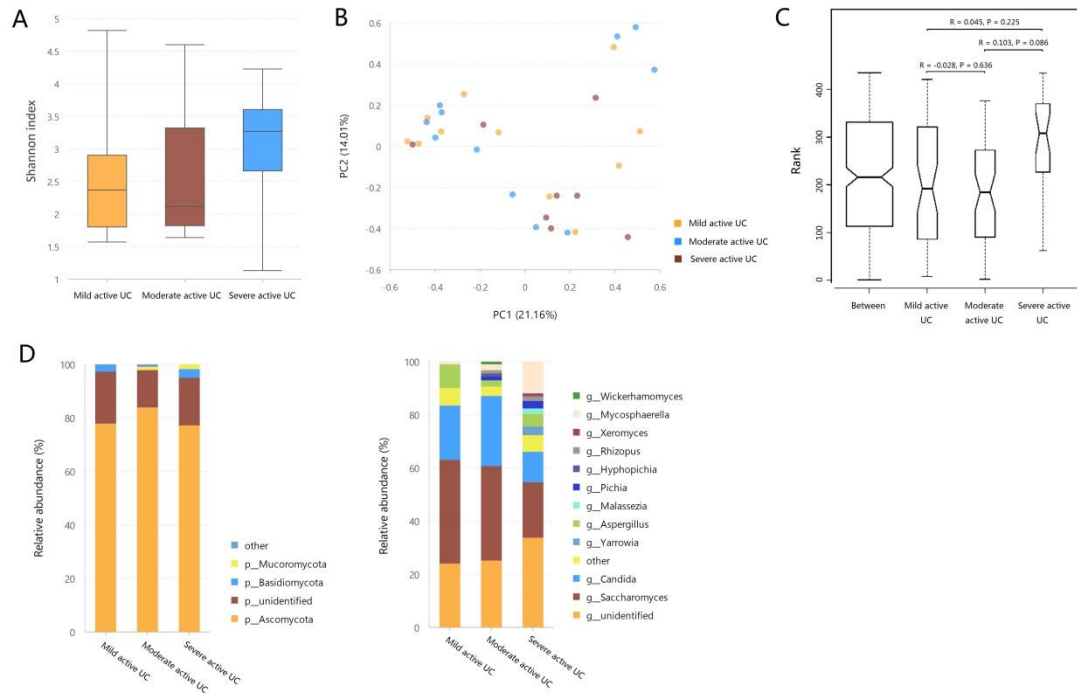
Supplementary Figure 3 The statistical analysis of the sequencing results of the microflora in mucosa samples from inflamed site and non-inflamed site. A: The α-diversity of microbiota evaluated by Shannon index. The ordinate showed the Sharnon index, and the abscissa showed the groups. The α-diversity of mucosal bacteria in inflamed site and that in the non-inflamed site were similar (Shannon index 4.63 ± 0.79 *vs* 4.42 ± 0.67, *P* = 0.075); B: Principal component analysis. The flora structure among these groups showed little difference in principal component analysis rectangular Coordinate; C: The analysis of similarities. The intergroup difference of these groups was not significant; D: The relative abundance of the bacteria at the phylum (the left bar graph) and genus (the right bar graph) level. The ordinate showed the relative abundance (%), and the abscissa axis showed the sample sites.

Supplementary Figure 4 The statistical analysis of the sequencing results of the fungal microflora in stool samples of ulcerative co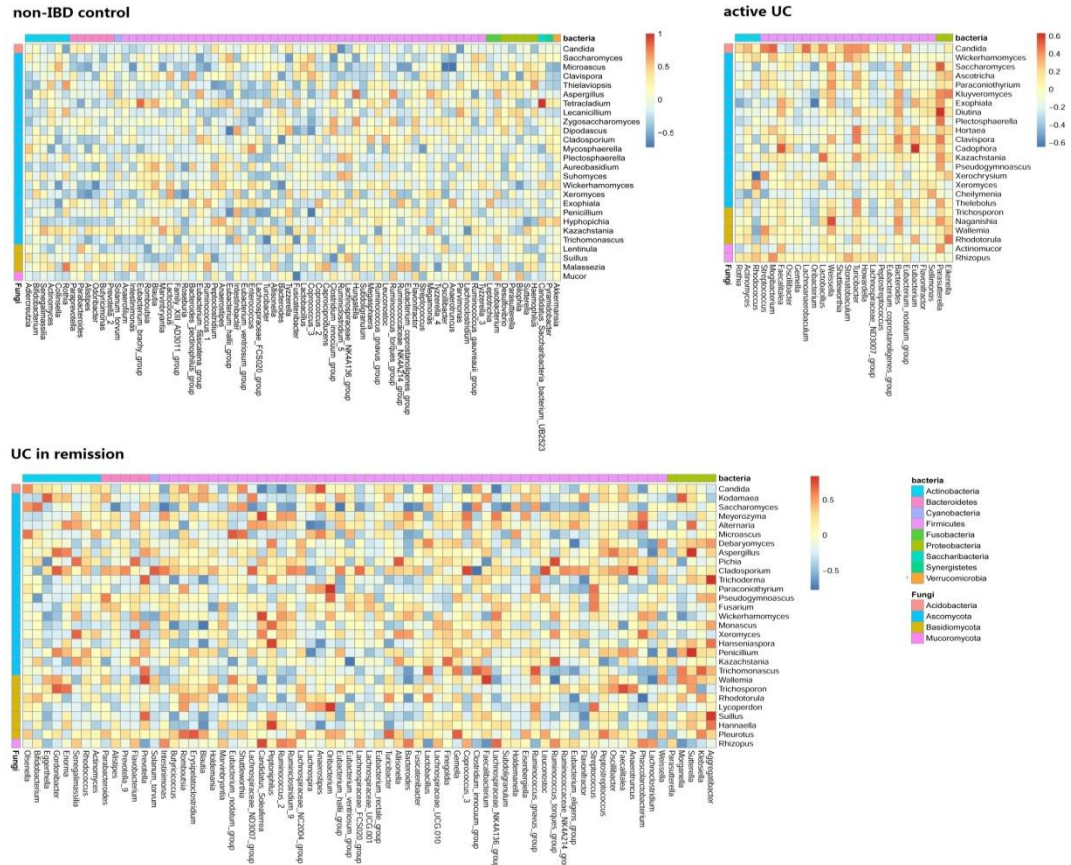litis patients and non-inflammatory bowel disease controls. A: The α-diversity of microbiota evaluated by Shannon index. The ordinate showed the Sharnon index, and the abscissa showed the groups. The α-diversity of stool fungal microflora evaluated by Shannon index in non-inflammatory bowel disease (IBD) controls, in ulcerative colitis (UC) in remission patients and in active UC patients [(Shannon index 2.40 ± 1.32 *vs* 2.84 ± 1.45 *vs* 2.72 ± 1.31) ($P_{Non-IBD–UC\ in\ remission}$ = 0.396, $P_{Non-IBD–active\ UC}$ = 0.454, $P_{UC\ in\ remission–active\ UC}$ = 0.786)]; B: Principal component analysis. The flora structure among these groups showed little difference in principal component analysis rectangular Coordinate; C: The analysis of similarities. The intergroup differences of these groups were insignificant; D: The relative abundance of the fungi at the phylum (the left bar graph) and genus (the right bar graph) level. The ordinate showed the relative abundance (%), and the abscissa axis showed the sample types where the miocrobiota were sequenced from.

Supplementary Figure 5 The statistical analysis of the sequencing results of the fungal microflora in stool samples of active ulcerative colitis patients with different inflammation degrees. A: The α-diversity of microbiota evaluated by Shannon index. The ordinate showed the Sharnon index, and the abscissa showed the groups. The α-diversity of stool fungal microflora in mild active ulcerative colitis (UC) subgroup, moderate active UC subgroup and severe active UC subgroup (Shannon index 2.57 ± 1.29 *vs* 2.61 ± 1.36 *vs* 3.03 ± 1.36) ($P_{mild-moderate}$ = 0.937, $P_{moderate-severe}$ = 0.507, $P_{mild-severe}$ = 0.462); B: Principal component analysis. The flora structure among these groups showed little difference in principal component analysis rectangular Coordinate; C: The analysis of similarities. The intergroup differences of these groups were insignificant; D: The relative abundance of the fungi at the phylum (the left bar graph) and genus (the right bar graph) level. The ordinate showed the relative abundance (%), and the abscissa axis showed the sample types where the miocrobiota were sequenced from.

Supplementary Figure 6 The heatmap of the bacteria-fungi correlations of intestinal microflora in non-inflammatory bowel disease controls (the left upper), ulcerative colitis in remission (the left lower) and active ulcerative colitis groups (the right). Bacterium-fungus pairs that at least one of the two genera had a relative abundance higher than 0.01, and their correlations with a *P* value smaller than 0.05 were showed in the heat map. The ordinate showed the bacteria phyla, and the abscissa showed the fungi phyla. In non-inflammatory bowel disease controls, bacteria genera from nine bacteria phyla were correlated with fungi genera from four fungi phyla, while for ulcerative colitis (UC) in remission the number of involved bacteria phyla decreased to five and for active UC the phyla number further reduced to three. Besides, the correlation intensity of the related bacterium-fungus pairs distributed evenly in controls, while the correlation intensity of some microbe pairs in patients with UC became prominent, indicating the bacteria-fungi interaction became single and circumscribed in patients with UC.

Supplementary Table 1 Subsampled sequences and corresponding operational taxonomic units in the subgroup analysis

Samples involved in the subgroup analysis	Number of subsampled sequences	Number of OTUs	Number of phyla	Number of genera
Fecal and mucosa bacteria from the same UC patients	14514	4251	34	497
Fecal bacteria of UC patients and non-IBD controls	14304	1560	19	269
Fecal bacteria of active UC patients with different disease activity	14304	949	17	226
Mucosa bacteria of UC patients and non-IBD controls	13504	6704	37	611
Mucosa bacteria of active UC patients with different disease activity	21613	4008	37	536
Fecal bacteria of UC patients with different disease subtype	16632	1172	17	231
Mucosa bacteria of UC patients with different disease subtype	21555	4023	37	542
Mucosa bacteria from non-inflamed and inflamed sites of UC patients	21637	2297	24	372

Fecal fungi of UC patients and non-IBD controls	17088	2401	6	159
Fecal fungi of active UC patients with different disease activity	17052	1173	5	106

In the subgroup analysis, qualified sequences were subsampled and clustered into operational taxonomic units (OTUs). The subsampled sequences and the number of corresponding OTUs, identified bacteria (or fungi) phyla and genera were listed in the table above. OTUs: Operational taxonomic units; IBD: Inflammatory bowel disease; UC: Ulcerative colitis.

Supplementary Table 2 The characteristics of ulcerative colitis patients provided paired stool and mucosa samples or paired mucosa samples from inflamed and non-inflamed sites for intestinal bacteria analysis

Clinical characteristic	Mean (SD)	
	Patients provided paired stool and mucosa samples	Patients provided paired mucosa samples from inflamed and non-inflamed sites
Total patients, *n* (%)	31	19
Age	45.4 (14.6)	47.6 (13.7)
Male/Female, *n* (%)	18/13	11/8
Disease activity		
UC in remission, *n* (%)	10	NA
Mild, *n* (%)	12	7
Moderate, *n* (%)	5	7
Severe, *n* (%)	4	5
Disease type		
E1 + E2, *n* (%)	15	8
E3, *n* (%)	16	11

UC: Ulcerative colitis; SD: Standard deviation; E1 + E2: Proctitis and distal colitis; E3: Pancolitis; NA: Not applicable.

Supplementary Table 3 The characteristics of ulcerative colitis patients with different levels of disease activity and the non-inflammatory bowel disease controls-the analysis of bacteria flora in stool or mucosa samples, or the analysis of fungi flora in stool samples

Group stratifications		Non-IBD	UC in remission	Active UC	Disease activity		
					Mild	Moderate	Severe
Analysis of bacteria flora in stool samples	Total patients, n (%)	21	16	56	20	21	15
	Mean age (SD)	55.5 (15.2)	41.8 (13.4)	43.4 (14.6)	44.1 (14.3)	46.3 (16.5)	40.1 (10.6)
	Male/Female, n (%)	13/8	10/6	31/25	12/8	13/8	6/9
	Disease type	\					
	E1 + E2, n (%)		14	15	8	6	1
	E3, n (%)		2	41	12	15	14
Analysis of bacteria flora in mucosa samples	Total patients, n (%)	12	13	35	16	13	6
	Mean age (SD)	56.1 (11.3)	43.1 (16.3)	44.2 (13.9)	40.8 (15.2)	49.1 (12.8)	42.8 (11.4)
	Male/Female, n (%)	7/5	8/5	20/15	9/7	9/4	2/4
	Disease type	\					
	E1 + E2, n (%)		9	10	5	3	2
	E3, n (%)		4	25	11	10	4
Analysis of fungi	Total patients, n (%)	15	12	30	11	11	8
	Mean age (SD)	59.7 (14.6)	44.2 (12.9)	39.3 (11.2)	41.5 (13.)	50.0 (13.1)	39.9 (10.7)

flora in stool samples				1)			
Male/Female, n (%)	9/6	8/4	15/15	5/6	6/5	4/4
Disease type	\					
E1 + E2, n (%)		10	4	2	2	0
E3, n (%)		2	26	9	9	8

For analysis of bacteria flora in stool sample, 93 stool samples were got from 21 non-inflammatory bowel disease (IBD) controls and 72 ulcerative colitis (UC) patients. Among the UC patients, 16 were in remission stage, and 56 were active UC. The mean age of non-IBD group was significantly different from remission stage UC group ($P = 0.007$) or active UC patients ($P = 0.002$). UC patients in remission stage and in active stage showed a similar age distribution ($P = 0.614$) but their constituent ratio of disease type differed significantly ($P = 0.000$). The gender ratio of all three groups showed little difference ($P = 0.809$). When the active UC patients were further classified as mild ($n = 20$), moderate ($n = 21$) and severe ($n = 15$) UC, the mean age ($P_{\text{mild-moderate}} = 0.620$, $P_{\text{mild-severe}} = 0.428$, $P_{\text{moderate-severe}} = 0.209$), gender ratio ($P = 0.373$) and the distribution of disease type ($P = 0.058$) of these three subgroups were similar. For analysis of bacteria flora in mucosa sample, 60 mucosa samples were got from 12 non-IBD controls and 48 UC patients. Among the UC patients, 13 were in remission, and 35 were in active stage. The mean age of non-IBD group was significantly different from remission stage UC group ($P = 0.031$) or active UC patients ($P = 0.011$). UC patients in remission stage and in active stage showed a similar age distribution ($P = 0.809$) but their constituent ratio of disease type differed significantly ($P = 0.010$). The gender ratio of all three groups showed little difference ($P = 0.963$). When the active UC patients were further classified as mild ($n = 16$), moderate ($n = 13$) and severe ($n = 6$) UC, the mean age ($P_{\text{mild-moderate}} = 0.130$, $P_{\text{mild-severe}} = 0.771$, $P_{\text{moderate-severe}} = 0.323$), gender ratio ($P = 0.335$) and the distribution of disease

type (P = 0.852) of these three subgroups were similar. 42 UC patients and 15 non-IBD controls were included in the analysis of fecal fungi flora. The mean age of non-IBD group was significantly different from UC in remission group (P = 0.000) or active UC patients (P = 0.000). Among the UC patients, 12 were in remission stage and 30 were in active stage. UC patients in remission stage and in active stage showed a similar age distribution (P = 0.274) but their constituent ratio of disease type differed significantly (P = 0.000). The gender ratio of non-IBD controls, UC in remission and active stage UC showed little difference (P = 0.580). When the active UC patients were further classified as mild (n = 11), moderate (n = 11) and severe (n = 8) UC, The mean age ($P_{\text{mild-moderate}}$ = 0.121, $P_{\text{mild-severe}}$ = 0.788, $P_{\text{moderate-severe}}$ = 0.093), gender ratio (P = 0.913) and the distribution of disease type (P = 0.259) of these active UC subgroups were similar. IBD: Inflammatory bowel disease; UC: Ulcerative colitis; SD: Standard deviation; E1 + E2: Proctitis and distal colitis; E3: Pancolitis.

Supplementary Table 4 The characteristics of ulcerative colitis patients with different disease extent-the analysis of bacteria flora in stool or mucosa sample

	Analysis of bacteria flora in stool sample		Analysis of bacteria flora in mucosa sample	
	Distal colitis and proctitis ($n = 15$)	Pancolitis ($n = 41$)	Distal colitis and proctitis ($n = 10$)	Pancolitis ($n = 25$)
Mean age (SD)	44.7 (13.1)	43.5 (14.9)	44.8 (13.4)	44.0 (14.4)
Male/Female, n (%)	8/7	23/18	6/4	14/11
Disease activity				
Mild, n (%)	8	12	5	11
Moderate, n (%)	6	15	3	10
Severe, n (%)	1	14	2	4

For analysis of bacteria flora in stool sample, among the 56 active-stage ulcerative colitis (UC) patients, 15 cases were "partial colitis" [2 proctitis (E1) and 13 distal colitis (E2)], and 41 cases were pancolitis. The basic clinical characteristics of these two groups were comparable (Age, $P = 0.780$. Gender, $P = 0.854$. Disease activity, $P = 0.086$). For analysis of bacteria flora in mucosa sample, among the 35 active-stage UC patients, 10 cases belonged to the "partial colitis" group (2 E1 and 8 E2), and 25 cases were pancolitis. The basic clinical characteristics of these two groups were comparable (Age, $P = 0.881$. Gender, $P = 0.829$. Disease activity, $P = 0.852$). UC: Ulcerative colitis; SD: Standard deviation; E1: Proctitis; E2: Distal colitis.

Supplementary Table 5 The relative abundance and *P* value of bacteria that significantly differed between stool and mucosa samples of the same ulcerative colitis patient

Bacteria	Relative abundance		*P* value
	Stool sample	**Mucosa sample**	
Phylum			
Bacteroidetes	0.2321 ± 0.0401	0.1078 ± 0.0138	0.007
Firmicutes	0.5068 ± 0.0489	0.3687 ± 0.0323	0.011
Proteobacteria	0.1544 ± 0.0415	0.3511 ± 0.0249	0.001
Unidentified phyla	0.0013 ± 0.0000	0.1000 ± 0.0146	0.001
Genus			
Acinetobacter	0.0008 ± 0.0000	0.0176 ± 0.0023	0.001
Bacteroides	0.2077 ± 0.0355	0.0890 ± 0.0138	0.005
Bifidobacterium	0.0903 ± 0.0129	0.0045 ± 0.0000	0.001
Blautia	0.0336 ± 0.0015	0.0113 ± 0.0002	0.004
Eubacterium rectale group	0.0163 ± 0.0014	0.0016 ± 0.0000	0.002
Faecalibacterium	0.0840 ± 0.0055	0.0335 ± 0.0019	0.003
Geobacillus	0.0025 ± 0.0000	0.0435 ± 0.0036	0.001
Lactococcus	0.0006 ± 0.0000	0.0106 ± 0.0002	0.001
Methylobacterium	0.0000 ± 0.0000	0.0194 ± 0.0020	0.001
Mobilitalea	0.0107 ± 0.0035	0.0000 ± 0.0000	0.001
Pseudomonas	0.0013 ± 0.0000	0.0163 ± 0.0004	0.001
Ralstonia	0.0008 ± 0.0000	0.0125 ± 0.0003	0.001
Rhodococcus	0.0002 ± 0.0000	0.0336 ± 0.0144	0.002
Roseburia	0.0312 ± 0.0021	0.0058 ± 0.0001	0.001
Turicibacter	0.0127 ± 0.0019	0.0003 ± 0.0000	0.001
Unidentified genera	0.0473 ± 0.0013	0.2754 ± 0.0280	0.001

Supplementary Table 6 The relative abundance and *P* value of bacteria significantly differed among the non-inflammatory bowel disease controls, ulcerative colitis in remission and active ulcerative colitis groups–stool or mucosa sample

Sample type	Bacteria	Relative abundance						$P_{N/R}$	$P_{N/A}$	$P_{A/R}$
		Non-IBD control		UC in remission		Active UC				
Stool sample	Phylum									
	Bacteroidetes	0.3374	±	0.1895	±	0.2221	±	0.005	0.012	0.520
		0.0243		0.0244		0.0550				
	Firmicutes	0.5445	±	0.7049	±	0.4255	±	0.003	0.023	0.001
		0.0258		0.0201		0.0557				
	Proteobacteria	0.0659	±	0.0355	±	0.2589	±	0.017	0.001	0.001
		0.0019		0.0009		0.0877				
	Genus									
	Alistipes	0.0108	±	0.0018	±	0.0018	±	0.001	0.006	0.984
		0.0001		0.0000		0.0000				
	Bacteroides	0.2769	±	0.1709	±	0.1813	±	0.039	0.050	0.814
		0.0237		0.0235		0.0443				
	Blautia	0.0349	±	0.0706	±	0.0221	±	0.064	0.252	0.021
		0.0016		0.0043		0.0017				
	Dialister	0.0139	±	0.0025	±	0.0064	±	0.019	0.136	0.162
		0.0004		0.0000		0.0002				
	Enterococcus	0.0012	±	0.0026	±	0.0468	±	0.554	0.001	0.002
		0.0000		0.0000		0.0151				
	Escherichia-Shigella	0.0365	±	0.0152	±	0.1783	±	0.039	0.001	0.002
		0.0015		0.0007		0.0684				
	Faecalibacterium	0.0931	±	0.1523	±	0.0595	±	0.104	0.068	0.021
		0.0040		0.0172		0.0086				

		Group 1		Group 2		Group 3		p1	p2	p3
	Haemophilus	0.0022 ± 0.0000	±	0.0007 ± 0.0000	±	0.0105 ± 0.0015	±	0.047	0.064	0.008
	Klebsiella	0.0087 ± 0.0003	±	0.0028 ± 0.0000	±	0.0245 ± 0.0085	±	0.170	0.203	0.036
	Lachnospira	0.0087 ± 0.0003	±	0.0251 ± 0.0004	±	0.0060 ± 0.0005	±	0.009	0.619	0.004
	Peptoclostridium	0.0035 ± 0.0000	±	0.0062 ± 0.0002	±	0.0119 ± 0.0006	±	0.521	0.027	0.298
	Roseburia	0.0377 ± 0.0013	±	0.0576 ± 0.0025	±	0.0090 ± 0.0004	±	0.194	0.007	0.005
	Ruminococcus 2	0.0153 ± 0.0013	±	0.0054 ± 0.0002	±	0.0003 ± 0.0000	±	0.285	0.003	0.203
	Ruminococcus torques group	0.0128 ± 0.0008	±	0.0220 ± 0.0018	±	0.0014 ± 0.0000	±	0.486	0.031	0.088
	Subdoligranulum	0.0296 ± 0.0011	±	0.0137 ± 0.0006	±	0.0022 ± 0.0000	±	0.106	0.002	0.207
Mucosa sample	**Phylum**									
	Actinobacteria	0.0082 ± 0.0000	±	0.0897 ± 0.0334	±	0.0409 ± 0.0020	±	0.028	0.001	0.435
	Firmicutes	0.2039 ± 0.0192	±	0.2929 ± 0.0288	±	0.3994 ± 0.0377	±	0.177	0.002	0.080
	Proteobacteria	0.1808 ± 0.0224	±	0.2553 ± 0.0203	±	0.3411 ± 0.0287	±	0.207	0.009	0.105
	Unidentified phyla	0.5229 ± 0.0597	±	0.2017 ± 0.0303	±	0.0748 ± 0.0099	±	0.002	0.001	0.031
	Genus									
	Acinetobacter	0.0003 ± 0.0000	±	0.0069 ± 0.0001	±	0.0308 ± 0.0094	±	0.000	0.001	0.210

				N/R	N/A	A/R
Bacillus	0.0000 ± 0.0000	0.0008 ± 0.0000	0.0410 ± 0.0165	0.028	0.006	0.013
Eubacterium rectale group	0.0132 ± 0.0002	0.0030 ± 0.0000	0.0019 ± 0.0000	0.004	0.050	0.445
Faecalibacterium	0.0186 ± 0.0004	0.0434 ± 0.0010	0.0391 ± 0.0024	0.006	0.088	0.741
Geobacillus	0.0000 ± 0.0000	0.0090 ± 0.0011	0.0438 ± 0.0034	0.952	0.001	0.021
Lactococcus	0.0000 ± 0.0000	0.0021 ± 0.0001	0.0106 ± 0.0002	0.001	0.001	0.017
Methylobacterium	0.0000 ± 0.0000	0.0244 ± 0.0010	0.0184 ± 0.0021	0.001	0.001	0.657
Peptoclostridium	0.0007 ± 0.0000	0.0210 ± 0.0035	0.0042 ± 0.0001	0.000	0.020	0.522
Prevotella group 9	0.0045 ± 0.0001	0.0005 ± 0.0000	0.0162 ± 0.0033	0.056	0.444	0.010
Pseudomonas	0.0000 ± 0.0000	0.0042 ± 0.0001	0.0162 ± 0.0004	0.006	0.001	0.023
Ralstonia	0.0000 ± 0.0000	0.0012 ± 0.0000	0.0153 ± 0.0004	0.348	0.001	0.002
Ruminococcus torques group	0.0177 ± 0.0002	0.0304 ± 0.0011	0.0030 ± 0.0001	0.216	0.012	0.010
Streptococcus	0.0019 ± 0.0000	0.0060 ± 0.0001	0.0164 ± 0.0003	0.078	0.001	0.020
Unidentified phyla	0.5955 ± 0.0576	0.3170 ± 0.0412	0.2567 ± 0.0268	0.069	0.001	0.371

IBD: Inflammatory bowel disease; UC: Ulcerative colitis; N/R: Normal versus UC in remission; N/A: Normal versus active UC; A/R: Active UC versus UC in remission.

Supplementary Table 7 The relative abundance and *P* value of bacteria that significantly differed among active ulcerative colitis subgroups with different level of disease activity–stool or mucosa sample

Sample type	Bacteria	Relative abundance			$P_{Mi/Mo}$	$P_{Mi/S}$	$P_{Mo/S}$
		Mild active UC	Moderate active UC	Severe active UC			
Stool sample	Phylum						
	Bacteroidetes	0.3405 ± 0.0568	0.2085 ± 0.0587	0.0845 ± 0.0159	0.104	0.001	0.500
	Proteobacteria	0.0906 ± 0.0061	0.2368 ± 0.0800	0.5152 ± 0.1097	0.024	0.001	0.016
	Genus						
	Bacteroides	0.2506 ± 0.0492	0.1931 ± 0.0527	0.0745 ± 0.0147	0.429	0.004	0.045
	Blautia	0.0285 ± 0.0009	0.0116 ± 0.0002	0.0232 ± 0.0051	0.024	0.882	0.899
	Escherichia-Shigella	0.0421 ± 0.0042	0.1884 ± 0.0649	0.3461 ± 0.1138	0.012	0.002	0.140
	Eubacterium rectale group	0.0164 ± 0.0013	0.0007 ± 0.0000	0.0000 ± 0.0000	0.028	0.001	0.012
	Faecalibacterium	0.0718 ± 0.0054	0.0807 ± 0.0152	0.0128 ± 0.0008	0.810	0.002	0.021
	Lachnospira	0.0142 ± 0.0013	0.0017 ± 0.0000	0.0008 ± 0.0000	0.068	0.034	0.422
	Parasutterella	0.0122 ± 0.0003	0.0062 ± 0.0005	0.0002 ± 0.0000	0.389	0.001	0.178
	Roseburia	0.0187 ± 0.0010	0.0061 ± 0.0001	0.0009 ± 0.0000	0.111	0.001	0.037

Mucosa sample	Phylum											
		Actinobacteria	0.0486 ± 0.0023	±	0.0426 0.0018	±	0.0120 0.0001	±	0.748	0.003	0.010	
		Unidentified phyla	0.0908 ± 0.0071	±	0.0689 0.0157	±	0.0366 0.0020	±	0.608	0.042	0.570	
	Genus											
		Blautia	0.0093 ± 0.0009	±	0.0187 0.0003	±	0.0021 0.0000	±	0.118	0.020	0.001	
		Methylobacterium	0.0372 ± 0.0040	±	0.0041 0.0001	±	0.0003 0.0000	±	0.021	0.010	0.266	

UC: Ulcerative colitis; Mi/Mo: Mild versus moderate subgroups; Mi/S: Mild versus severe subgroups; Mo/S: Moderate versus severe subgroups.

Supplementary Table 8 The relative abundance and *P* value of the bacteria significantly differed among groups

Stool bacteria	Relative abundance		*P* value
	Partial colitis	**Pancolitis**	
Phylum			
Fusobacteria	0.0001 ± 0.0000	0.0113 ± 0.0017	0.020
Genus			
Fusobacterium	0.0001 ± 0.0000	0.0113 ± 0.0017	0.019
Mucosal bacteria	Relative abundance		
	Non-IBD control	UC in remission	
Phylum			
unidentified phyla	0.0211 ± 0.0003	0.0982 ± 0.0112	0.004
Genus			
Methylobacterium	0.0007 ± 0.0000	0.0256 ± 0.0028	0.031

IBD: Inflammatory bowel disease; UC: Ulcerative colitis.

Supplementary Table 9 The relative abundance and *P* value of the fungi significantly differed among controls, ulcerative colitis in remission and active ulcerative colitis patients, or among mild, moderate and severe active ulcerative colitis patients

	Relative abundance			$P_{N/R}$	$P_{N/A}$	$P_{A/R}$
	Non-IBD control	UC in remission	Active UC			
Genus						
Malassezia	0.0017 ± 0.0000	0.0048 ± 0.0000	0.0102 ± 0.0003	0.184	0.003	0.172
Mycosphaerella	0.0036 ± 0.0001	0.0032 ± 0.0000	0.0439 ± 0.0264	0.973	0.008	0.008
Suillus	0.0204 ± 0.0058	0.0008 ± 0.0000	0.0000 ± 0.0000	0.562	0.023	0.198
	Mild active UC	Moderate active UC	Severe active UC	$P_{Mi/Mo}$	$P_{Mi/S}$	$P_{Mo/S}$
Genus						
Rhizopus	0.0005 ± 0.0000	0.0119 ± 0.0003	0.0176 ± 0.0024	0.031	0.658	0.918
Xeromyces	0.0000 ± 0.0000	0.0021 ± 0.0000	0.0109 ± 0.0009	0.079	0.018	0.657
Yarrowia	0.0000 ± 0.0000	0.0000 ± 0.0000	0.0324 ± 0.0084	0.062	0.822	0.001

IBD: Inflammatory bowel disease; UC: Ulcerative colitis; N/R: Normal versus UC in remission; N/A: Normal versus active UC; A/R: Active UC versus UC in remission; Mi/Mo: Mild versus moderate; Mi/S: Mild versus severe; Mo/S: Moderate versus severe.