

Dysbiosis of Fungal Microbiota in the Intestinal Mucosa of Patients with Colorectal Adenomas

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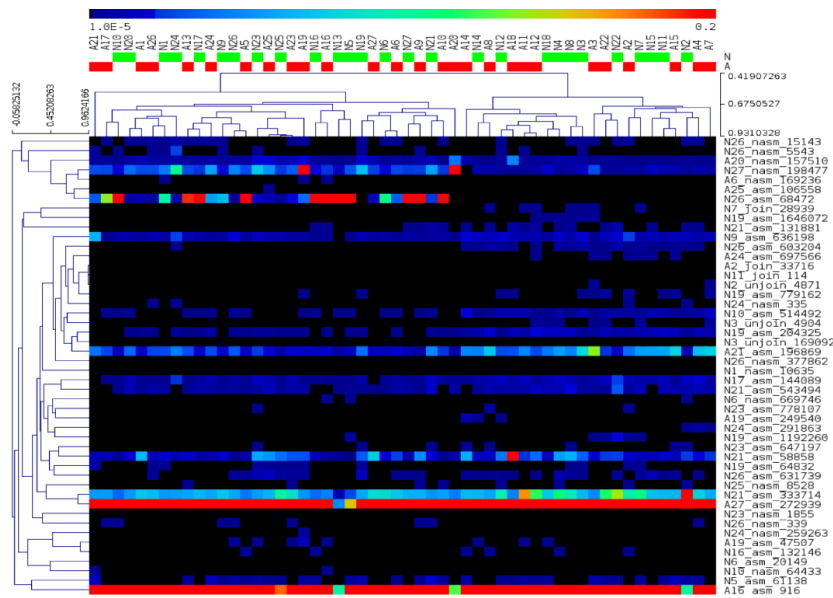
Supplementary Information

The supplementary information includes:

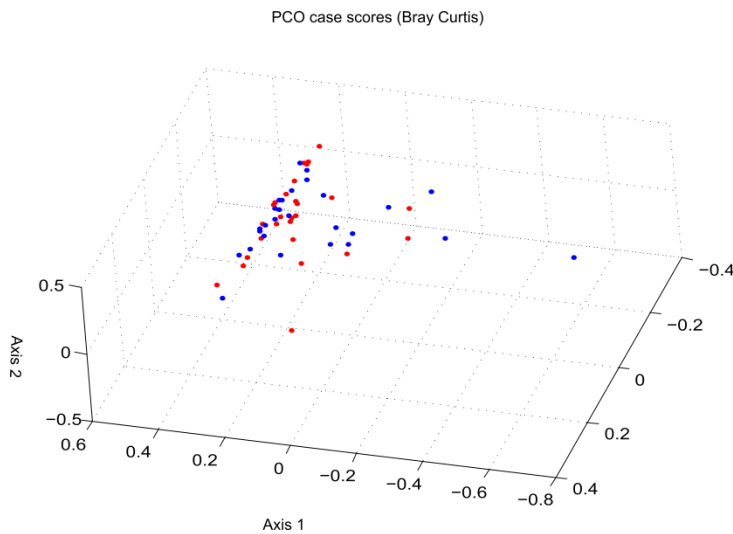
Supplementary Figures S1 and S2.

Supplementary Tables S1 and S2.

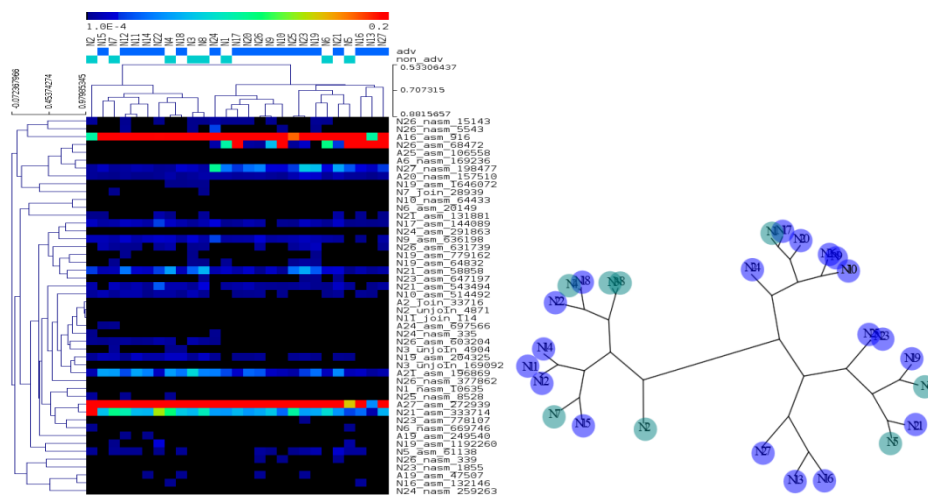
Supplementary Figures



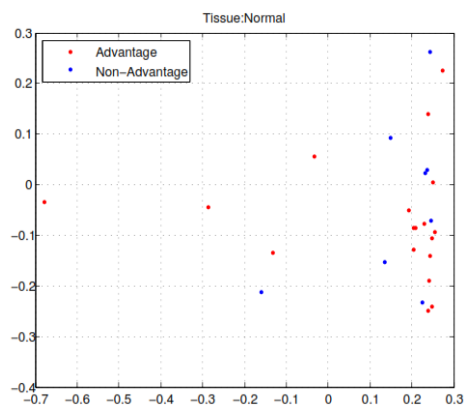
Supplement figure 1 A. The heat-map of the global mycobiome of the adenomas and normal mucosa biopsies based on the core OTUs.



Supplement figure 1 B. The relationship of PCA component between adenomas and normal mucosa biopsies based on the core OTUs. Red dots indicate the adenomas mucosa biopsies, blue dots indicates the normal mucosa biopsies.



Supplement figure 2 A. The heatmap and hierarchical clustering of normal mucosal biopsies in advanced and non advanced stage subjects based on the core OTUs.



Supplement figure 2 B. The PCA analysis of normal mucosa biopsies in advanced and non advanced stage subjects.

Lobulomyces	0	0	0	0	0	3.56E-06	0	0	0	0	0.00047	2.35E-06	0	0	0	0	0	0.000164	0	0	0	8.71E-05	0	0.00E+00	0	0.00E+00	
Malassezia	0.00E+00	7.00E-05	0	0	0	0	0	0.00E+00	0	0	0	0	0	0	0.00134	6.02E-05	0	0	0	1.50E-03	0.00E+00	0.00E+00	3.37E-04	0.00E+00	2.10E-05	0	
Microdochium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Penicillium	8.77E-07	0	4.05E-05	1.90E-06	5.83E-07	0	3.49E-06	0	0	0	0	0	0	0.00E+00	0.00E+00	0	0	0.013336	7.40E-07	0	0	0	0	0	0	0	
Phaeosphaeria	0	0	0	0	0	0	0	0	0	0	0.000136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Phaeosphaeriopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Phoma	0.509196	0.617107	0.30555	0.432677	0.286389	0.503919	0.270465	0.329619	0.436188	0.401132	0.504965	0.551297	0.407544	0.382901	0.320634	0.312495	0.372342	0.294553	0.344273	0.308488	0.395964	0.542347	0.601565	0.426352	0.450364	0.476528	0.577796
Pichia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00E+00	0	
Piromyces	0	0	0	0	0	7.12E-07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Plectosphaerella	8.77E-07	0.00237	0	0.00022	0	0	0	0	0	0	0	0	0	0	0	0	1.59E-05	0.002103	0	0.006388	0	0.002112	0.00E+00	0.002587	0.001724	0.00039	
Pseudozyma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00E+00	0.000302	0	0	0	0	0	0	
Pterygellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Puccinia	0	0	0	0	0	0	0	0.00E+00	0	0	0	0	0	0	0.000751	0	0	0	0	0	0	0	0	0	0	0	
Pyrenochaeta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Rhizophagus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Rhizophydium	0	0.00253	0	0	0	0	0	0	0	0.00E+00	0.00033	0	0	0	0	0	0	0	0	0	0	0.000522	0	0	0	0	
Rhodotorula	0.000697	0.005704	0.001334	0.007577	1.32E-03	0.00081	0.012755	0.002852	0.001205	0.00063	0.008981	0.003094	0.001273	0.017563	0.003562	0.000242	0.002571	0.008238	0.000934	2.22E-06	3.01E-06	0.007701	0.000544	0.001475	0.000623	3.19E-05	0.00036
Saccharomyces	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00E+00	0	
Schizophyllum	0	0.00347	0.001058	0	0	0	0.002996	0	0	0	0.000627	0	0	0.004079	0	0	0.001159	0.001518	0	0	0.004273	0	0	0	0	0	
Shiraia	0.00E+00	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Sporobolomyces	0	6.67E-06	0.001201	0	0.00E+00	0	0	0	0	1.01E-04	0	0	0	0.001785	0	6.16E-07	0	0	0	0	0	0	0	0	0	0	0
Synchytrium	3.07E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Thanatephorus	3.07E-06	0	0	0	6.56E-05	0	5.23E-05	0	0	0.00E+00	0	0	0	3.21E-05	0.00E+00	0	0.00E+00	0.00E+00	0	0	0	0	0	0.00E+00	1.93E-05	0.000112	0
Trichocladium	6.01E-04	0.000347	0	0.001519	0.00284	0.000924	0	0.001638	0.001349	4.97E-07	0	0.000911	0	0.002981	0.003455	0	0	0.001159	0.002382	0	1.80E-06	0	0.002567	0	0.012528	0.003244	0.000391
Trichoderma	0.00024	0	0	0.000875	0	8.26E-05	0	0	9.97E-04	0.00E+00	0	0	0	0.000657	0	0	0.002361	0	1.73E-06	0	0	0	0.000946	0	0	0.000239	

333714	167338	28330	9243	41369	73695	102621	17409	19646	125838	115384	30593	51847	137958	21048	24510	74619	98558	20037	58457	59284	91087	19699	99770	92775	50175	99576	186902
198477	64048	2061	5370	3827	49027	38230	1975	2836	47191	45215	772	2523	62084	189	3539	35301	48818	1578	261225	663730	48226	605	38583	89200	40164	41064	54673
196869	33486	11824	25916	36118	23385	21271	22051	24111	7012	42979	8707	11468	65816	14743	29871	24434	46619	12752	17450	8377	68235	3581	21310	43428	13293	38257	31394
58858	150426	4212	2551	10266	10741	35133	6229	5161	95864	4163	3875	16128	31079	19341	5354	7042	16187	146376	34188	10500	13289	3987	35795	10243	41238	13696	166088
636198	10309	7457	291	3347	7290	4515	2696	3434	6831	12217	1635	3379	21390	5731	3950	3859	2854	4357	5860	3174	107763	1752	5190	5458	6274	12745	9098
157510	29723	387	391	960	8020	7353	742	490	15215	4614	610	1762	11106	2143	505	6264	8413	20834	20873	56440	6819	715	12094	9001	13502	7634	21372
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204325	4619	2093	819	5130	1874	1485	2202	5282	817	3164	1354	8191	2723	1574	4292	1345	0	4688	1983	1241	0	1672	2623	8228	2430	1340	1421
631739	1369	104	0	800	4871	1298	0	545	2653	1	0	388	0	930	1318	0	0	511	3792	0	3	0	2976	0	9738	4784	877
514492	1588	1711	261	3992	2272	1138	3657	949	2370	1267	1646	1318	2957	5479	1359	393	4610	3633	1079	3	5	1283	631	2279	484	47	806
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169236	859	2	4	6	775	330	0	1	120	573	1	0	374	0	0	1455	751	3	1106	476	58	0	418	531	462	932	401
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2574	0	0	37	0	0	0	0	0	0	0	11	0	0	1	0	0	0	0	15311	0	0	0	0	0	0	0	0
8528	638	291	42	151	835	99	28	41	3128	3105	9	0	1975	55	30	0	0	12	280	0	0	0	1016	0	119	0	161
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0

15143	3540	1429	423	209	0	2973	0	535	3348	1206	358	802	0	69	0	0	3006	291	9080	3852	0	395	0	9337	0	466	0
5543	1393	67	425	29	521	900	44	280	1623	2011	181	1018	0	123	208	291	270	276	3787	459	313	0	1057	42591	180	626	329
131881	1084	529	0	326	404	550	0	2186	0	0	145	12	176	252	432	2918	251	0	2067	801	1766	1886	254	131	0	0	2587
64832	4029	0	845	0	0	0	895	870	0	0	0	0	0	229	0	0	2	0	8066	0	0	0	6855	0	1899	0	0
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647197	0	295	6	0	0	663	0	1672	5	0	119	0	0	276	0	0	900	0	5200	106	2846	0	1187	0	356	0	0
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339	0	0	9	0	0	0	0	222	1676	3056	0	0	0	0	0	0	0	0	0	0	2434	0	0	0	39	1988	0
2574	0	71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1308	0	0	0	0	0	0	0
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142	0	0	0	0	14450	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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608222	0	22	0	0	0	0	10	0	0	0	0	0	0	0	1	0	0	0	7	0	0	0	0	1	0	0	0
132146	2	2	5	540	0	0	14	2	9	2	0	1	5	14	0	4738	68	290	0	10	0	0	92	12	90	108	0
259263	389	2	0	0	0	18	1	0	246	76	0	1	121	0	0	342	94	1	0	33	0	1	188	516	229	374	1
185140	0	0	0	0	0	295	0	0	0	0	0	0	113	0	0	3875	836	0	0	0	0	0	0	0	0	0	1039
1646072	449	0	954	455	0	37	0	1168	10	75	0	0	99	0	0	44	187	913	839	68	0	54	92	12	1	52	1034
669746	0	552	0	0	2068	4	0	0	321	0	46	0	0	9	0	0	430	0	0	0	0	0	0	0	0	0	0
4904	2	19	113	299	2	2	1474	65	3	3	142	67	0	228	77	1	2	862	3	4	2	152	1	3	0	1	1
249540	0	0	14	0	0	86	0	0	0	0	0	95	747	467	0	0	0	0	0	713	0	0	896	0	0	0	0
335	0	325	0	0	0	0	119	8	0	0	0	0	0	0	257	0	0	0	0	0	0	0	0	3687	0	0	0
28939	5	0	401	0	1	9	433	623	3	733	0	14	0	0	0	1	41	0	190	130	19	0	9	0	7	1	182
1003119	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	1160	404	0	0	0	0	0	1595	0	0	0	0

Table S2. Primers were used for sequencing library construction.

ITS Forward Primer	5'→3'
ITS1 Forward-1	aatgatacggcgaccaccgagatctacactcttccctacacgacgctctccgatctCTTGGTCATTTAGAGGAAGTAA
ITS1 Forward-2	aatgatacggcgaccaccgagatctacactcttccctacacgacgctctccgatctTTGGTCATTTAGAGGAAGTAAA
ITS1 Forward-3	aatgatacggcgaccaccgagatctacactcttccctacacgacgctctccgatctTGGTCATTTAGAGGAAGTAAAA
ITS1 Forward-4	aatgatacggcgaccaccgagatctacactcttccctacacgacgctctccgatctGGTCATTTAGAGGAAGTAAAAAG
ITS1 Forward-5	aatgatacggcgaccaccgagatctacactcttccctacacgacgctctccgatctGTCATTTAGAGGAAGTAAAAAGT

ITS Reverse Primer	5'→3'
ITS2 Reverse-1	caagcagaagacggcatacagagatATCACGtgactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-2	caagcagaagacggcatacagagatCGATGTgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-3	caagcagaagacggcatacagagatTAGGCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-4	caagcagaagacggcatacagagatTGACCAgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-5	caagcagaagacggcatacagagatACAGTgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-6	caagcagaagacggcatacagagatGCCAATgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-7	caagcagaagacggcatacagagatCAGATgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-8	caagcagaagacggcatacagagatACTTAGgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-9	caagcagaagacggcatacagagatGATCAGgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-10	caagcagaagacggcatacagagatTAGCTTgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-11	caagcagaagacggcatacagagatGGCTACgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATG
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ITS2 Reverse-13	caagcagaagacggcatacagagatAGTCAAgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-14	caagcagaagacggcatacagagatAGTTCCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-15	caagcagaagacggcatacagagatATGTCAgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-16	caagcagaagacggcatacagagatCCGTCCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-17	caagcagaagacggcatacagagatGTCCGCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-18	caagcagaagacggcatacagagatGTAAAGtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-19	caagcagaagacggcatacagagatGTGGCCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-20	caagcagaagacggcatacagagatGTTTCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-21	caagcagaagacggcatacagagatCGTACGgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-22	caagcagaagacggcatacagagatGAGTGGgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
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ITS2 Reverse-30	caagcagaagacggcatacagagatTATTCgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-31	caagcagaagacggcatacagagatTAGTACgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC
ITS2 Reverse-32	caagcagaagacggcatacagagatTCTGATgtactggagttcagacgtgtgctctccgatctGCTGCGTTCTTCATCGATGC