

**Alteration of gut microbiota and inflammatory cytokine/chemokine profiles in 5-fluorouracil induced **intestinal** mucositis**

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**Running title:** Gut microbiota and 5-Fu induced **intestinal** mucositis

Table S1 The composition of the flora community at the level of phylum in feces (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobia	0.4356±0.06799	0.4027±0.04211	0.6799
Bacteroidetes	0.4231±0.08080	0.4768±0.02934	0.5153
Firmicutes	0.1452±0.02328	0.06948±0.01062	0.0253 *
Proteobacteria	0.02551±0.005710	0.008886±0.0003568	0.0272 *
Cyanobacteria	0.002693±0.0007608	0.0001695±0.0001695	0.0084 **
Actinobacteria	0.0002417±0.00009627	0.0008819±0.00008486	0.0016 **
Candidate division TM7	0.003212±0.0006694	0.0006372±0.0002150	0.0049 **
Deferribacteres	0.00009818±0.00007302	0.0002962±0.00007995	0.1172
Tenericutes	0.00238574		

Table S2 The composition of the flora community at the level of class in feces (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobiae	0.4356±0.06799	0.4027±0.04211	0.6799
Bacteroidia	0.4917±0.09291	0.4768±0.02934	0.8818
Clostridia	0.1229±0.02367	0.09086±0.03353	0.4573
Eosilonproteobactera	0.001462±0.0003436	0.004515±0.001169	0.0367 *
Grammaproteobacteria	0.006617±0.001381	0.003769±0.001427	0.2018
Alphaproteobacteria	0.01415±0.005350	0.0007946±0.0007084	0.0264 *
Deltaproteobacteria	0.003296±0.0005752	0.002056±0.0005849	0.1789
Erysipelotrichia	0.005560±0.002444	0.007786±0.002730	0.5603
Bacilli	0.001445±0.0005651	0.0004300±0.0002130	0.1722
Deferribacteres	0.0005289±0.0004344	0.0006517±0.0003609	0.8333
Unclassified	0.004468±0.001312	0.001754±0.0001729	0.0861
Nollocutes	0.00192405		
Actinobacteri		0.00020656	

Table S3 The composition of the flora community at the level of order in feces  
(T-test)

Composition	Control	5-Fu	P value
Verrucomicrobiales	0.3488±0.1015	0.4027±0.04211	0.6373
Bacteroidales	0.4917±0.09291	0.4768±0.02934	0.8818
Clostridiales	0.1229±0.02367	0.09086±0.03353	0.4573
Campylobacterales	0.001462±0.0003436	0.004515±0.001169	0.0367 *
Enterobacteriales	0.004595±0.001510	0.002709±0.001111	0.3439
Rhodospirillales	0.01134±0.005009	0.0007946±0.0007084	0.0706
Desulfovibrionales	0.003296±0.0005752	0.002056±0.0005849	0.1789
Erysipelotrichales	0.005560±0.002444	0.007786±0.002730	0.5603
Lactobacillales	0.001445±0.0005651	0.001322±0.0009072	0.9113
Deferribacterales	0.001541±0.0005151	0.0004616±0.0002204	0.0700
Unclassified	0.006959±0.002331	0.001013±0.0001832	0.0346 *
Coriobacterales	0.0005489±0.0003161	0.0006753±0.0001439	0.7253
Pseudomonadales	0.0007853±0.0003274	0.001060±0.0003241	0.5669

Table S4 The composition of the flora community at the level of family in feces (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobiaceae	0.3934±0.07540	0.4287±0.04275	0.6807
Proteobacterales	0.1128±0.05667	0.1216±0.03597	0.8990
Unclassified	0.3037±0.06738	0.2634±0.02136	0.5841
Lachnospiraceae	0.07114±0.01841	0.01895±0.004308	0.0435 *
Helicobacteraceae	0.001462±0.0003436	0.004515±0.001169	0.0367 *
Ruminococcaceae	0.04628±0.01201	0.04308±0.01064	0.8467
Bacteroidaceae	0.01186±0.003274	0.05655±0.01451	0.0170 *
Rikenellaceae	0.04755±0.01876	0.02050±0.002595	0.1911
Enterobacteriaceae	0.005657±0.001386	0.002709±0.001111	0.1363
Porphyromonadaceae	0.02587±0.008819	0.01738±0.003607	0.3988
Rhodospirillaceae	0.01415±0.005350	0.0007946±0.0007084	0.0264 *
Peptococcaceae	0.001619±0.0004530	0.0008538±0.00005141	0.1316
Desulfovibrionaceae	0.003296±0.0005752	0.009170±0.007128	0.4352
Erysipelotrichaceae	0.005560±0.002444	0.007786±0.002730	0.5603
Lactobacillaceae	0.001445±0.0005651	0.001322±0.0009072	0.9113
Coriobacteriaceae	0.0005489±0.0003161	0.0006753±0.0001439	0.7253
Defluviitaleaceae	0.0007847±0.0005116	0.00009102±0.00003922	0.2134
Deferribacteraceae	0.0005289±0.0004344	0.0006517±0.0003609	0.8333
Moraxellaceae	0.0007853±0.0003274	0.001060±0.0003241	0.5669
Propionibacteriaceae		0.00020656	

Table S5 The composition of the flora community at the level of genus in feces (T-test)

Composition	Control	5-Fu	P value
<i>Akkermansia</i>	0.3488±0.1015	0.4027±0.04211	0.6373
<i>Alloprevotella</i>	0.0957±0.04885	0.1190±0.03555	0.7196
<i>Unclassified</i>	0.4189±0.08401	0.3219±0.03140	0.3112
<i>Blautia</i>	0.04596±0.01108	0.02530±0.01775	0.3524
<i>Helicobacter</i>	0.001462±0.0003436	0.004515±0.001169	0.0367 *
<i>Anaerotruncus</i>	0.002597±0.0007430	0.003980±0.001194	0.3542
<i>Bacteroides</i>	0.01186±0.003274	0.05655±0.01451	0.0170 *
<i>Odoribacter</i>	0.01156±0.003767	0.0002374±0.002374	0.0171 *
<i>Parabacteroides</i>	0.01432±0.005142	0.01714±0.003700	0.6674
<i>Ruminococcus</i>	0.0008885±0.0002775	0.006665±0.002870	0.0801
<i>Alistipes</i>	0.01134±0.005009	0.0007946±0.0007084	0.0706
<i>Desulfovibrio</i>	0.01631±0.004094	0.01467±0.001775	0.7231
<i>Oscillibacter</i>	0.002673±0.0004783	0.008237±0.006620	0.4262
<i>Rikenella</i>	0.002713±0.0009053	0.002134±0.0005740	0.6035
<i>Bilophila</i>	0.003474±0.0009356	0.005814±0.001140	0.1513
<i>Coprococcus</i>	0.0006230±0.0001093	0.0009331±0.0005116	0.5697
<i>Roseburia</i>	0.001666±0.0006232	0.002461±0.002059	0.7213
<i>Lactobacillus</i>	0.0004067±0.0001320	0.001268±0.0007312	0.2330
<i>Enterorhabdus</i>	0.001445±0.0005651	0.001322±0.0009072	0.9113
<i>Candidatus Saccharimonas</i>	0.0005489±0.0003161	0.0006753±0.0001439	0.7253
<i>Candidatus Arthromitus</i>	0.002690±0.0007351	0.0006372±0.0002150	0.0279 *
<i>Marvinbryantia</i>	0.0009203±0.0002350	0.0001595±0.00009371	0.0169 *
<i>Mucispirillum</i>	0.0001703±0.00006582	0.001123±0.0004301	0.0600
<i>Turicibacter</i>	0.0005289±0.0004344	0.0006517±0.0003609	0.8333
<i>Acinetobacter</i>	0.0008098±0.0003323	0.00007907±0.00003480	0.0602
<i>Propionibacterium</i>	0.0007853±0.0003274	0.001060±0.0003241	0.5669
<i>Thalassospira</i>		0.00020656	

Table S6 The composition of the flora community at the level of species in feces (T-test)

Composition	Control	5-Fu	P value
<i>Unclassified</i>	0.7238±0.06837	0.6403±0.02355	0.2815
<i>Uncultured bacyperoidales bacterium</i>	0.2062±0.04252	0.2685±0.02144	0.2272
<i>Helicobacter ganmani</i>	0.001051±0.0003576	0.002833±0.0007646	0.0678
<i>Anaerotruncus sp. G3</i>	0.002067±0.0006848	0.003487±0.0009402	0.2568
<i>Gut metagenome</i>	0.0307932		
<i>Bacteroides vulgatus(ATCC 8428)</i>	0.0002376±0.00005330	0.03796±0.01395	0.0269 *
<i>Eubacterium coprostanoligenes</i>	0.00515534		
<i>Firmicutes bacterium ASF500</i>	0.003883±0.001304	0.002433±0.0005846	0.3402
<i>Parabacteroides goldsteinii</i>	0.0003321±0.0001730	0.009337±0.002903	0.0147 *
<i>Clostridium papyrosolvans</i>	0.01048±0.009080	0.002972±0.001697	0.4397
<i>Mouse gut metagenome</i>	0.0003874±0.0001732	0.001335±0.0007863	0.2730
<i>Bacteroides acidifaciens</i>	0.004226±0.0006173	0.01081±0.002800	0.0508
<i>Lachnospiraceae bacterium 610</i>	0.0000327765		
<i>Uncultured rikenellaceae bacterium</i>	0.0005278±0.0001933	0.005373±0.001754	0.0252 *
<i>Bacteroids uniformis</i>	0.00005299±0.00003684	0.005662±0.002817	0.0816
<i>Desulfovibrio sp. ABHUISB</i>	0.0005155±0.0004584	0.0004687±0.0002772	0.9326
<i>Unidentified rumen bacterium RFN71</i>	0.001409±0.0004383	0.002340±0.0009056	0.3817
<i>Clostridium sp. ABHUISB</i>	0.00007113±0.00005451	0.0003307±0.0001612	0.1656
<i>Bacteroides bacterium ph8</i>	0.0002058±0.00008006	0.0003478±0.0001581	0.4462
<i>Lachnospiraceae bacterium 10-1</i>	0.0006687±0.0004080	0.0001456±0.0001066	0.2500
<i>Dorea sp. 5-2</i>	0.0005632±0.0001401	0.0006022±0.0001472	0.8524
<i>Clostridium sp. Culture-41</i>	0.0009228±0.0002589	0.0001941±0.0001198	0.0339 *
<i>Clostridiales bacterium CIEAF 020</i>	0.00274196		
<i>Clostridiales bacterium CIEAF 012</i>	0.0001703±0.00006582	0.001123±0.0004301	0.0600
<i>Unclutured clostridiales bacterium</i>		0.000437517	
<i>Unclutured rumen bacterium</i>	0.001691±0.0009883	0.0007946±0.0007084	0.4819
<i>Bacteroides stercoris(ATCC 43183)</i>	0.0001507±0.00001942	0.0002309±0.0001230	0.5376
<i>Clostridium sp. Culture-27</i>	0.000163524		
<i>Clostridium leptum</i>	0.0002351±0.00004341	0.0007264±0.0003916	0.2477
<i>Lactobacillus murinus</i>	0.001206±0.0005052	0.0009966±0.0008175	0.8327
<i>Clostridium sp. ATCC 29733</i>		0.000525516	

Table S7 The composition of the flora community at the level of phylum in cecum contents (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobia	0.3007±0.06402	0.4991±0.03395	0.0135 *
Bacteroidetes	0.3284±0.07683	0.3162±0.03796	0.8877
Firmicutes	0.2881±0.03875	0.1530±0.02468	0.0088 **
Proteobacteria	0.05923±0.01809	0.02911±0.005661	0.1149
Cyanobacteria	0.001784±0.0004976	0.00005597±0.00003290	0.0019 **
Actinobacteria	0.0002655±0.00005982	0.001087±0.0003288	0.0243 *
Candidate division TM7	0.002187±0.0007248	0.0009700±0.0003831	0.1549
Deferribacteres	0.001541±0.0005151	0.0004616±0.0002204	0.0700
Tenericutes	00.000594389	0	

Table S8 The composition of the flora community at the level of class in cecum contents (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobiae	0.3007±0.06402	0.4991±0.03395	0.0135 *
Bacteroidia	0.3007±0.06402	0.3162±0.03796	0.8374
Clostridia	0.2828±0.03895	0.1471±0.02481	0.0088 **
Eosilonproteobacteia	0.02848±0.01498	0.003005±0.001033	0.1070
Grammaproteobacteria	0.02528±0.01890	0.006593±0.003346	0.3430
Alphaproteobacteria	0.006536±0.001600	0.00005132±0.00001819	0.0007***
Deltaproteobacteria	0.01481±0.002172	0.01946±0.005544	0.4444
Erysipelotrichia	0.003592±0.0008929	0.003617±0.0009385	0.9849
Bacilli	0.001685±0.0004087	0.002254±0.0007671	0.5207
Deferribacteres	0.00154063		
Unclassified	0.005586±0.001437	0.002113±0.0004704	0.0338 *
Nollocutes	0.000594389		
Actinobacteri			

Table S9 The composition of the flora community at the level of order in cecum contents (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobiales	0.3007±0.06402	0.4991±0.03395	0.0135 *
Bacteroidales	0.3284±0.07683	0.3162±0.03796	0.8877
Clostridiales	0.2828±0.03895	0.1471±0.02481	0.0088 **
Campylobacterales	0.02848±0.01498	0.003005±0.001033	0.1070
Enterobacteriales	0.02507±0.01889	0.006409±0.003345	0.3435
Rhodospirillales	0.02507±0.01889	0.00005132±0.00001819	0.2019
Desulfovibrionales	0.01481±0.002172	0.01946±0.005544	0.4444
Erysipelotrichales	0.003592±0.0008929	0.003617±0.0009385	0.9849
Lactobacillales	0.003592±0.0008929	0.002254±0.0007671	0.2708
Deferribacterales	0.001541±0.0005151	0.0004616±0.0002204	0.0700
Unclassified	0.005915±0.001555	0.001026±0.0003808	0.0068 **
Coriobacterales	0.0002655±0.00005982	0.001087±0.0003288	0.0243 *
Pseudomonadales	0.0002146±0.00004695	0.0001840±0.00003676	0.6135

Table S10 The composition of the flora community at the level of family in cecum contents (T-test)

Composition	Control	5-Fu	P value
Verrucomicrobiaceae	0.2314±0.05465	0.4991±0.03395	0.0005 ***
Provotellaceae	0.04876±0.01510	0.01844±0.008162	0.0944
Unclassified	0.005915±0.001555	0.2317±0.05744	0.0010 ***
Lachnospiraceae	0.1813±0.03122	0.06647±0.01143	0.0033 **
Helicobacteraceae	0.02848±0.01498	0.003005±0.001033	0.1070
Ruminococcaceae	0.09544±0.01282	0.05507±0.008728	0.0180 *
Bacteroidaceae	0.02718±0.007717	0.02695±0.004670	0.9796
Rikenellaceae	0.01653±0.004766	0.01273±0.003335	0.5220
Enterobacteriaceae	0.03553±0.02653	0.001483±0.0004226	0.1910
Porphyromonadaceae	0.01925±0.005374	0.008768±0.003003	0.1060
Rhodospirillaceae	0.006536±0.00600	0.00005132±0.00001819	0.0007 ***
Peptococcaceae	0.005148±0.001245	0.002500±0.0004356	0.0599
Desulfovibrionaceae	0.01481±0.002172	0.01946±0.005544	0.4444
Erysipelotrichaceae	0.003592±0.0008929	0.003617±0.0009385	0.9849
Lactobacillaceae	0.001685±0.0004087	0.002254±0.0007671	0.5207
Coriobacteriaceae	0.0002655±0.00005982	0.001087±0.0003288	0.0243 *
Defluviitaleaceae	0.001467±0.0004206	0.0002832±0.00008852	0.0130 *
Deferribacteraceae	0.001541±0.0005151	0.0004616±0.0002204	0.0700
Moraxellaceae	0.0002146±0.00004695	0.0001840±0.00003676	0.6135
Propionibacteriaceae			

Table S11 The composition of the flora community at the level of genus in cecum contents (T-test)

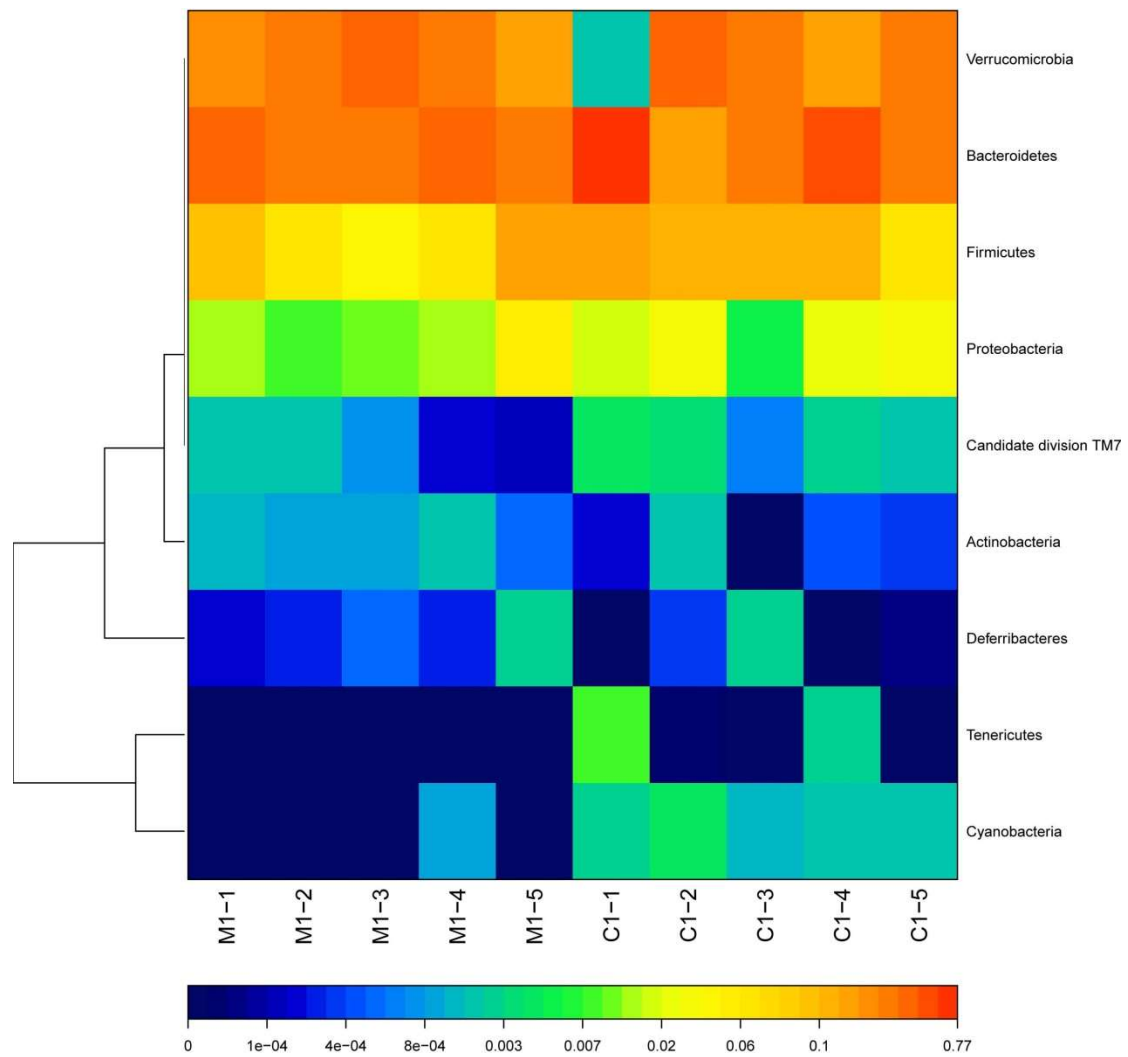
Composition	Control	5-Fu	P value
<i>Akkermansia</i>	0.3007±0.06402	0.4991±0.03395	0.0135 *
<i>Alloprevotella</i>	0.03761±0.01341	0.01793±0.007925	0.2223
<i>Unclassified</i>	0.4034±0.05140	0.3519±0.02861	0.3931
<i>Blautia</i>	0.1039±0.02636	0.03301±0.01495	0.0311 *
<i>Helicobacter</i>	0.02848±0.01498	0.003005±0.001033	0.1070
<i>Anaerotruncus</i>	0.01379±0.002957	0.007140±0.001857	0.0728
<i>Bacteroides</i>	0.02718±0.007717	0.02695±0.004670	0.9796
<i>Odoribacter</i>	0.0029127		
<i>Parabacteroides</i>	0.01633±0.004065	0.008768±0.003003	0.1518
<i>Ruminococcus</i>	0.002033±0.0008483	0.003741±0.001548	0.3461
<i>Alistipes</i>	0.006536±0.001600	0.00005132±0.00001819	0.0007 ***
<i>Desulfovibrio</i>	0.01250±0.003088	0.009522±0.002762	0.4819
<i>Oscillibacter</i>	0.008491±0.0009494	0.01775±0.005683	0.1256
<i>Rikenella</i>	0.01271±0.004157	0.004426±0.0009961	0.0684
<i>Bilophila</i>	0.0009718±0.0004100	0.003209±0.0009055	0.0371 *
<i>Coprococcus</i>	0.006316±0.001997	0.001716±0.0004276	0.0370 *
<i>Roseburia</i>	0.007069±0.001690	0.003934±0.001230	0.1511*
<i>Lactobacillus</i>	0.001019±0.0003167	0.002077±0.0005648	0.1130
<i>Enterorhabdus</i>	0.001685±0.0004087	0.002254±0.0007671	0.5207
<i>Candidatus Saccharimonas</i>	0.0002655±0.00005982	0.001087±0.0003288	0.0243 *
<i>Candidatus Arthromitus</i>	0.002187±0.0007248	0.0009700±0.0003831	0.1549
<i>Marvinbryantia</i>	0.000399286		
<i>Mucispirillum</i>	0.0001978±0.00004584	0.0007044±0.0002342	0.0479 *
<i>Turicibacter</i>	0.001541±0.0005151	0.0004616±0.0002204	0.0700
<i>Acinetobacter</i>	0.0007593±0.0002504	0.0004597±0.0002337	0.3933
<i>Propionibacterium</i>	0.0002146±0.00004695	0.0001840±0.00003676	0.6135
<i>Thalassospira</i>			



Table S12 The composition of the flora community at the level of species in cecum contents (T-test)

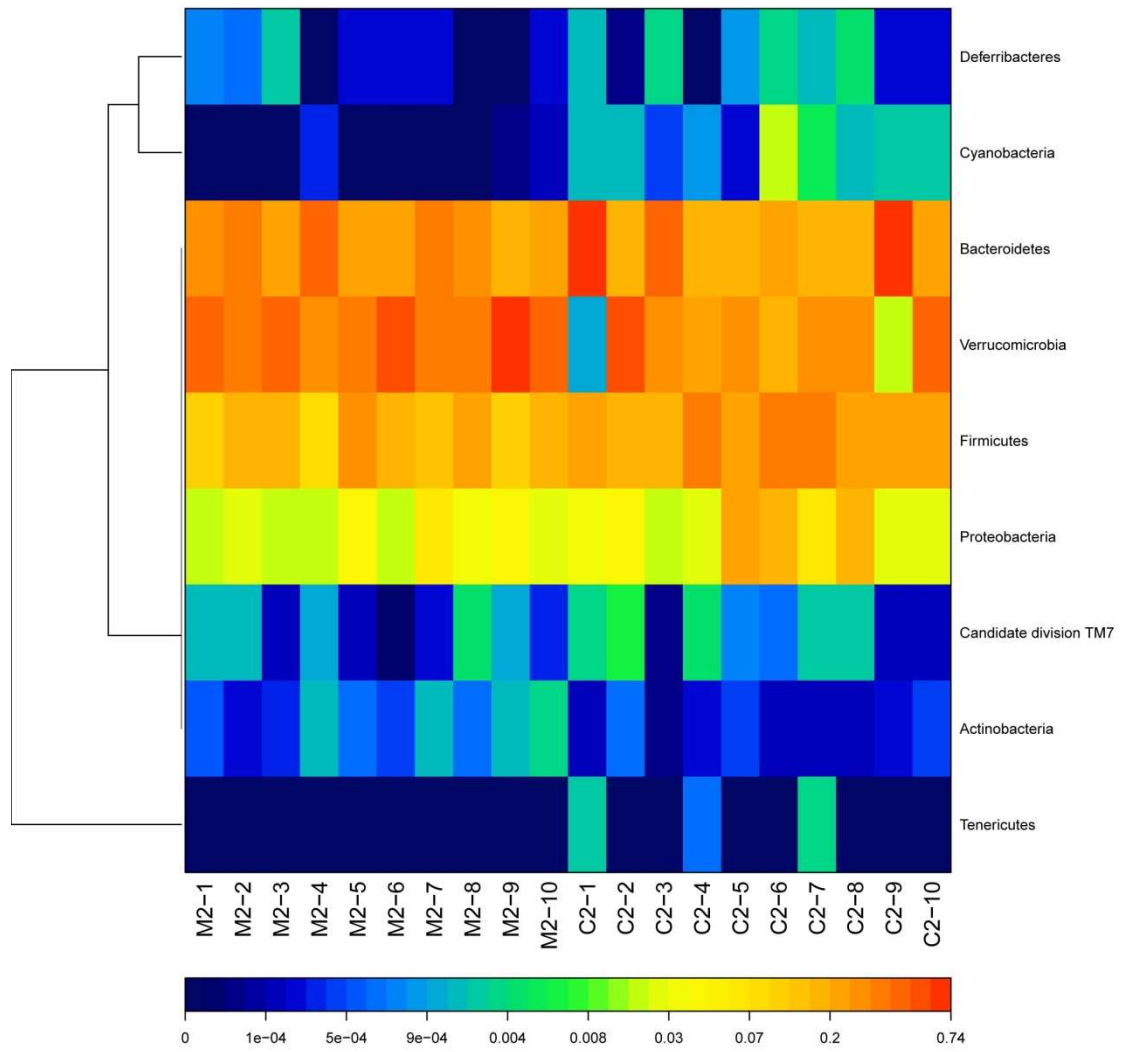
Composition	Control	5-Fu	P value
<i>Unclassified</i>	0.7847±0.03792	0.7725±0.03184	0.8078
<i>Uncultured bacyeroidales bacterium</i>	0.09597±0.03631	0.1617±0.02930	0.1762
<i>Helicobacter ganmani</i>	0.02848±0.01498	0.003005±0.001033	0.1070
<i>Anaerotruncus sp. G3</i>	0.01256±0.002904	0.005846±0.001412	0.0523
<i>Gut metagenome</i>	0.021095		
<i>Bacteroides vulgatus(ATCC 8428)</i>	0.002781±0.001524	0.01700±0.004454	0.0073 **
<i>Eubacterium coprostanoligenes</i>	0.00326508		
<i>Firmicutes bacterium ASF500</i>	0.01333±0.003497	0.004081±0.0007758	0.0188 *
<i>Parabacteroides goldsteinii</i>	0.001758±0.0009900	0.006612±0.002554	0.0932
<i>Clostridium papyrosolvens</i>	0.004695±0.003216	0.0006296±0.0004238	0.2261
<i>Mouse gut metagenome</i>	0.004054±0.001139	0.007068±0.003249	0.3930
<i>Bacteroides acidifaciens</i>	0.004621±0.001216	0.005861±0.001077	0.4549
<i>Lachnospiraceae bacterium 610</i>	0.005703±0.003249	0.000008447±0.000008447	0.0967
<i>Uncultured rikenellaceae bacterium</i>	0.0001016±0.00005553	0.001995±0.0004610	0.0007 ***
<i>Bacteroids uniformis</i>	0.0001741±0.00007605	0.002450±0.0006886	0.0041 **
<i>Desulfovibrio sp. ABHUISB</i>	0.0009436±0.0005257	0.002500±0.001007	0.1874
<i>Unidentified rumen bacterium RFN71</i>	0.001332±0.0005893	0.001433±0.0002636	0.8775
<i>Clostridium sp. ABHUISB</i>	0.0004405±0.00008135	0.0004785±0.0002046	0.8651
<i>Bacteroides bacterium ph8</i>	0.0001064±0.00006598	0.0002876±0.00007040	0.0768
<i>Lachnospiraceae bacterium 10-1</i>	0.0009771±0.0005363	0.0001268±0.00004718	0.1316
<i>Dorea sp. 5-2</i>	0.001606±0.0003919	0.001874±0.0004092	0.6413
<i>Clostridium sp. Culture-41</i>	0.002975±0.0008249	0.001083±0.0005509	0.0725
<i>Clostridiales bacterium CIEAF 020</i>	0.00287277		
<i>Clostridiales bacterium CIEAF 012</i>	0.0001978±0.00004584	0.0007044±0.0002342	0.0479 *
<i>Unclutured clostridiales bacterium</i>		0.000808674	
<i>Unclutured rumen bacterium</i>	0.001336±0.0008452	0.00005132±0.00001819	0.1461
<i>Bacteroides stercoris(ATCC 43183)</i>	0.00004030±0.00001657	0.00002747±0.00001878	0.6146
<i>Clostridium sp. Culture-27</i>	0.001982±0.001365	0.00005977±0.00005977	0.1766
<i>Clostridium leptum</i>	0.0004466±0.0001533	0.0004523±0.0001761	0.9809
<i>Lactobacillus murinus</i>	0.001417±0.0003773	0.0008577±0.0002453	0.2295
<i>Clostridium sp. ATCC 29733</i>		0.000525516	

Fig.S1



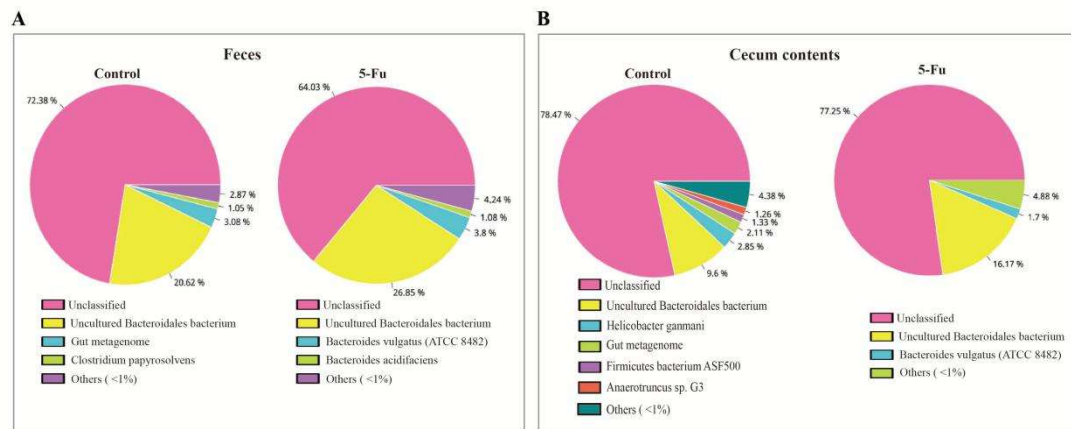
The heatmap of relative abundance of gut microbiota at phylum level in feces of mice  
M: 5-Fu treated mice; C: normal mice

Fig.S2



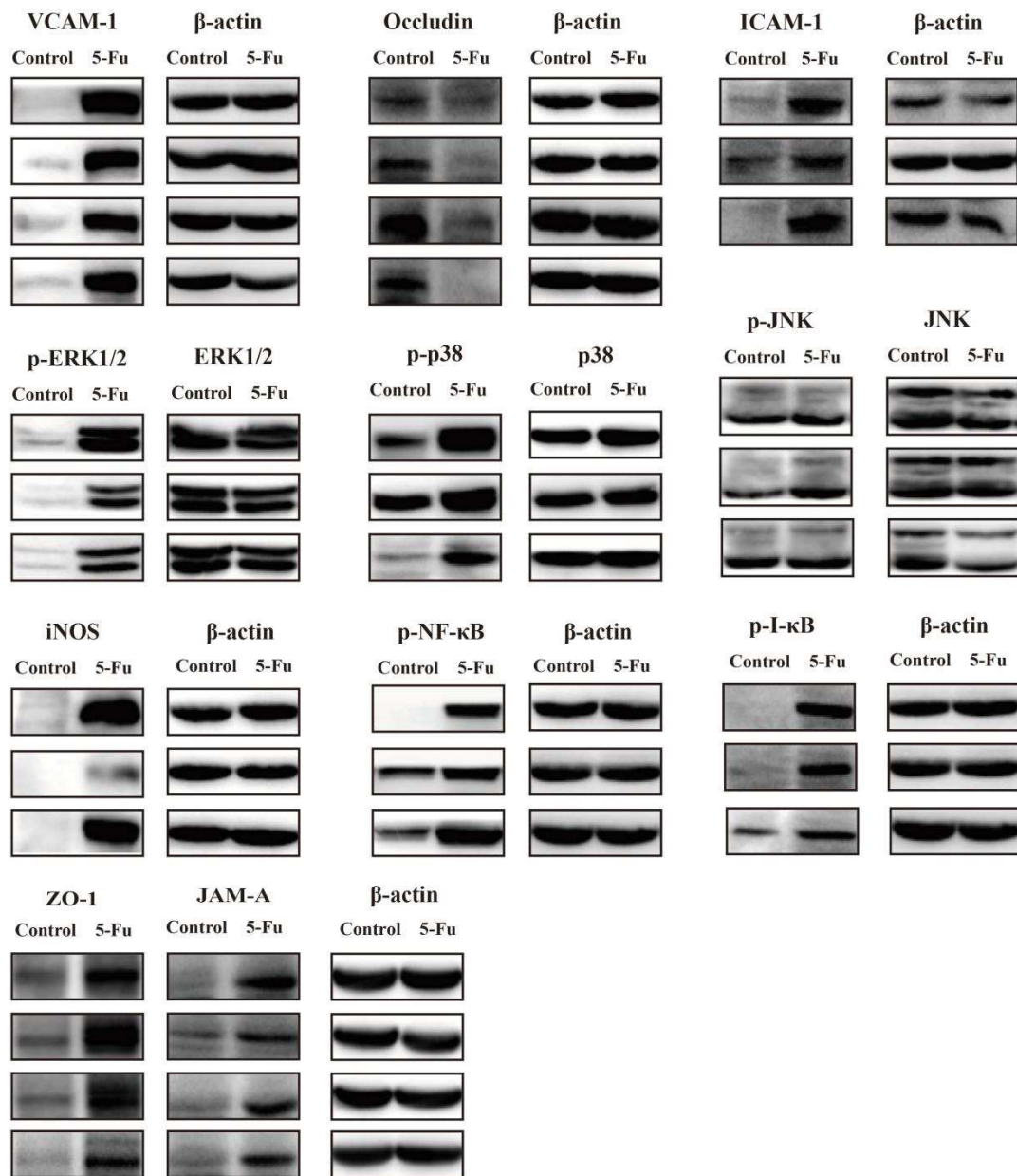
The heatmap of relative abundance of gut microbiota at phylum level in cecum contents of mice  
M: 5-Fu treated mice; C: normal mice

Fig.S3



The pie charts depicting the mean relative abundances for feces and cecum contents at species level

Fig.S4



All the WB images for all the mice used in present study