

**Supplementary Table S3.** Microbial communities and abundance changed in different groups

genus	S1C	S1L	S1N	S2C	S2L	S2N
<i>Parabacteroides</i>	0.14±0.0371	0.0343±0.0197				
<i>Ruminococcaceae_V9D2013_group</i>	2.13±0.064		0.856±0.243			
<i>Ruminiclostridium_1</i>	0.0328±0.00417		0.0769±0.0126			
<i>Ruminococcaceae_UCG-005</i>	0.442±0.0993		0.128±0.0532			
<i>Parasutterella</i>	0.993±0.0801		0.456±0.192			
<i>Roseburia</i>	0.00612±0.00159		0.0338±0.0108			
<i>Subdoligranulum</i>	0.405±0.0645		0.233±0.0221			
<i>Parasutterella</i>	0.315±0.0244			0.993±0.0801		
<i>Barnesiella</i>	0.212±0.0259			0.0635±0.0321		
<i>Ruminococcaceae_V9D2013_group</i>	1.32±0.235			2.13±0.064		
<i>Ruminiclostridium_1</i>	0.0987±0.0228			0.0328±0.00417		
<i>dgA-11_gut_group</i>	2.53±0.964			0.118±0.118		
<i>Ruminococcus_1</i>	11.5±1.7			16.4±1.05		
<i>Christensenellaceae_R-7_group</i>		12.1±1.52	6.94±0.547			
<i>Gelria</i>		0.0158±0.0052	0±0			
<i>Ruminococcaceae_UCG-001</i>		0.0114±0.0041	0±0			
<i>Enterorhabdus</i>		0.00939±0.00375	0.0236±0.00374			
<i>[Eubacterium]_ventriosum_group</i>		0.00736±0.00121			0.0168±0.000546	
<i>Anaerotruncus</i>		0.339±0.0961			0.643±0.0228	
<i>[Eubacterium]_nodatum_group</i>		0.0113±0.00406			0.0852±0.0275	
<i>Ruminococcus_1</i>			16.3±0.31			12.5±0.12
<i>Hydrogenoanaerobacterium</i>			0.00412±0.00107			0.0122±0.00306
<i>Clostridiales_bacterium</i>				0.197±0.039	0.0396±0.0122	
<i>Anaerovorax</i>				0.0762±0.0104	0.154±0.0197	
<i>Alistipes</i>				3.54±0.19		1.15±0.0776
<i>Hydrogenoanaerobacterium</i>				0±0		0.0122±0.00306
<i>Tyzzarella_3</i>				0.0536±0.00711		0.132±0.0225
<i>Bacteroides</i>				3.34±0.309		1.31±0.597
<i>[Eubacterium]_ruminantium_group</i>				0.0102±0.00368		0.168±0.0594
<i>Alistipes</i>					3.14±0.162	1.15±0.0776
<i>Family_XIII_AD3011_group</i>					0.0717±0.00552	0.0508±0.00585