

Table S1

Relative abundances of the top 50 most abundant bacterial genera in the intestine mucosa of turbot fed with fed with different experiment diets as determined by 16S rRNA gene high throughput sequencing<sup>1</sup>.

Taxonomy	% sequence per treatment		
	SBM	CTS	COS
Stenotrophomonas	23.02±2.27	33.7±1.81	28.94±2.62
Phyllobacterium	17.78±1.86	9.47±1.86	20.6±1.78
Sphingomonas	8.03±1.52	11.35±1.97	8.22±1.57
Vibrio	6.70±3.63	9.13±0.11	9.03±0.24
Dubosiella	3.80±0.57	0.32±0.03	0.61±0.10
Limnohabitans	3.31±0.12	5.50±0.85	1.70±0.49
Acinetobacter	1.90±0.35	2.37±0.93	1.75±0.10
Skermanella	1.69±0.08	0.94±0.01	0.61±0.01
Methylophilus	1.62±0.17	3.41±0.44	2.42±1.24
Mycobacterium	1.52±0.15	2.53±0.15	0.96±0.09
Cutibacterium	1.19±0.03	0.27±0.03	0.22±0.08
Bacteroides	0.95±0.07	0.55±0.03	0.18±0.04
Rhodoluna	0.89±0.05	1.39±0.09	0.57±0.05
Lawsonella	0.88±0.04	0.08±0.01	0.05±0.01
Tumebacillus	0.77±0.33	0	0
unidentified_Clostridiales	0.75±0.07	0.50±0.02	0.23±0.01
Lentilitoribacter	0.74±0.08	0.16±0.08	0.07±0.06
Polynucleobacter	0.74±0.13	2.38±0.33	0.67±0.06
Pseudomonas	0.73±0.06	1.54±0.19	1.81±0.08
Faecalibacterium	0.69±0.06	0.55±0.04	0.09±0.01
Streptococcus	0.68±0.07	0.09±0.04	0.14±0.01
Staphylococcus	0.64±1.08	0.25±0.01	0.09±0.01
Sulfitobacter	0.61±0.03	0.25±0.03	0.15±0.01
unidentified_Cyanobacteria	0.61±0.06	1.45±0.66	0.96±0.15
Boseongicola	0.57±0.06	0.46±0.07	0.06±0.06
Halioglobus	0.56±0.06	0.69±0.08	0.06±0.01
Fusobacterium	0.44±0.04	0.02±0.01	0.02±0.02
Bradyrhizobium	0.43±0.18	0.12±0.06	0.47±0.04
Serratia	0.42±0.04	0.22±0.08	0.23±0.01
Salegentibacter	0.4±0.19	0.64±0.04	0.19±0.02
Alistipes	0.37±0.12	0.55±0.03	0.05±0.01
Lactobacillus	0.37±0.07	1.55±0.37	1.36±0.13
Helicobacter	0.36±0.03	0.16±0.11	0.11±0.01
unidentified_Lachnospiraceae	0.36±0.03	0.16±0.08	0.08±0.01
Arcobacter	0.34±0.03	0.20±0.03	0.04±0.02
unidentified_Burkholderiaceae	0.34±0.09	0.17±0.04	0.06±0.01
Perlucidibaca	0.33±0.03	0.40±0.05	1.93±0.31

Nocardioides	0.30±0.11	0.62±0.07	0.27±0.08
Bifidobacterium	0.29±0.04	0.23±0.03	0.05±0.02
Arthrobacter	0.28±0.04	2.42±0.41	0.01±0.01
Romboutsia	0.27±0.12	0.26±0.06	0.08±0.02
unidentified_Ruminococcaceae	0.27±0.03	0.16±0.01	0.10±0.01
Pelomonas	0.26±0.01	0.88±0.06	0.44±0.03
Pseudarcicella	0.20±0.06	0.54±0.07	0.12±0.02
Gramella	0.16±0.01	0.31±0.02	0.10±0.01
Novosphingobium	0.14±0.01	0.15±0.02	0.32±0.04
Marinobacter	0.14±0.07	0.20±0.08	0.21±0.01
unidentified_Corynebacteriaceae	0.14±0.07	0.26±0.03	0.06±0.01
Microbacterium	0.09±0.04	0.10±0.08	0.09±0.02
Bacillus	0.08±0.01	0.23±0.16	0.23±0.11

<sup>1</sup>Values are expressed as means ± S.D. SBM, a basal diet containing 400 g kg<sup>-1</sup> of soybean meal; CTS, inclusion of 7.5 g kg<sup>-1</sup> of chitosan in SBM diet; and COS, inclusion of 2 g kg<sup>-1</sup> of chitooligosaccharide in SBM diet.