

Supplementary Material

Table S1: Effect of different diets on relative abundance (%) of intestinal microbiota on Phylum level in *T. fulvidraco*. (Mean \pm SD, n=4)

	UCD	MFLD	SSFD
Foreintestine			
<i>Firmicutes</i>	34.15 \pm 19.23	28.98 \pm 2.06	27.86 \pm 11.42
<i>Fusobacteriota</i>	37.15 \pm 19.49 ^b	9.50 \pm 8.55 ^a	11.32 \pm 7.74 ^a
<i>Proteobacteria</i>	10.87 \pm 6.96 ^a	33.52 \pm 14.93 ^b	46.15 \pm 12.35 ^b
<i>Bacteroidota</i>	11.55 \pm 9.35	12.88 \pm 16.53	6.09 \pm 3.51
<i>Acidobacteriota</i>	3.61 \pm 2.74 ^a	10.73 \pm 6.48 ^b	5.81 \pm 2.06 ^{ab}
Other	2.67 \pm 1.85	4.40 \pm 2.94	2.77 \pm 1.49
Midintestine			
<i>Firmicutes</i>	24.68 \pm 23.28	30.55 \pm 9.78	29.00 \pm 9.45
<i>Fusobacteriota</i>	45.57 \pm 31.69	21.08 \pm 5.64	34.11 \pm 8.24
<i>Proteobacteria</i>	10.34 \pm 4.88 ^a	25.96 \pm 14.43 ^b	18.51 \pm 6.33 ^{ab}
<i>Bacteroidota</i>	15.00 \pm 13.70	13.61 \pm 14.43	10.40 \pm 5.37
<i>Acidobacteriota</i>	2.69 \pm 1.82	5.42 \pm 3.12	5.92 \pm 3.06
Other	1.72 \pm 1.67	3.38 \pm 1.74	2.07 \pm 0.71
Hindintestine			
<i>Firmicutes</i>	21.88 \pm 20.72	27.43 \pm 20.81	17.64 \pm 18.82
<i>Fusobacteriota</i>	58.82 \pm 27.97	55.49 \pm 9.23	59.59 \pm 19.73
<i>Proteobacteria</i>	7.07 \pm 7.42	1.48 \pm 1.04	2.12 \pm 2.03
<i>Bacteroidota</i>	9.80 \pm 11.18	15.49 \pm 13.84	20.28 \pm 13.82
<i>Acidobacteriota</i>	1.39 \pm 1.52	0.06 \pm 0.06	0.19 \pm 0.15
Other	1.05 \pm 1.15	0.07 \pm 0.06	0.19 \pm 0.17

Note: UCD, untreated commercial diet (control treatment); MFLD, the commercial diet mixed with fermented liquid; SSFD, solid-state fermented diet. Values in the same rows with different superscript letter are significantly different ($P < 0.05$), while values in the same rows with same or without superscript letter are not significantly different ($P > 0.05$). The values presented were average \pm standard deviation (n=4).

Table S2: Effect of different diets on relative abundance (%) of intestinal microbiota on Genus level in *T. fulvidraco*. (Mean \pm SD, n=4)

	UCD	MFLD	SSFD
Foreintestine			
<i>Cetobacterium</i>	37.14 \pm 19.49 ^b	9.45 \pm 5.90 ^a	11.31 \pm 6.62 ^a
norank_f_Barnesiellaceae	8.14 \pm 7.64	7.24 \pm 12.17	3.71 \pm 3.12
<i>Ralstonia</i>	1.02 \pm 0.84 ^a	5.76 \pm 5.06 ^a	27.38 \pm 10.47 ^b
<i>Turicibacter</i>	3.84 \pm 5.76	2.36 \pm 2.61	1.00 \pm 0.28
<i>Acinetobacter</i>	3.98 \pm 3.75	12.71 \pm 10.44	7.61 \pm 3.33
<i>Mycoplasma</i>	2.78 \pm 4.54	5.94 \pm 5.81	1.63 \pm 1.33
<i>Clostridium_sensu_stricto_1</i>	4.68 \pm 4.76	2.54 \pm 2.75	0.94 \pm 0.64
<i>Romboutsia</i>	6.69 \pm 10.78	1.44 \pm 0.85	1.24 \pm 0.71
<i>Macellibacteroides</i>	2.40 \pm 2.09	2.67 \pm 4.39	0.53 \pm 0.56
<i>Geobacillus</i>	1.52 \pm 1.33 ^a	3.91 \pm 1.36 ^{ab}	6.66 \pm 3.49 ^b
<i>Lactobacillus</i>	0.63 \pm 0.53 ^a	1.69 \pm 1.04 ^a	7.17 \pm 3.85 ^b
<i>Rhodococcus</i>	0.94 \pm 0.67 ^a	3.73 \pm 1.73 ^b	2.36 \pm 0.74 ^{ab}
<i>Plesiomonas</i>	1.08 \pm 1.02	0.85 \pm 0.65	0.37 \pm 0.24
<i>Epulopiscium</i>	1.73 \pm 1.57	0.80 \pm 1.21	0.18 \pm 0.19
<i>Bacillus</i>	3.02 \pm 5.56	0.25 \pm 0.11	2.40 \pm 3.79
Other	20.44 \pm 15.73	38.66 \pm 18.11	25.53 \pm 7.61
Midintestine			
<i>Cetobacterium</i>	45.56 \pm 31.70	21.08 \pm 5.64	34.11 \pm 8.24
norank_f_Barnesiellaceae	10.39 \pm 9.48	8.36 \pm 10.07	7.77 \pm 5.44
<i>Ralstonia</i>	0.80 \pm 1.24	8.96 \pm 15.52	4.14 \pm 4.03
<i>Turicibacter</i>	4.38 \pm 3.05	1.84 \pm 0.79	3.02 \pm 1.95
<i>Acinetobacter</i>	2.46 \pm 2.00 ^a	6.50 \pm 1.50 ^b	5.60 \pm 2.43 ^{ab}
<i>Mycoplasma</i>	4.04 \pm 7.55	10.98 \pm 9.16	8.20 \pm 8.80
<i>Clostridium_sensu_stricto_1</i>	5.03 \pm 4.24	1.83 \pm 1.06	2.46 \pm 0.97
<i>Romboutsia</i>	4.47 \pm 6.30	1.54 \pm 0.32	2.13 \pm 1.39
<i>Macellibacteroides</i>	3.67 \pm 3.92	2.91 \pm 4.27	1.29 \pm 0.79
<i>Geobacillus</i>	0.99 \pm 0.84 ^a	3.51 \pm 1.23 ^b	2.35 \pm 0.63 ^{ab}
<i>Lactobacillus</i>	0.31 \pm 0.26 ^a	2.12 \pm 1.14 ^b	1.24 \pm 0.38 ^{ab}
<i>Rhodococcus</i>	0.74 \pm 0.55	2.34 \pm 1.47	1.85 \pm 1.42
<i>Plesiomonas</i>	2.51 \pm 1.07	1.37 \pm 1.87	0.82 \pm 0.33
<i>Epulopiscium</i>	1.26 \pm 0.96	0.60 \pm 0.71	1.26 \pm 1.15
<i>Bacillus</i>	0.12 \pm 0.08	0.39 \pm 0.34	0.24 \pm 0.18
Other	13.30 \pm 9.33	25.66 \pm 9.45	23.55 \pm 7.38
Hindintestine			
<i>Cetobacterium</i>	58.82 \pm 27.97	55.49 \pm 9.23	59.59 \pm 19.73
norank_f_Barnesiellaceae	7.26 \pm 8.79	12.09 \pm 11.83	15.65 \pm 14.87
<i>Ralstonia</i>	1.67 \pm 3.03	0.15 \pm 0.30	0.25 \pm 0.41
<i>Turicibacter</i>	4.13 \pm 4.62	14.99 \pm 12.24	5.56 \pm 5.47

	UCD	MFLD	SSFD
<i>Acinetobacter</i>	2.08±2.41	0.05±0.07	0.14±0.08
<i>Mycoplasma</i>	3.38±4.58	0.12±0.18	0.80±0.87
<i>Clostridium_sensu_stricto_1</i>	4.70±5.59	5.14±3.79	4.75±6.22
<i>Romboutsia</i>	4.71±8.43	6.47±8.85	3.29±4.95
<i>Macellibacteroides</i>	1.73±1.87	2.79±2.48	4.01±1.74
<i>Geobacillus</i>	1.01±1.38	0.01±0.02	0.09±0.09
<i>Lactobacillus</i>	0.21±0.24	0.01±0.01	0.03±0.04
<i>Rhodococcus</i>	0.56±0.62	0.02±0.02	0.06±0.05
<i>Plesiomonas</i>	1.14±1.34	1.14±1.09	1.39±1.43
<i>Epulopiscium</i>	1.20±1.89	0.37±0.61	1.40±1.46
<i>Bacillus</i>	0.13±0.05	0.07±0.08	0.17±0.20
Other	7.28±6.24	1.11±1.39	2.82±0.83

Note: UCD, untreated commercial diet (control treatment); MFLD, the commercial diet mixed with fermented liquid; SSFD, solid-state fermented diet. Values in the same rows with different superscript letter are significantly different ($P<0.05$), while values in the same rows with same or without superscript letter are not significantly different ($P>0.05$). The values presented were average \pm standard deviation (n=4).

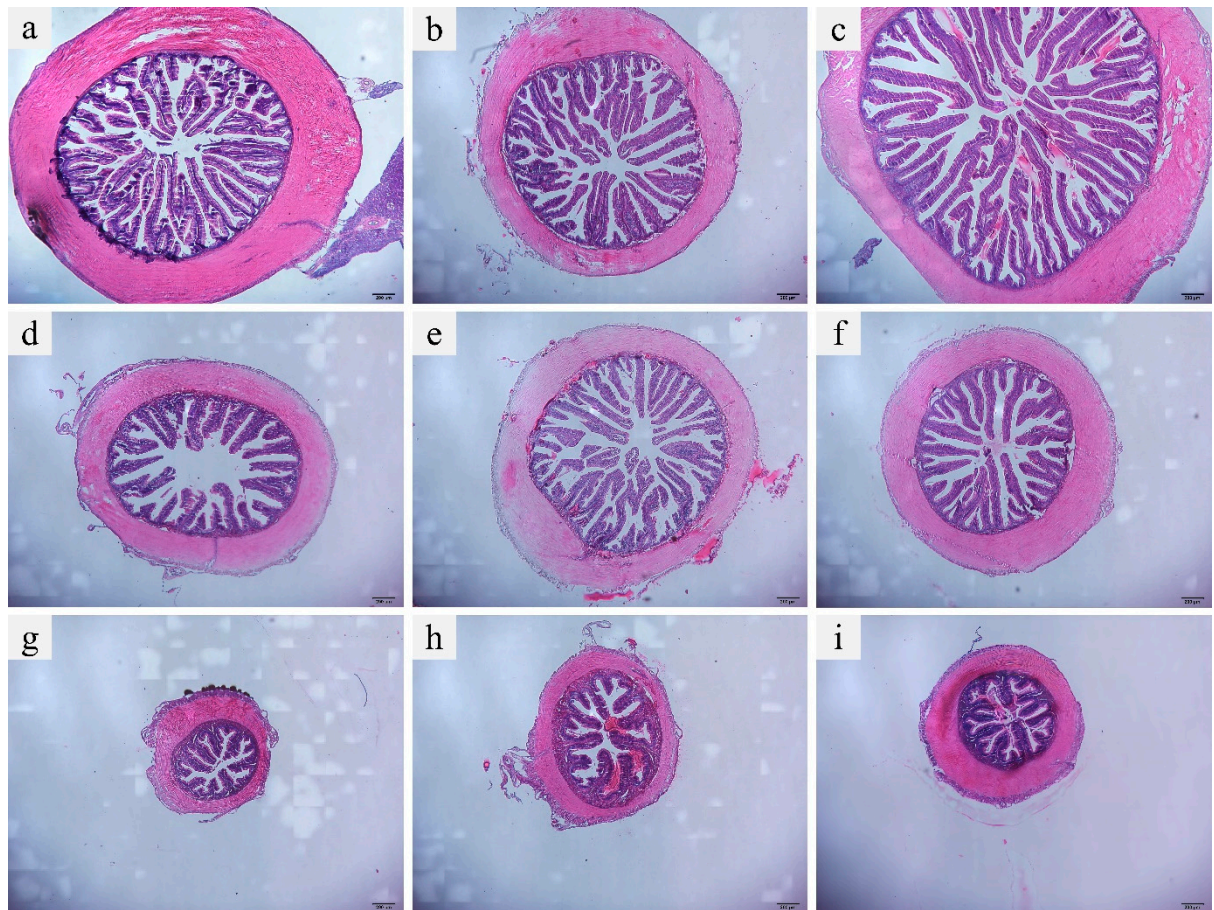


Figure S1: Histologically-observed intestine of *T. fulvidraco* fed with experiment diets ($\times 40$, scale bar = 200 μm);.

(a), (b) and (c) represent the foreintestine of UCD, MFLD and SSFD treatment, respectively. (e), (f) and (g) represent the midintestine of UCD, MFLD and SSFD treatment, respectively. (g), (h) and (e) represent the hindintestine of UCD, MFLD and SSFD treatment, respectively. UCD means untreated commercial diet (control treatment). MFLD means the commercial diet mixed with fermented liquid. SSFD means solid-state fermented diet.