Supplementary materials

Table S1. Basic information of sequencing data.

Sample ID	Number of merged tags	Number of clean tags	Number of effective tags	Number of resampling tags
JX01F	24,067	23,736	21,687	19,850
JX02F	29,181	28,774	26,166	19,850
JX03F	23,126	22,790	20,427	19,850
JX04F	25,155	24,824	22,623	19,850
JX05F	24,576	24,252	22,172	19,850
JX06F	24,055	23,741	21,591	19,850
JX01M	28,440	28,117	25,993	19,850
JX02M	31,468	31z,106	28,556	19,850
JX03M	29,752	29,412	26,780	19,850
JX04M	27,404	27,054	24,747	19,850
JX05M	32,409	31,966	29,561	19,850
JX06M	30,292	29,793	27,538	19,850
JX01H	21,929	21,584	19,850	19,850
JX02H	30,446	30,017	27,473	19,850
JX03H	24,489	24,071	22,003	19,850
JX04H	26,088	25,732	23,109	19,850
JX05H	23,895	23,584	21,552	19,850
JX06H	25,641	25,329	22,929	19,850
Mean	26,800.72	26,437.89	24,153.17	19,850
SD	3,177.94	3,145.66	2,981.22	0
Total	482,413	475,882	434,757	357,300

Table S2. Differences in α-diversity indices of gut microbiota in different segments of *Spinibarbus caldwelli*.

Index	Foregut	Midgut	Hindgut
Phylogenetic diversity distance	18.35 ± 1.13	15.70 ± 1.98	17.80 ± 1.79
Chao1 index	1097.40 ± 75.43[a]	860.68 ± 97.34[b]	1070.96 ± 61.72[a]
Richness	762.67 ± 51.84[a]	567.00 ± 68.75[b]	737.00 ± 54.14[a]
Shannon index	2.84 ± 0.29[a]	2.01 ± 0.20[b]	2.84 ± 0.25[a]
Goods coverage	0.986 ± 0.00[b]	0.990 ± 0.00[a]	0.987 ±0.00[b]
Simpson index	0.82 ± 0.06[a]	0.70 ± 0.05[b]	0.82 ± 0.04[a]

Table S3. Differences in the relative abundances of dominant phyla of gut microbiota among different gut segments of *Spinibarbus caldwelli*.

Phylum	Foregut	Midgut	Hindgut
Proteobacteria	66.70%±7.65%	62.06%±13.47%	72.67%±6.14%
Fusobacteria	17.23%±5.03%^{ab}	25.58%±10.85%^{a}	13.62%±4.57%^{b}
Bacteroidota	5.32%±3.56%	4.03%±3.27%	5.45%±4.28%
Firmicutes	10.04%±4.51%	7.55%±7.01%	7.47%±3.74%
Others	0.71%±0.24%	0.78%±0.30%	0.79%±0.24%

Table S4. Differences in the relative abundances of dominant genera of gut microbiota among different gut segments of *Spinibarbus caldwelli*.

Genus	Foregut	Midgut	Hindgut
Stenotrophomonas	0.042%±0.016%	0.005%±0.004%	0.045%±0.014%
Brevibacterium	0.007%±0.003%	0.002%±0.005%	0.013±0.007
Aurantimicrobium	0	0.006%±0.007%	0
mle1-7	0	0	0.003%±0.004%
Cyanobium PCC-6307	0.014%±0.015%	0.001%±0.002%	0.003%±0.004%
Cetobacterium	17.228%±5.033%^{ab}	25.584%±10.847%^{a}	13.616%±4.573%^{b}
Bacillus	1.230%±0.214%^{a}	0.201%±0.043%^{b}	1.161%±0.174%^{a}
Microbacterium	0.276%±0.077%^{ab}	0.363%±0.090%^{a}	0.216%±0.033%^{b}
Cupriavidus	0.427%±0.069%^{a}	0.169%±0.047%^{b}	0.405%±0.111%^{a}

Table S5. Weighted nearest sequenced taxon index (NSTI) of functional prediction based on gut microbiota composition using PICRUSt2. KO, KEGG Orthology.

sample	KO weighted NSTI
JX01F	0.101
JX01M	0.049
JX01H	0.116
JX02F	0.104
JX02M	0.094
JX02H	0.066
JX03F	0.103
JX03M	0.092
JX03H	0.094
JX04F	0.098
JX04M	0.102
JX04H	0.116
JX05F	0.080
JX05M	0.076
JX05H	0.075
JX06F	0.077
JX06M	0.051
JX06H	0.082
Mean	0.088±0.020

Figure S1. Sample photos (A) and intestinal segments (B).

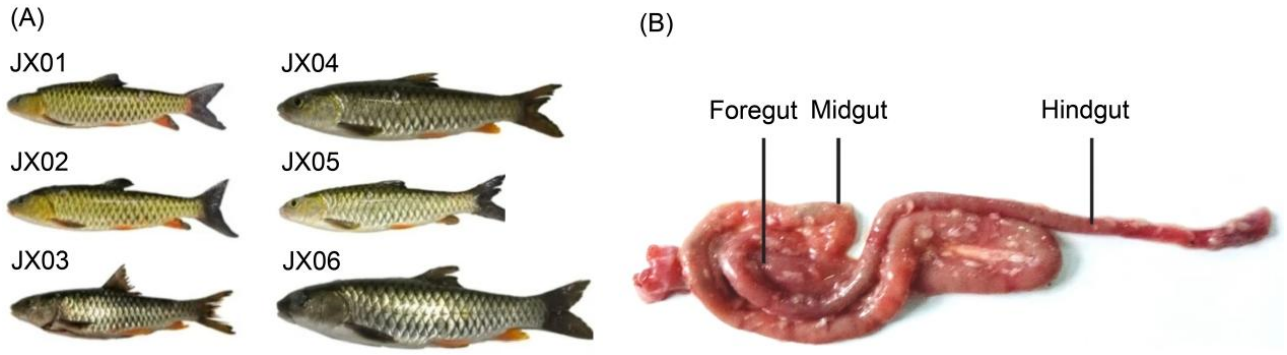


Figure S2. Non-metric multidimensional scaling (NMDS) profile shows the difference in predicted gene composition among different gut segments.

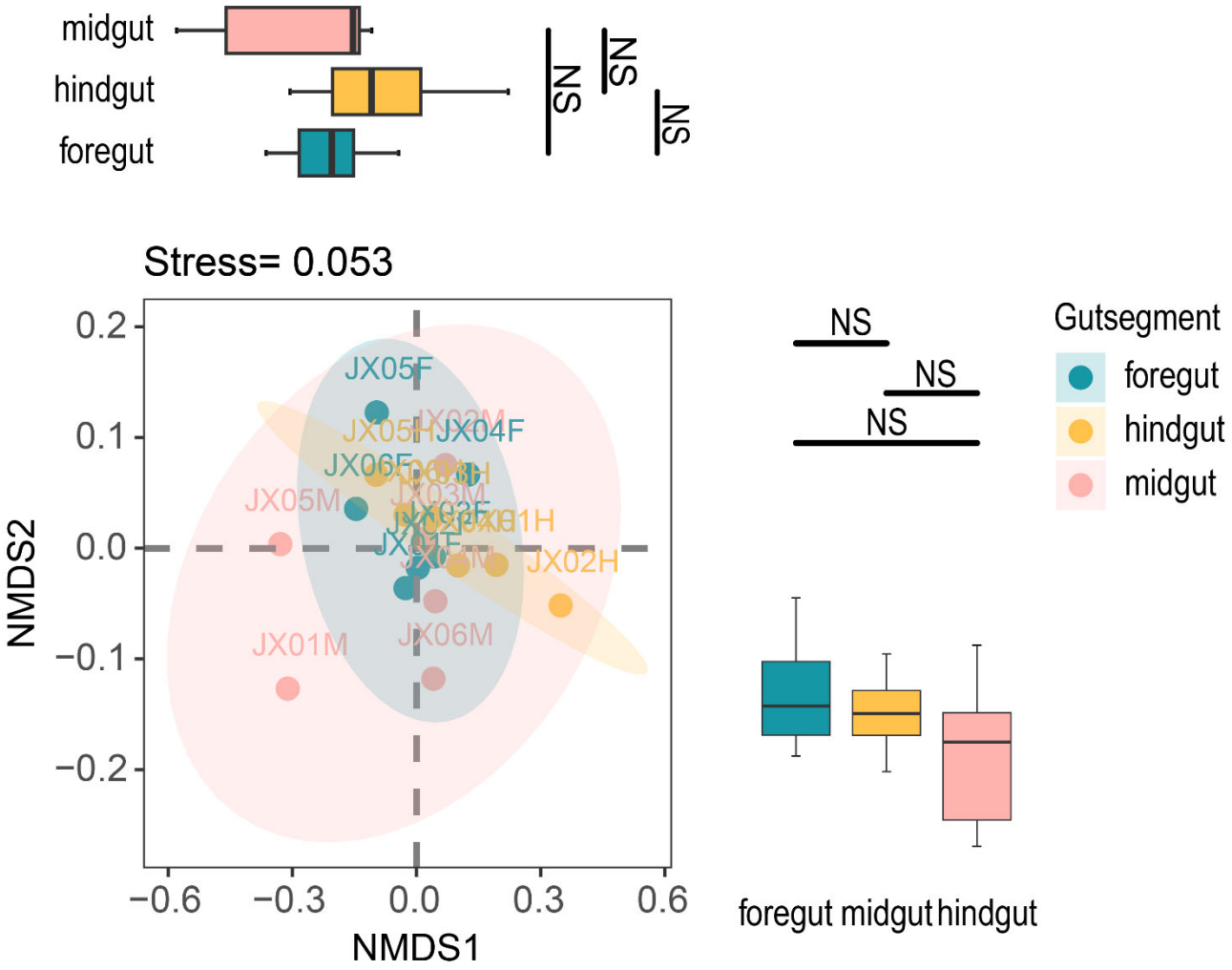


Figure S3. Functional composition of the gut microbiota in *Spinibarbus caldwelli*. F, foregut microbiota; M, midgut microbiota; H, hindgut microbiota; GIP, genetic information processing; EIP, environmental information processing.

