

Table S1. Primers used in this study

Primer	Accession No.	Sequence (5'-3')	Amplicon size (bp)
tlr4-F tlr4-R	AY388400.1	ACAGATCACCTGGACAGCAAGA CGGCTTGAAAGTCCCCGCAT	153
myd88-F myd88-R	DQ100359.1	GGGACTGACACCTGAGACCTT CGATAAGCTCACTGGCGATGG	176
nfkb-F nfkb-R	DQ066717	AAGGAATCATGGCTGGCGAG GTAAGCAAGGCCCATCAACTGC	156
il1 β -F il1 β -R	BC098597	CGGCAGCTCCATAAACACCTTC CGCTCGGTGTCTTTCCTGT	108
il6-F il6-R	NM_001261449	CAGCTGCAGGTGAGAGACG GCAGGCGTCGATCATCACG	132
tnf α -F tnf α -R	AY427649.1	GCTTTTCTGAATCCTACGGAGGC CGTGTCTGTGCCCAGTCTG	155
sod1-F sod1-R	NM_131294.1	AGACCTGGGTAATGTGACCGC GCCACCCTTCCCCAAGT	145
sod2-F sod2-R	NM_199976.1	TGCAGAGTCGGATATGTTTCGGAG GTGAGGCTCAAGTGCACCAT	123
hsp90-F hsp90-R	L35587.1	CCAAACTGGACAGCGGCAA AGATCGGCTTTGGTCATCCCA	106
cat-F cat-R	NM_130912.2	GATCGCTGTCCGCTTTTCCA CAGTTGCCCTCATCGGTGT	105
gpx-F gpx-R	AY216589.1	TGGCGTCGCTTTGAGGC TCCTGGTGCCCGAACTG	121
muc2.2-F muc2.2-R	XM 002667543	ACACGCTCAAGTAATCGCACAGTC TCAGCGAGTGTTTGGCTCACTT	137
mmp9-F mmp9-R	NM 213123.1	CCAACATTAAAGATGCCCTGATGTAT CCC AGTGGTGGTCCGTGGTTGA	146
β -def-1-F β -def-1-R	NM 001081553.1	TGTCCTTGTCGTACTAGCATTGCAC ACACACTCCTTGTCTGCAAACACC	100
β -actin-F β -actin-R	AF057040.1	AGGCTCCCCTGAATCCCAA GTCACACCATCACCAGAGTCC	160

Table S2. Relative abundance of zebrafish gut microbiome in phylum level

Phylum ^{a)}	Relative abundance (%)			
	Ctrl.	Otc	Smx/Tmp	Ery
Fusobacteria	57.11±2.6	55.72±4.3	52.09±6.4	52.83±4.6
Proteobacteria	18.89±2.5	22.02±2.7	27.77±10.5	36.02±3.7
Firmicutes	13.26±1.5	11.91±2.1	13.78±5.7	5.01±2.3
Bacteroidetes	10.25±0.9	8.28±3.5	5.61±1.6	5.55±2.8
Actinobacteria	0.36±0.1	1.63±1.2	0.40±0.3	0.10±0.0
Planctomycetes	0.02±0.0	0.13±0.1	0.16±0.1	0.19±0.1
Verrucomicrobia	0.01±0.0	0.08±0.1	0.12±0.0	0.25±0.2
Tenericutes	0.09±0.1	0.22±0.4	0.02±0.0	0.001±0.0
Chlamydiae	0.00±0.0	0.001±0.0	0.03±0.0	0.03±0.0
Armatimonadetes	0.00±0.0	0.00±0.0	0.02±0.0	0.00±0.0
Deinococcus-Thermus	0.003±0.0	0.00±0.0	0.006±0.0	0.00±0.0
Acidobacteria	0.00±0.0	0.001±0.0	0.002±0.0	0.002±0.0
Spirochaetes	0.00±0.0	0.00±0.0	0.005±0.0	0.00±0.0
Cyanobacteria	0.00±0.0	0.00±0.0	0.00±0.0	0.004±0.0
Other	0.00±0.0	0.00±0.0	0.00±0.0	0.007±0.0

^{a)} Values are presented as means±SD.

Table S3. Relative abundance of zebrafish gut microbiome in species level

Species ^{a)}	Relative abundance (%)			
	Ctrl.	Otc	Smx/Tmp	Ery
<i>Cetobacterium somerae</i>	57.10±2.6	55.72±4.3	52.08±6.4	52.83±4.6
<i>Aeromonas veronii</i>	10.06±0.6	10.02±3.3	9.24±1.5	25.57±1.4
KM585593	9.47±1.0	9.23±2.1	9.10±4.6	3.41±1.6
<i>Cellvibrio fibrivorans</i>	1.27±0.8	1.23±0.3	9.63±9.1	2.65±3.3
<i>Shewanella xiamenensis</i>	2.75±0.5	4.25±2.1	3.88±0.4	0.66±0.2
KM585593_g_uc ^{b)}	3.61±0.3	2.04±0.9	3.74±2.0	1.44±0.7
Bacteroides_uc	4.36±3.6	2.46±1.5	1.28±0.6	0.06±0.0
Bacteroidaceae_uc	3.75±2.1	0.72±0.6	0.30±0.1	0.01±0.0
<i>Flavobacterium ginsenosidimutans</i>	0.07±0.0	0.24±0.2	0.03±0.0	3.30±1.8
<i>Flavobacterium granuli</i>	0.18±0.0	2.13±2.2	0.30±0.2	0.41±0.2
GQ360021_g_uc	1.55±0.7	0.75±0.2	0.56±0.2	0.02±0.0
<i>Gemmobacter fontiphilus</i>	0.75±0.4	0.65±0.5	0.56±0.2	0.72±0.4
Rhodobacteraceae_uc	0.02±0.0	2.13±1.7	0.25±0.2	0.25±0.3
<i>Flavobacterium succinicans</i>	0.05±0.0	0.73±0.9	1.13±0.8	0.66±0.5
<i>Aeromonas caviae</i>	1.60±0.3	0.01±0.0	0.00±0.0	0.004±0.0
<i>Flavobacterium cutihirudinis</i>	0.002±0.0	0.01±0.0	1.44±0.8	0.01±0.0
<i>Rhodococcus erythropolis</i>	0.01±0.0	1.39±1.1	0.01±0.0	0.00±0.0
<i>Rhizobium arenae</i>	0.11±0.1	0.003±0.0	0.003±0.0	1.28±0.2
<i>Kinneretia asaccharophila</i>	0.96±0.4	0.01±0.0	0.29±0.1	0.03±0.0
<i>Plesiomonas shigelloides</i>	0.002±0.0	0.07±0.1	0.06±0.1	0.90±1.5
<i>Flavobacterium notoginsengisoli</i>	0.16±0.1	0.37±0.2	0.003±0.0	0.35±0.3
Hyphomicrobium_uc	0.002±0.0	0.35±0.2	0.042±0.3	0.08±0.0
EU234324	0.001±0.0	0.35±0.2	0.25±0.1	0.19±0.1
<i>Pseudomonas alcaligenes</i>	0.002±0.0	0.00±0.0	0.00±0.0	0.77±0.6
<i>Bacteroides vulgatus</i>	0.02±0.0	0.61±1.0	0.08±0.1	0.05±0.0

^{a)} Values are presented as means±SD.

^{b)} ‘uc’ means unclassified.

Table S4. Number of goblet cells per villus

Number of goblet cells (n = 10) ^{a)}				<i>p</i> value ^{b)}		
Ctrl.	Otc	Smx/Tmp	Ery	Ctrl.-Otc	Ctrl.-Smx/Tmp	Ctrl.-Ery
2.5±1.3	3.9±1.9	5.6±2.3	4.9±1.6	0.0696	0.0016	0.0016

^{a)} Values are presented as means±SD.

^{b)} Significance was determined by *t*-test.

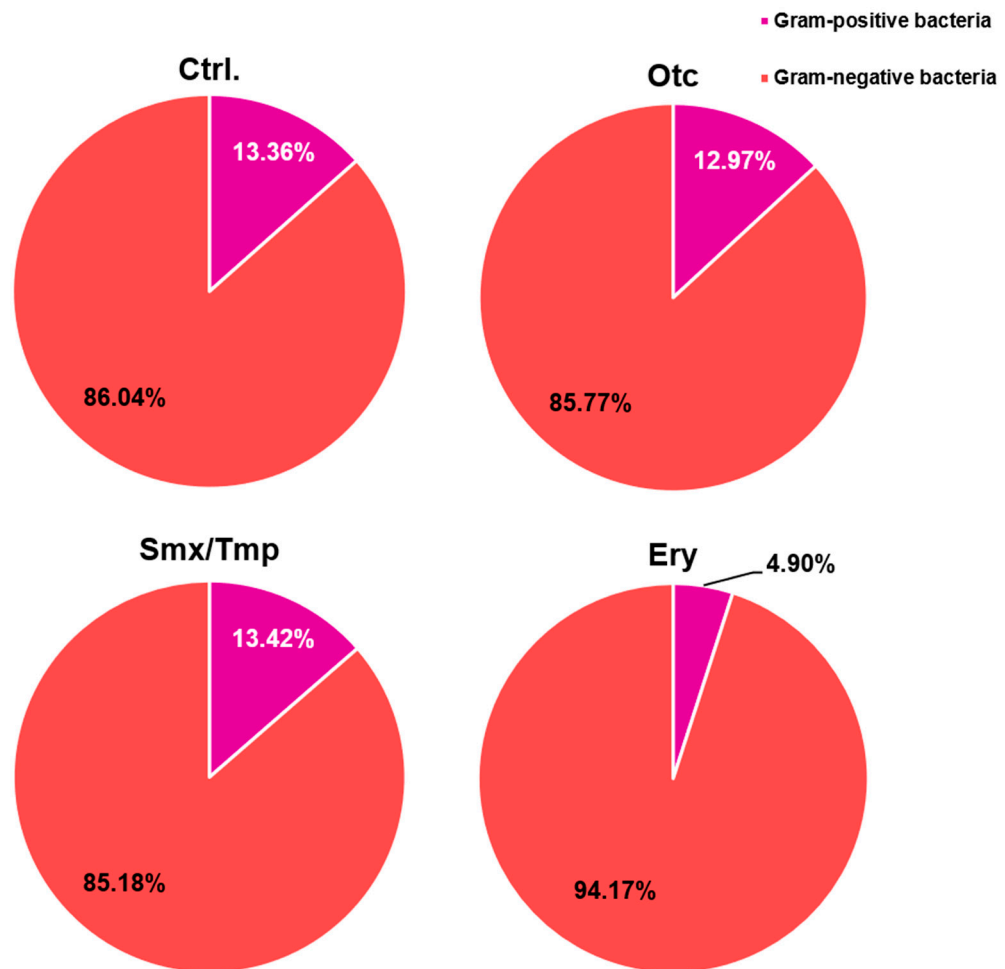


Figure S1. Relative abundance of Gram-positive bacteria and Gram-negative bacteria in zebrafish gut microbiome.