

Figure S1. Wound healing rate of diverse fish species.

(A) Representative images of wounds. Wound images from 7 fish species at 0, 8, and 16 dpw.

Scale bars: 3 mm. (B, C) Changes in wound size percent (B) and pigment percent (C).

Wound size (pigment) percent: (wound size (pigment) at (n) dpw/0 dpw)*100. (D, E)

Quantification of wound healing rate based on changes in wound size (D) and pigment (E).

Wound healing rates between the families Cyprinidae and Cobitidae were compared by

wound size (pigment) percent at 10 dpw. Sample size (n) is denoted next to the graph. *** p

≤ 0.001 , **** $p \leq 0.0001$.

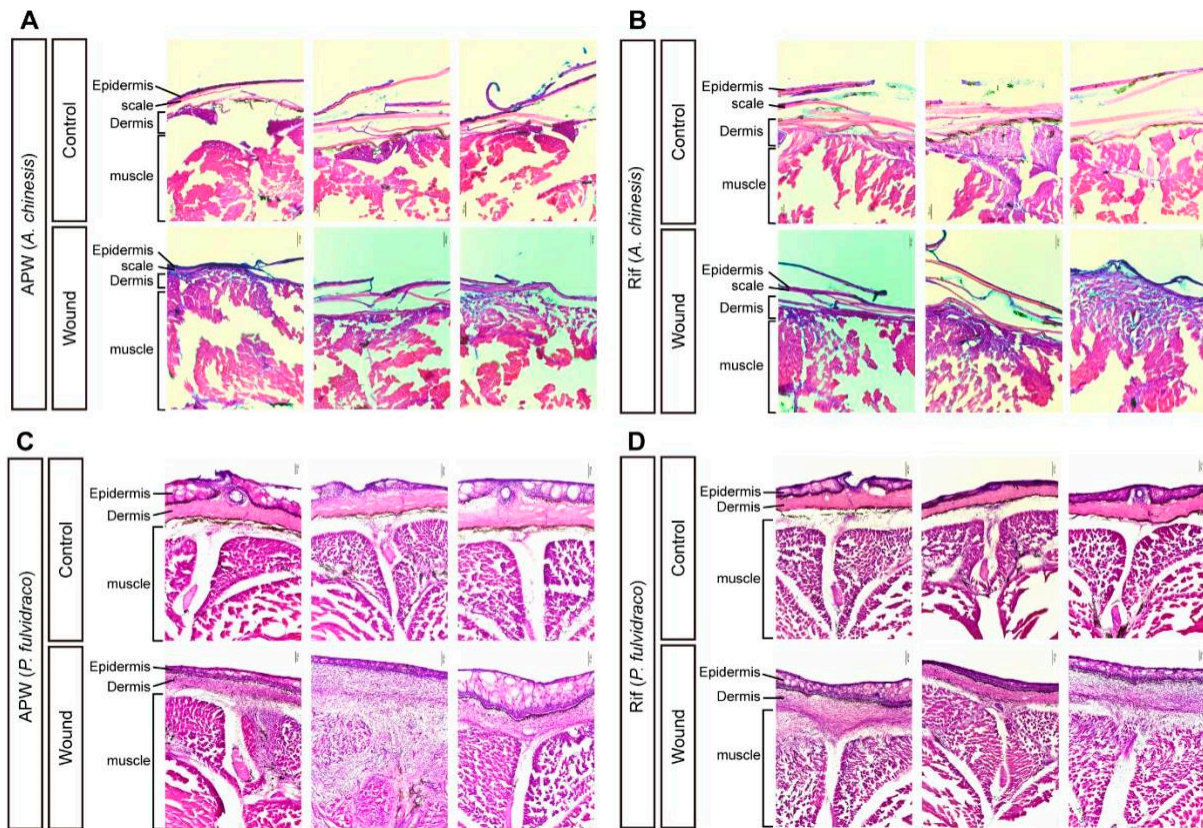


Figure S2. Skin organization after wound healing.

(A~D) H&E staining images showing transverse sections through the recovered wound tissue of Korean bullhead and Chinese bleak at 16 dpw. Representative images of 3 samples from each condition are shown here. (A, B) H&E staining on control side (top) and wounded side (bottom) of Chinese bleak reared in APW (A) and APW with rifampicin (B). (C, D) H&E staining on control side (top) and wounded side (bottom) of Korean bullhead reared in APW (C) and APW with rifampicin (D). Scale bars: 100 μm .

A

<i>Aphyocypris chinensis</i> APW	%	<i>Aphyocypris chinensis</i> Rif	%
<i>Muribaculaceae</i> (Bacteroidia)	20.92	<i>Muribaculaceae</i> (Bacteroidia)	18.50
<i>Muribaculaceae*</i> (Bacteroidia)	11.71	<i>Lactobacillus</i> (Bacilli)	11.12
<i>Lactobacillus</i> (Bacilli)	11.38	<i>Muribaculaceae*</i> (Bacteroidia)	10.28
<i>Muribaculum</i> (Bacteroidia)	10.74	<i>Muribaculum</i> (Bacteroidia)	9.35
<i>Lachnospiraceae*</i> (Clostridia)	9.71	<i>Lachnospiraceae*</i> (Clostridia)	7.81
<i>Campylobacter</i> (Campylobacteria)	5.73	<i>Campylobacter</i> (Campylobacteria)	4.55
<i>Bacteroides</i> (Bacteroidia)	3.08	<i>Bacteroides</i> (Bacteroidia)	3.41
<i>Bacteroidales**</i> (Bacteroidia)	2.27	unclassified (Gammaproteobacteria)	2.96
<i>Oscillospiraceae*</i> (Clostridia)	2.17	<i>Akkermansia</i> (Verrucomicrobiae)	2.21
<i>Akkermansia</i> (Verrucomicrobiae)	2.11	<i>Bacteroidales**</i> (Bacteroidia)	2.19
<i>Parasutterella</i> (Gammaproteobacteria)	1.62	<i>Oscillospiraceae*</i> (Clostridia)	1.50
<i>Lachnospiraceae_NK4A136_group</i> (Clostridia)	1.39	<i>Clostridia_UCG-014</i> (Clostridia)	1.48
<i>Burkholderia-Caballeronia-Paraburkholderia</i> (Gammaproteobacteria)	1.28	<i>Parasutterella</i> (Gammaproteobacteria)	1.44
<i>Desulfovibrio</i> (Desulfovibrionia)	1.22	<i>Lachnospiraceae_NK4A136_group</i> (Clostridia)	1.30
<i>Clostridia_UCG-014</i> (Clostridia)	1.15	<i>Enterococcus</i> (Bacilli)	1.19
<i>Oscillibacter</i> (Clostridia)	0.84	<i>Bacillus</i> (Bacilli)	1.00
<i>Allistipes</i> (Bacteroidia)	0.81	<i>Desulfovibrio</i> (Desulfovibrionia)	1.00
<i>Colidextribacter</i> (Clostridia)	0.66	<i>Burkholderia-Caballeronia-Paraburkholderia</i> (Gammaproteobacteria)	0.88
<i>Helicobacter</i> (Campylobacteria)	0.61	<i>Oscillibacter</i> (Clostridia)	0.74
<i>Blautia</i> (Clostridia)	0.52	<i>Enhydrobacter</i> (Gammaproteobacteria)	0.67
others	10.09	others	16.39
Total Sum	100.00	Total Sum	100.00

<i>Pseudobagrus fulvidraco</i> APW	%	<i>Pseudobagrus fulvidraco</i> Rif	%
<i>Muribaculaceae</i> (Bacteroidia)	17.75	<i>Muribaculaceae</i> (Bacteroidia)	19.09
<i>Lactobacillus</i> (Bacilli)	9.98	<i>Lactobacillus</i> (Bacilli)	13.17
<i>Muribaculaceae*</i> (Bacteroidia)	9.78	<i>Muribaculaceae*</i> (Bacteroidia)	11.08
<i>Muribaculum</i> (Bacteroidia)	8.68	<i>Muribaculum</i> (Bacteroidia)	10.12
<i>Lachnospiraceae*</i> (Clostridia)	7.55	<i>Lachnospiraceae*</i> (Clostridia)	9.08
<i>Elizabethkingia</i> (Bacteroidia)	4.61	<i>Campylobacter</i> (Campylobacteria)	4.46
<i>Campylobacter</i> (Campylobacteria)	4.24	<i>Bacteroides</i> (Bacteroidia)	3.76
<i>Bacteroides</i> (Bacteroidia)	2.77	<i>Akkermansia</i> (Verrucomicrobiae)	2.59
unclassified (Gammaproteobacteria)	2.71	<i>Bacteroidales**</i> (Bacteroidia)	2.27
<i>Niveispirillum</i> (Alphaproteobacteria)	2.56	<i>Parasutterella</i> (Gammaproteobacteria)	1.82
<i>Akkermansia</i> (Verrucomicrobiae)	2.28	<i>Oscillospiraceae*</i> (Clostridia)	1.59
<i>Bacteroidales**</i> (Bacteroidia)	2.16	<i>Clostridia_UCG-014</i> (Clostridia)	1.57
unclassified (Verrucomicrobiae)	2.15	<i>Lachnospiraceae_NK4A136_group</i> (Clostridia)	1.38
<i>Oscillospiraceae*</i> (Clostridia)	1.73	<i>Burkholderia-Caballeronia-Paraburkholderia</i> (Gammaproteobacteria)	1.09
<i>Parasutterella</i> (Gammaproteobacteria)	1.40	unclassified (Gammaproteobacteria)	0.96
<i>Clostridia_UCG-014</i> (Clostridia)	1.33	<i>Enterobacterales**</i> (Gammaproteobacteria)	0.95
<i>Lachnospiraceae_NK4A136_group</i> (Clostridia)	1.26	<i>Helicobacter</i> (Campylobacteria)	0.89
<i>Desulfovibrio</i> (Desulfovibrionia)	0.98	<i>Desulfovibrio</i> (Desulfovibrionia)	0.80
<i>Comamonadaceae*</i> (Gammaproteobacteria)	0.85	<i>Allistipes</i> (Bacteroidia)	0.75
<i>Burkholderia-Caballeronia-Paraburkholderia</i> (Gammaproteobacteria)	0.82	<i>Oscillibacter</i> (Clostridia)	0.69
others	14.42	others	11.89
Total Sum	100.00	Total Sum	100.00

B

Genus name	percentage	log2FoldChange	padj
<i>Aphyocypris chinensis</i> APW			
<i>Chryseobacterium</i> (Bacteroidia)	0.35%	-6.13	8.08 × 10 ⁻⁴
<i>RF39</i> (Bacilli)	0.12%	-3.03	9.79 × 10 ⁻²
<i>ASF356</i> (Clostridia)	0.04%	-5.09	4.79 × 10 ⁻²
<i>Moraxellaceae*</i> (Gammaproteobacteria)	0.04%	-5.05	5.23 × 10 ⁻²
<i>Comamonas</i> (Gammaproteobacteria)	0.03%	-4.44	9.79 × 10 ⁻²
<i>Aphyocypris chinensis</i> Rif			
unclassified (Gammaproteobacteria)	2.96%	3.81	1.39 × 10 ⁻¹¹
<i>Bacillus</i> (Bacilli)	1.00%	6.02	5.95 × 10 ⁻²
<i>Cetobacterium</i> (Fusobacteriia)	0.18%	6.90	8.58 × 10 ⁻³
<i>Sphingomonas</i> (Alphaproteobacteria)	0.03%	4.76	6.49 × 10 ⁻²
<i>Intestinimonas</i> (Clostridia)	0.03%	4.86	9.79 × 10 ⁻²
<i>Pseudobagrus fulvidraco</i> APW			
<i>Elizabethkingia</i> (Bacteroidia)	4.61%	-12.33	2.06 × 10 ⁻¹²
<i>Niveispirillum</i> (Alphaproteobacteria)	2.56%	-11.16	8.62 × 10 ⁻¹⁵
unclassified (Verrucomicrobiae)	2.15%	-11.00	1.46 × 10 ⁻¹⁴
<i>Shewanella</i> (Gammaproteobacteria)	0.37%	-5.89	2.55 × 10 ⁻⁵
<i>Stella</i> (Alphaproteobacteria)	0.37%	-8.43	7.00 × 10 ⁻⁸
<i>Fimbrimonadaceae*</i> (Fimbrimonadida)	0.20%	-4.56	7.55 × 10 ⁻⁴
<i>Fluviicola</i> (Bacteroidia)	0.14%	-7.02	1.13 × 10 ⁻⁵
<i>Arsenicibacter</i> (Bacteroidia)	0.13%	-6.90	8.01 × 10 ⁻⁶
<i>Cloacibacterium</i> (Bacteroidia)	0.12%	-6.93	4.93 × 10 ⁻⁴
<i>Crenobacter</i> (Gammaproteobacteria)	0.11%	-6.66	1.13 × 10 ⁻⁵
<i>Enhydrobacter</i> (Gammaproteobacteria)	0.11%	-4.77	1.97 × 10 ⁻²
<i>Cerasicoccus</i> (Verrucomicrobiae)	0.06%	-5.84	6.32 × 10 ⁻⁴
<i>OM190</i> (Planctomycetota***)	0.06%	-3.44	8.98 × 10 ⁻²
<i>Sphingopyxis</i> (Alphaproteobacteria)	0.03%	-5.14	2.49 × 10 ⁻³
<i>pirellula</i> (Planctomycetes)	0.03%	-5.01	3.98 × 10 ⁻³
unclassified (Alphaproteobacteria)	0.03%	-4.80	2.19 × 10 ⁻²
<i>Legionella</i> (Gammaproteobacteria)	0.02%	-4.24	4.89 × 10 ⁻²
<i>Mycobacterium</i> (Actinobacteria)	0.02%	-4.19	7.09 × 10 ⁻²
<i>Proteus</i> (Gammaproteobacteria)	0.02%	-4.56	5.46 × 10 ⁻²
<i>Candidatus Odysseia</i> (Alphaproteobacteria)	0.02%	-3.96	8.98 × 10 ⁻²
<i>Candidatus Branchiomonas</i> (Gammaproteobacteria)	0.02%	-4.14	7.17 × 10 ⁻²
<i>Candidatus simlichlamydia</i> (Chlamydiae)	0.02%	-4.19	5.57 × 10 ⁻²
<i>methylothera</i> (Gammaproteobacteria)	0.02%	-4.62	2.85 × 10 ⁻²
<i>Noviherbaspirillum</i> (Gammaproteobacteria)	0.02%	-4.19	2.85 × 10 ⁻²
<i>CCM19a</i> (Gammaproteobacteria)	0.02%	-4.29	6.54 × 10 ⁻²
<i>Intestinimonas</i> (Clostridia)	0.02%	-4.08	5.57 × 10 ⁻²
<i>Dyadobacter</i> (Bacteroidia)	0.02%	-4.52	3.57 × 10 ⁻²
<i>Weeksellaceae*</i> (Bacteroidia)	0.02%	-4.29	6.54 × 10 ⁻²
<i>Geothermophilum</i> (Bacilli)	0.02%	-4.16	7.17 × 10 ⁻²
<i>Planococcaceae*</i> (Bacilli)	0.02%	-4.32	6.54 × 10 ⁻²
<i>Vogesella</i> (Gammaproteobacteria)	0.02%	-4.29	6.54 × 10 ⁻²
<i>Fusobacterium</i> (Fusobacteriia)	0.01%	-3.84	7.04 × 10 ⁻²
<i>Empedobacter</i> (Bacteroidia)	0.01%	-3.69	6.35 × 10 ⁻²
<i>Nitrosomonas</i> (Gammaproteobacteria)	0.01%	-3.90	9.67 × 10 ⁻²
<i>Pseudobagrus fulvidraco</i> Rif			
<i>Pseudoxanthomonas</i> (Gammaproteobacteria)	0.12%	3.54	0.05
<i>Chitinophagaceae*</i> (Bacteroidia)	0.06%	3.75	0.03
<i>Enterococcus</i> (Bacilli)	0.04%	3.84	0.05
unclassified (Firmicutes***)	0.04%	5.01	0.02
<i>Enterococcus</i> (Bacilli)	0.04%	3.84	0.05
<i>UCG-003</i> (Clostridia)	0.03%	4.57	0.03
<i>Barnesiellaceae*</i> (Bacteroidia)	0.03%	4.62	0.05
<i>Faecalibacterium</i> (Clostridia)	0.02%	4.39	0.04
<i>Gordoniabacter</i> (Coriobacteriia)	0.02%	3.88	0.07
<i>UCS-1-2E3</i> (Clostridia)	0.02%	3.78	0.07
<i>Bosea</i> (Alphaproteobacteria)	0.01%	3.78	0.06

Figure S3. Microbiome abundance in each group.

(A) The top 20 taxonomic diversity and relative abundance in Figure 3. Genus (class) is

shown and if the genus level is not identifiable, an additional level is included. * family,

**order. (B) Relative abundance of bacteria shown in Figure 4 at the genus (class) level.

