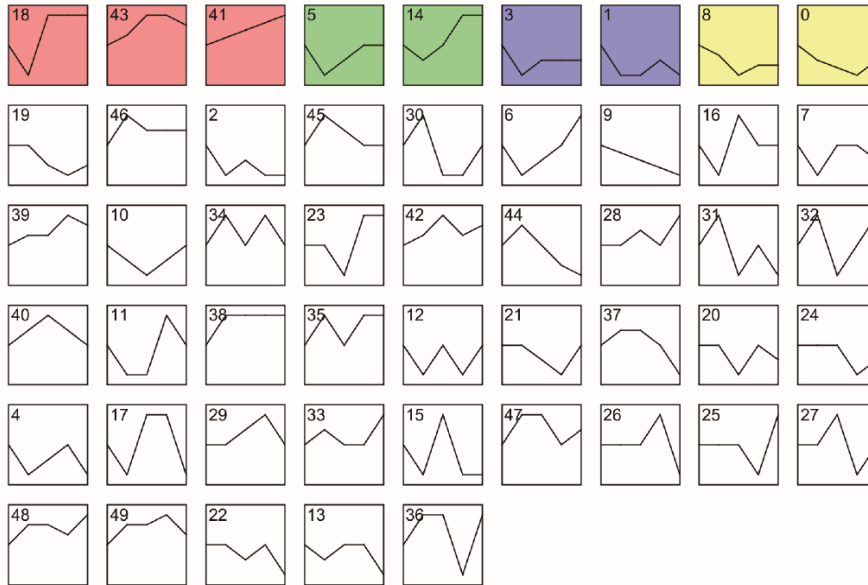


Supplementary Figures

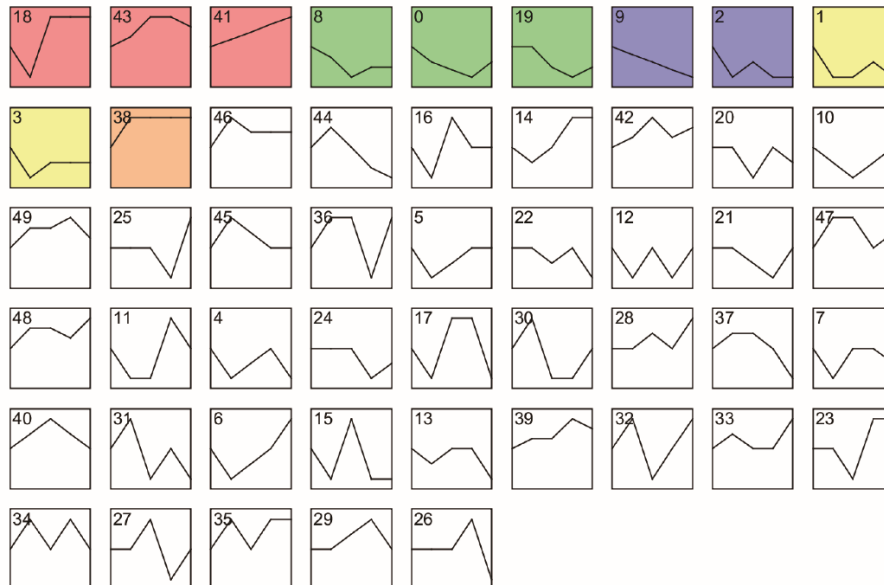
A

Clusters ordered based on number of genes and profiles ordered by significance (default)



B

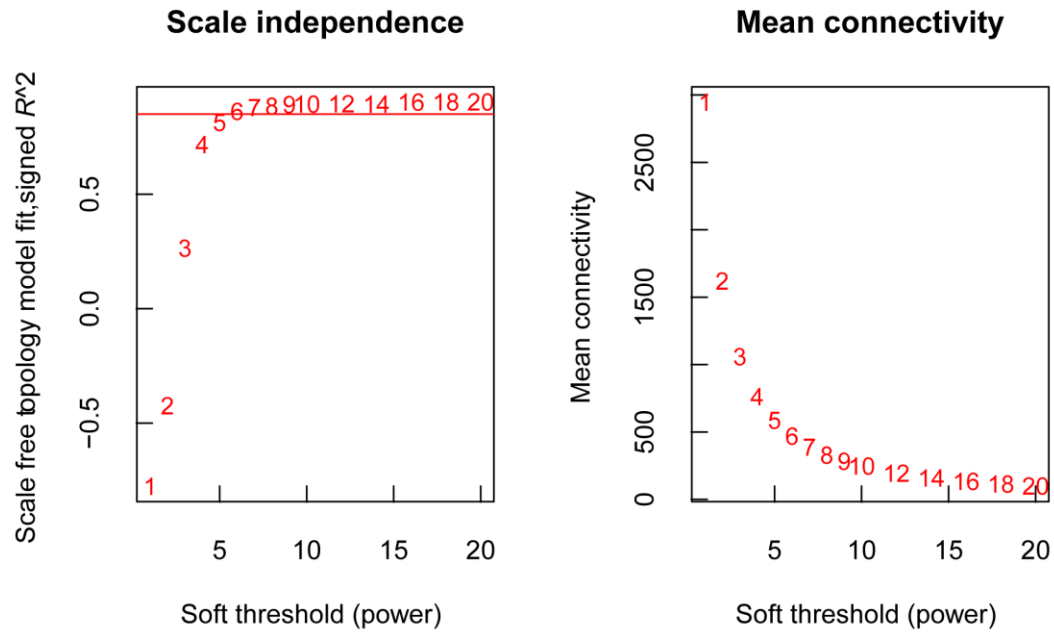
Clusters ordered based on number of genes and profiles ordered by significance (default)



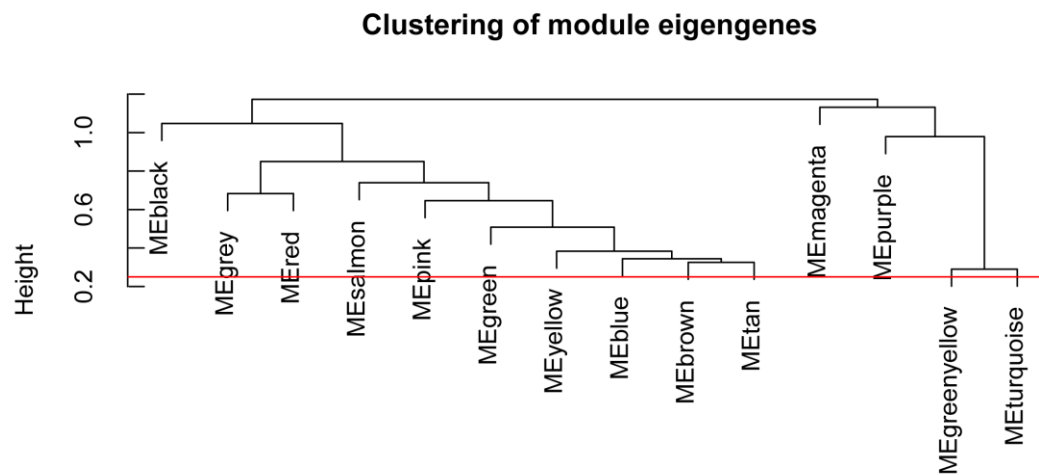
Supplementary Figure S1 STEM analysis result

(A) *Larimichthys crocea*; (B) *Pseudomonas plecoglossicida*.

A



B



Supplementary Figure S2 Result of weighted gene correlation network analysis (WGCNA) analysis

(A) Determination of parameter β of the adjacency function in the weighted gene correlation network analysis (WGCNA) algorithm. (B) Relatedness between clusters generated by WGCNA analysis.

Supplementary Tables
Supplementary Table S1 Sequencing statics

Sample_ID	Mapped reads/Total reads	Mapping rate
<i>Larimichthys crocea</i>		
mock_PI_1	60560526/68374542	88.57%
mock_PI_2	53536892/60620642	88.31%
mock_PI_3	65093420/73839154	88.16%
WT_1d_1	170471769/190128514	89.66%
WT_1d_2	177957855/198458648	89.67%
WT_1d_3	203336580/227370882	89.43%
WT_2d_1	179300790/200048168	89.63%
WT_2d_2	169575247/190546784	88.99%
WT_2d_3	182875898/203641328	89.80%
WT_3d_1	181758753/206533094	88.00%
WT_3d_2	193505042/216481594	89.39%
WT_3d_3	175427210/199704300	87.84%
WT_4d_1	168505171/194250978	86.75%
WT_4d_2	154738080/207548980	74.55%
WT_4d_3	173441469/199386590	86.99%
<i>Pseudomonas plecoglossicida</i>		
mock_cj_1	20883456/21107326	98.94%
mock_cj_2	20925696/21157930	98.90%
mock_cj_3	20690483/20896468	99.01%
WT_1d_1	33156/190128514	0.02%
WT_1d_2	32033/198458648	0.02%
WT_1d_3	24392/227370882	0.01%
WT_2d_1	378935/200048168	0.19%
WT_2d_2	164994/190546784	0.09%

WT_2d_3	149782/203641328	0.07%
WT_3d_1	3524199/206533094	1.71%
WT_3d_2	282724/216481594	0.13%
WT_3d_3	2836803/199704300	1.42%
WT_4d_1	5042046/194250978	2.60%
WT_4d_2	31878030/207548980	15.36%
WT_4d_3	3967360/199386590	1.99%

Supplementary Table S2 Primers Sequence for PCR and qRT-PCR

Gene Name	Base sequence (From 5' to 3')
<i>gyrB</i>	F:5' TGCTGAAGGACGAGCGTTTCG 3'
	R:5' ATCATCTTGCCGACAACAGC 3'
<i>16s</i>	F:5' TCAGTATCAGTCCAGGTGGTCGC 3'
	R:5' CGTTACCGACAGAATAAGCACCG 3'
<i>pcM130</i>	F:5' CTCCTGGTTGGCTTGGTTTC 3'
	R:5' GGTGTTCCCTTCTTCACTGTCCCT 3'
<i>actf (β-actin)</i>	F:5' GACCTGACAGACTACCTCATG 3'
	R:5' AGTTGAAGGTGGTCTCGTGGA 3'
<i>LOC104920199</i>	F:5' TCCTTTGCGGGACTTCTGCT 3'
	R:5' TTGGTGGGAGTGGTGGCTGT 3'
<i>LOC104932156</i>	F:5' CTGGAATGGGAGAATGGAAC 3'
	R:5' AACAGGAGCAGGGTAGAAAA 3'
<i>LOC104922235</i>	F:5' GGAGAATGGAAATGGGTG 3'
	R:5' GGAGCAGGGAACATCGTA 3'
<i>LOC104919239</i>	F:5' TGAGCAATAAAGTGACACCCAT 3'
	R:5' GGCAAGAGGCAGTACGAGGT 3'
<i>LOC109139448</i>	F:5' CTACCAGCAGCAGACAAGAGC 3'
	R:5' GATGTGCCGGATACCGTGAG 3'
<i>LOC104936237</i>	F:5' GGCTCTGCCCTCGCTGCTTT 3'
	R:5' TTCCTGTAGTCCCCTCTGTCTT 3'
<i>hsp90b1</i>	F:5' GACTGGGAACTGATGAACGA 3'
	R:5' CCATAAAGTGGATGTGAGCC 3'
<i>pak1ip1</i>	F:5' TCACAACGGAAGCATCACCT 3'
	R:5' GGATTTTCAGACACTCCCCT 3'
<i>dyrk2</i>	F:5' ATTCTAGGCTCTAGGTATGGGATG 3'
	R:5' CAACTGGTCGGCTTCGTCTT 3'
<i>LOC104938114</i>	F:5' CAGGGCATGAGGCGGGTAGT 3'
	R:5' CGGAGGGTGGTGCTGTTGAG 3'
<i>LOC104932572</i>	F:5' TAAGACACGGAAGCCCAGTA 3'
	R:5' CATGTATTTCGAGCCAAACG 3'

<i>LOC104939072</i>	F:5' ACTGGGAGGTGGACTATGA 3'
	R:5' CCTGGGTATTGACGCTGA 3'
<i>fliG</i>	F:5' TCACTCCGTCCAGTTGATGCC 3'
	R:5' CCCTTGATGCTGCTTTGCTC 3'
<i>flgD</i>	F:5' GCGCCAGGCAAATACGACAT 3'
	R:5' GATACGACTGAACGGCACCC 3'
<i>L321_RS18300</i>	F:5' AGCCCAGCAGCAAACCCTCA 3'
	R:5' AATGCCGCCGAATGCGATGT 3'
<i>L321_RS06430</i>	F:5' TTGGAAGTGCTGACGCTGATC 3'
	R:5' CGGCTGGAGTGGTAGTTGCT 3'
<i>L321_RS04795</i>	F:5' GCCTTCGCCGAGCAGGTGTT 3'
	R:5' AGGTGTCGCCCTTGTGGTTGC 3'
<i>L321_RS23835</i>	F:5' CAACTGGTTCACGCCCAATGTC 3'
	R:5' GCAACACGGGCAGGTTCTTTT 3'
<i>L321_RS17435</i>	F:5' TGAGTTCATCGACCGCTATGTG 3'
	R:5' TCTCCAGGTTCTCGCTCCAGT 3'
<i>L321_RS01350</i>	F:5' CCGCATATCGCAGGTTACAGCC 3'
	R:5' GGCGACATCCTCACTCAGGCTAC 3'
<i>F:L321_RS07175</i>	F:5' TCGGTGGCGCAGGATTGTTT 3'
	R:5' CGGGCATTTCCTTGAGCACATC 3'
<i>L321_RS15215</i>	F:5' ACCAGGAAATGCTCGCTGACCC 3'
	R:5' CAGCACCTGCGACCGATGT 3'
<i>L321_RS06550</i>	F:5' GCAAGGCACTCATCCAGACACTG 3'
	R:5' GGCACGCCCTGCTCTTCATAG 3'
<i>L321_RS20240</i>	F:5' CTGGCGGCTATTTCTGTGGC 3'
	R:5' TGATCCGTCCGAGCGTTTCC 3'
<i>L321_RS24165</i>	F:5' CGTGGTGATCTTCGTGGTCG 3'
	R:5' TTCAGCGTTCGGCAGTTGTT 3'
<i>L321_RS10520</i>	F:5' GCAAACGCATCGTTACCAC 3'
	R:5' CGCCTGAGTAATCACGCTAAAT 3'
