frontiers

Supplementary Material

Transcriptome, intestinal microbiome and histomorphology profiling of differences in the response of Chinese sea bass (*Lateolabrax maculatus*) to *Aeromonas hydrophila* infection

Supplementary Table 1

Sequence information of primers for qRT-PCR.

Primer No.	Primer name	Sequence (5' - 3')
1	C6-F	ACCAAGTTCTGCCTGTTTCCA
2	C6-R	CCCTGAGCTGTAGTAGTGCGTC
3	LBP-F	AGCGTTTCCCAGGTCTGATGATGA
4	LBP-R	AGGGTGGCGTTGGGTTGGATAG
5	NFATC1-F	CAACATGCGGGCCATGATCG
6	NFATC1-R	ACCATCCGCACTCGTGTGTT
7	RIPK2-F	GACCTGCGGCTGGACCTCTAACC
8	RIPK2-R	GACCCCTCATCACTCCTCTTCTCACA
9	SIPA1L2-F	GACAGCGGCATCGACACTAATCC
10	SIPA1L2-R	GGACATAATGGCAGAGGCGTAGC
11	C7-F	TGACAAAACGCCTCCCAACTC
12	C7-R	CTGCACTGCCCTCCGAAACTC
13	IRAK4-F	CGACTTGCTTGCTTGGAGGG
14	IRAK4-R	ACGCTCTCGTCAGCCCAAAG

15	β-actin-F	CGTGCTGTCTTCCCCTCCA
16	β-actin-R	TCACCAACGTAGCTGTCCTTCTG

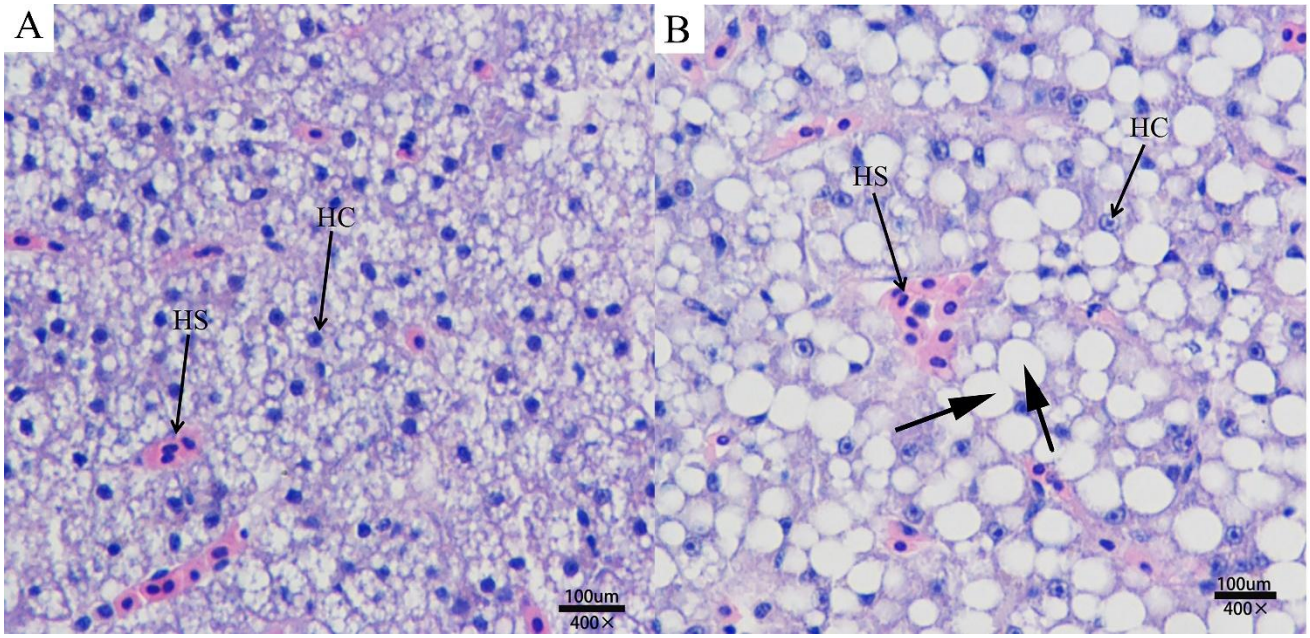
Supplementary Table 2 Partial of DEGs involved in signaling pathway related to immune response

Gene name	Gene ID in transcriptome	Log_2FC	Regulated	*p*-value
Toll−like receptor signaling pathway				
TLR5	evm.TU.scaffold_129.16	7.15	up	1.16×10^{-6}
CASP8	evm.TU.scaffold_255.49	1.54	up	1×10^{-3}
CD40	evm.TU.scaffold_11.322	1.34	up	2.81×10^{-3}
NOD-like receptor signaling pathway				
HSP90	evm.TU.scaffold_1.108	-1.52	down	1.06×10^{-3}
ASC	evm.TU.scaffold_14.2	2.00	up	1.43×10^{-4}
IL-1β	evm.TU.scaffold_287.11	4.55	up	5.43×10^{-6}
IRF3/7	evm.TU.scaffold_4.273	2.71	up	1.17×10^{-5}
C-type lectin receptor signaling pathway				
IκBα	evm.TU.scaffold_137.4	3.24	up	1.79×10^{-11}
MALT1	evm.TU.scaffold_6.267	1.41	up	1.22×10^{-3}
RELB	evm.TU.scaffold_56.112	1.54	up	1.46×10^{-3}
Cox-2	evm.TU.scaffold_12.30	1.67	up	4.31×10^{-3}

Supplementary Table 3 Relationship between differentially expressed genes and microbial community composition on genus level

Gene ID	NR	Chr	regulated	Correlation	P-value	Genus
evm.TU.scaffold_6.46	CD44 antigen	6	Down	0.828	0.042	*Ralstonia*
evm.TU.scaffold_76.153	Zinc finger protein 362-like isoform X1	4	Down	0.848	0.033	*Ralstonia*
evm.TU.scaffold_19.80	Ankyrin repeat and SOCS box protein 5-like isoform X1	14	Down	0.863	0.027	*Ralstonia*
evm.TU.scaffold_188.45	Growth/differentiation factor 10-like	13	Up	-0.872	0.024	*Ralstonia*
novel.1379	Unknown	23	Up	-0.831	0.040	*Ralstonia*
novel.2442	Uncharacterized protein LOC108881995(predicted)	scaffold_446	Down	0.814	0.049	*Ralstonia*
evm.TU.scaffold_25.115	Serum amyloid A	1	Up	0.983	0.000	*Pseudomonas*
evm.TU.scaffold_98.14	Metalloreductase STEAP4 isoform X2	7	Up	0.955	0.003	*Pseudomonas*
evm.TU.scaffold_24.251	Unknown	7	Up	0.944	0.005	*Pseudomonas*
evm.TU.scaffold_25.76	Haptoglobin-like isoform X1	1	Up	0.992	0.000	*Pseudomonas*

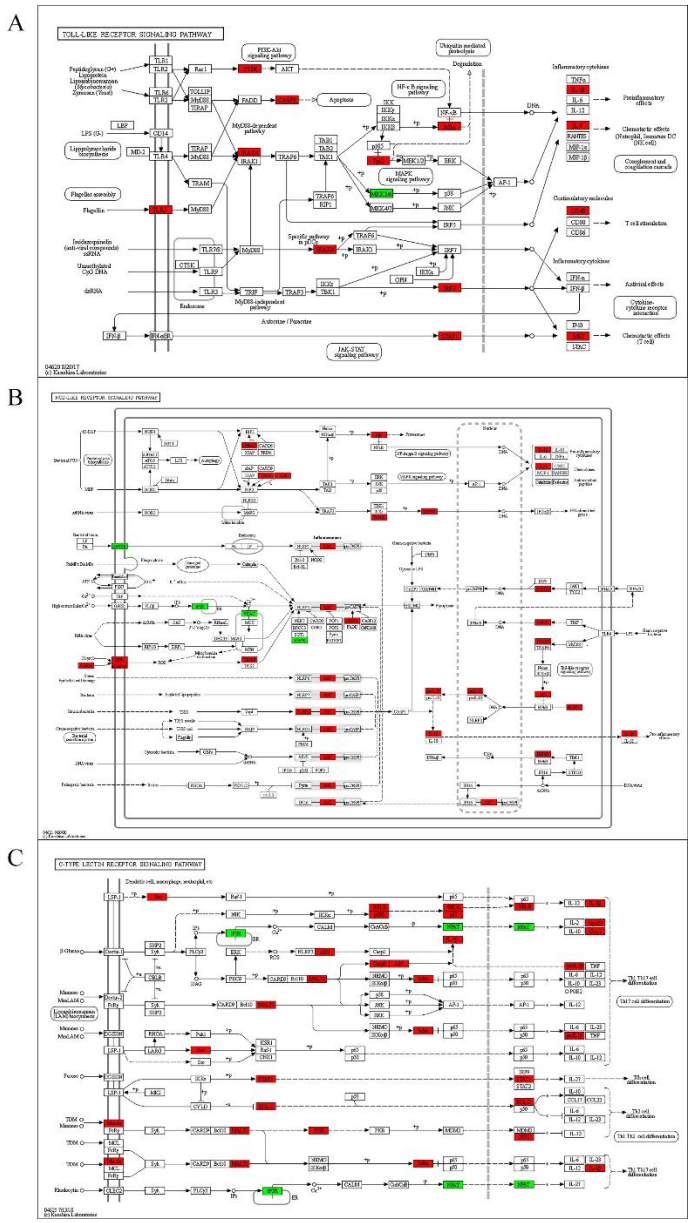
Supplementary Fig. 1



Supplementary Fig.1 Histopathological changes in the liver of the control and *A. hydrophila* groups.

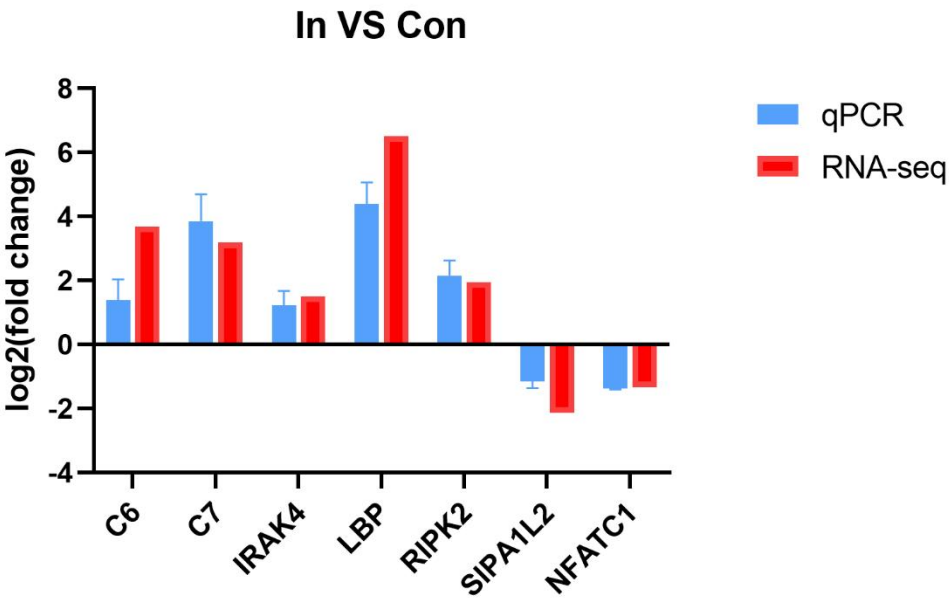
Note: A. The liver of the control group. B. The liver of the *A. hydrophila* group. Thick arrows= vacuolated hepatocytes, HS = hepatic sinusoid, HC = hepatocyte.

Supplementary Fig. 2



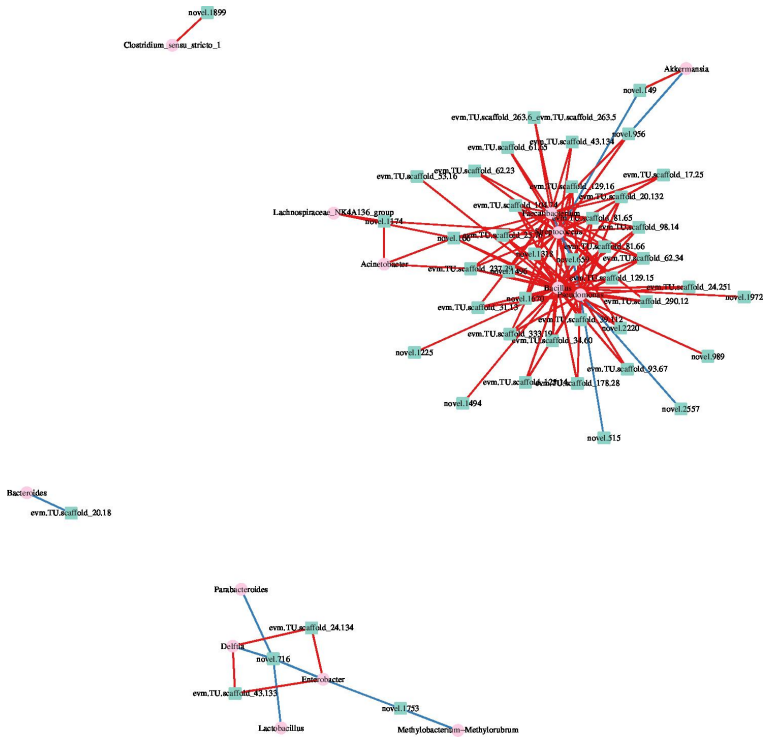
Supplementary Fig. 2 KEGG pathways annotation of differentially expressed genes. (A) DEGs are annotated to the Toll-like receptor signaling pathway. (B) DEGs are annotated to the NOD-like receptor signaling pathway. (C) C-type lectin receptor signaling pathway. For the infected group, the red box labeled protein is related to the up-regulated gene, and the green box labeled protein is related to the down-regulated gene. According to the differences of samples, the differential expression of genes related to metabolic pathway was mainly studied.

Supplementary Fig. 3



Supplementary Fig. 3 Validation of RNA-seq data by qRT-PCR analysis. X-axis, gene names; Y-axis, $\log_2$(fold change) in gene expression. The relative expression of seven DEGs related to complement pathways and defense responses were determined by qRT-PCR with the *β-actin* as the internal reference.

Supplementary Fig. 4



Supplementary Fig. 4 Network interaction diagram of association analysis with the top 30 genera and significantly differentially expressed genes. The genes with significant differences (|log2foldchange| ≥ 5) were screened for association analysis with the top 30 genera of relative abundance.