

Supplementary Materials

Table S1. Primer sequences for qPCR.

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
Clpro	CACCCACGCAGATTGGAAC	TGACGATGGTGCCACAGAC
Durt1	TACCACGCCGCCATACCCAA	GCAGGCTGACTGATACTGAAGGC
Chymotrypsin	ACATCAGGTTGGAAGAAGCGTC	GTGTTGAATGTGACGGGGCT
Hemocyanin	TGGTGTGGCTCGCATCAGA	GCACCCACGACATCAATACCAT
Vmo1	AAGAGGGGTGACTGGCAAGG	TCCACTCCAAAGTCATCGCC
Hemocyanin A	GAAGTCAAGGCTGGAACGCA	CATCATTCACAGCCTCGTCAGTC
Nodulin-75	CACCTACACTCCTTCCCTGGCA	TTAGGCAGCGACGAACCTGAA
CD97	CCTACAAGAACGGTGGAGCG	TGGGGAAAAGAATGTTGGGA
Durt2	TGACATCTTACCTGAACTGCCAAA	AGGCGGTAGTTATCCATCCCA
Iscw	AAGATGGAATAATAGTCCTTACGGC	AGGCGGGAGCAAATCACTG
TLR1	GCTTGGAGTACACCCAGAA	TTAACAAGTCCGTCCAGGTG
TLR2	GATCCCAGCAGAGTCTGAGC	CAAGATCTGGTGGATGGGGC
SR	GCACTACTGTCCCTGGCAAT	GCCCTCCACACCATTGAGAA
Mapkkk4	TTCAGTCTGTGTGAGGAGCC	GGTGGGTGGATGGGTATCA
Mapkkk7	GTGGCAGTGAAGAAGGTAGAAA	GCAAACCTCAATGACCAGGCA
Mapkk6	CGCTCAGATGTGTGGTCACT	GAAAGTTCCAGGAGGGAGGC

Table S2. Statistics of the transcriptome sequencing from blood samples of *P. trituberculatus*.

Sample	Raw_reads	Clean_reads	Q20 (%)	Q30 (%)	Mapped to genome (%)	Coverage depth
0h_1	45,218,876	44,011,870	97.46	93.1	88.54%	7.97
0h_2	37,195,138	36,084,876	97.69	93.63	88.79%	8.27
0h_3	45,525,094	44,600,106	97.89	94.35	88.59%	8.01
Ls_12h_1	46,859,006	45,828,352	98.17	94.92	87.23%	8.24
Ls_12h_2	45,279,026	44,062,912	98.06	94.5	87.70%	7.93
Ls_12h_3	42,583,858	41,359,654	98.08	94.65	86.33%	7.43
Ls_24h_1	47,453,074	46,231,682	97.92	94.35	84.48%	8.31
Ls_24h_2	45,837,770	44,449,438	98.01	94.57	84.96%	8.00
Ls_24h_3	44,245,524	43,263,644	97.93	94.29	85.09%	7.78
Ls_48h_1	46,152,442	45,084,506	98.13	94.79	85.96%	8.11
Ls_48h_2	49,249,936	48,575,640	97.65	93.72	87.32%	8.74
Ls_48h_3	45,747,746	45,034,808	97.61	93.64	87.06%	8.11
Ls_72h_1	45,811,612	44,415,824	97.65	93.74	86.42%	7.99
Ls_72h_2	41,454,254	40,265,614	97.8	94.12	86.06%	7.24
Ls_72h_3	45,655,424	44,919,668	97.54	93.63	85.94%	8.08
Vp_12h_1	43,997,912	43,196,466	97.35	93.14	86.61%	7.77
Vp_12h_2	38,543,930	37,381,920	97.52	93.57	86.82%	6.73
Vp_12h_3	43,404,780	42,550,502	97.59	93.71	86.88%	7.65
Vp_24h_1	44,069,140	43,047,190	97.56	93.43	85.74%	7.75

Vp_24h_2	38,601,836	37,812,006	97.24	92.7	85.78%	6.80
Vp_24h_3	42,987,796	41,768,994	97.64	93.8	87.00%	7.52
Vp_48h_1	46,401,016	45,466,782	97.7	93.83	86.12%	8.18
Vp_48h_2	42,439,408	41,578,678	97.74	93.98	86.02%	7.48
Vp_48h_3	47,674,034	46,769,312	97.68	93.88	85.73%	8.42
Vp_72h_1	46,008,204	45,190,418	97.43	93.35	85.65%	8.13
Vp_72h_2	43,930,664	43,097,034	97.42	93.3	85.56%	7.75
Vp_72h_3	40,381,368	39,615,108	97.55	93.58	86.07%	7.12

Table S3. KEGG of DEGs with opposite trends in expression patterns post pathogen infection and low salinity stress.

	KEGG ID	Description	BgRatio	padj	Gene name	Count
Vp_up & ls_down	dme04310	Wnt signaling pathway	64/2203	0.001662	receptor tyrosine kinase	2
	dme04150	mTOR signaling pathway	73/2203	0.06519	Frizzled-4	1
	dme00760	Nicotinate and nicotinamide metabolism	16/2203	0.053146	Frizzled-4	1
	dme00260	Glycine, serine and threonine metabolism	25/2203	0.053146	Cytosolic purine 5'-nucleotidase	1
	dme00513	Various types of N-glycan biosynthesis	25/2203	0.053146	sarcosine dehydrogenase	1
Vp_down & ls_up	dme00510	N-Glycan biosynthesis	31/2203	0.053146	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase C-like	1
	dme00240	Pyrimidine metabolism	33/2203	0.053146	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase C-like	1
	dme00230	Purine metabolism	72/2203	0.09492	Cytosolic purine 5'-nucleotidase	1

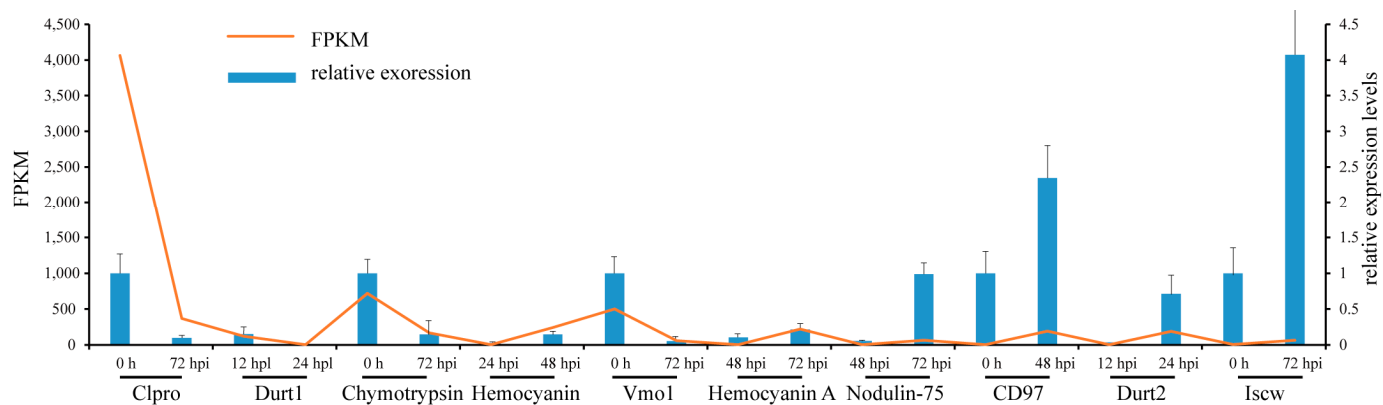


Figure S1. qPCR validation of transcriptome data. The RT-qPCR data was presented as the mean \pm S.D.

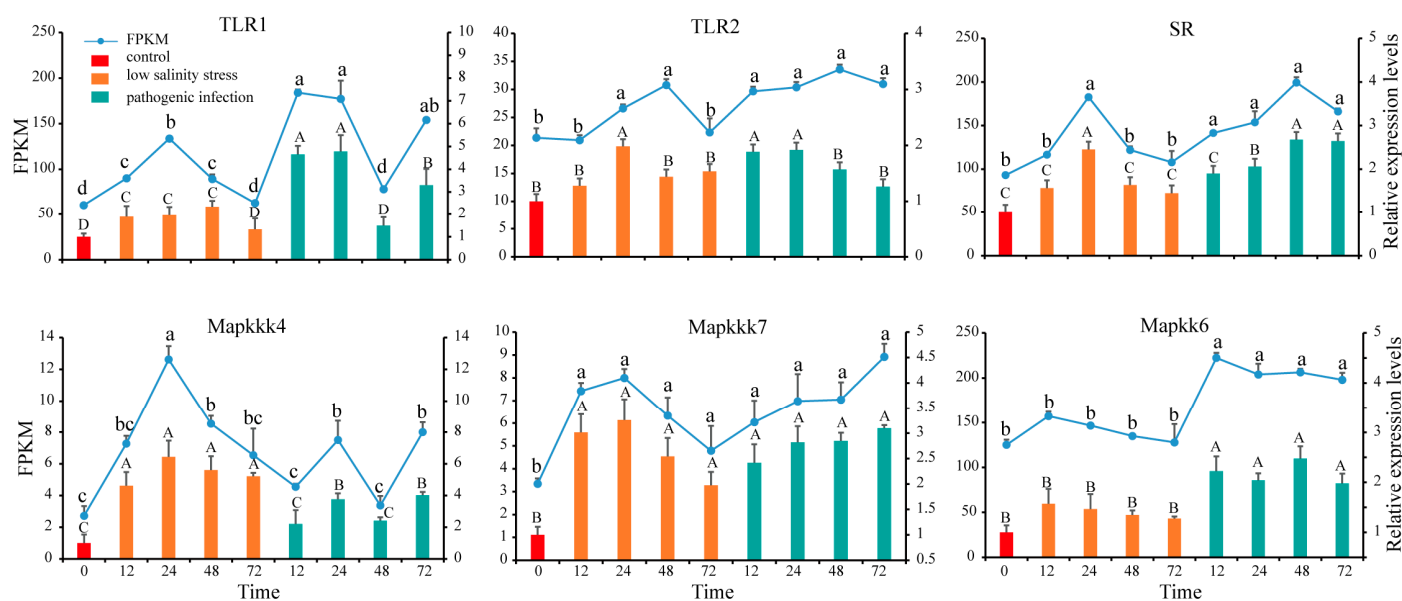


Figure S2. qPCR validation of genes in the Toll and IMD signaling pathways. TLR1, Toll-like receptors 1; TLR2, Toll-like receptors 2; SR, scavenger receptor; Mapkkk4, mitogen-activated protein kinase kinase kinase 4; Mapkkk7, mitogen-activated protein kinase kinase kinase 7; Mapkk6, mitogen-activated protein kinase kinase 6. Different lowercase letters indicate significant differences ($P < 0.05$) in RNA-seq; different uppercase letters indicate significant differences ($P < 0.05$) in qPCR.

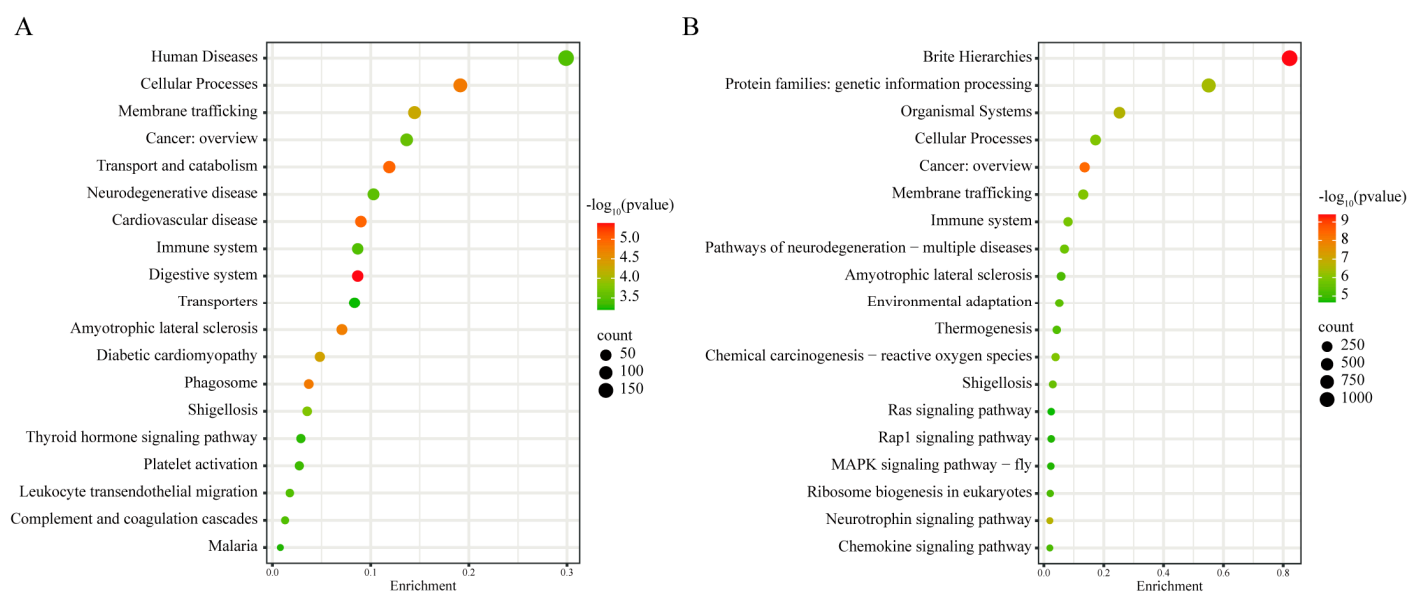


Figure S3. KEGG annotation of DEGs under low salinity and *V. parahaemolyticus*. (A) KEGG annotation of shared DEGs under low salinity stress. (B) KEGG annotation of shared DEGs under pathogen stress.