

Table S1. Bacterial strains and media used in this study.

Bacterial strain	Culture medium	Source
<i>Vibrio alginolyticus</i> ATCC17749	TSB	ATCC, United States
<i>Vibrio alginolyticus</i> ATCC33787	TSB	ATCC, United States
<i>Vibrio fluvialis</i> ATCC33809	Marine 2216	ATCC, United States
<i>Vibrio harvey</i> ATCC BAA-1117	Marine 2216	ATCC, United States
<i>Vibrio harveyi</i> ATCC33842	Marine 2216	ATCC, United States
<i>Vibrio metschnikovii</i> ATCC700040	Marine 2216	ATCC, United States
<i>Vibrio mimicus</i> bio-56759	TSB	Biobw, China
<i>Vibrio parahaemolyticus</i> ATCC17802	TSB	ATCC, United States
<i>Vibrio parahaemolyticus</i> ATCC33847	TSB	ATCC, United States
<i>Vibrio vulnificus</i> ATCC27562	TSB	Biobw, China
<i>Aeromonas hydrophila</i> ATCC35654	TSB	ATCC, United States
<i>Bacillus cereus</i> A1-1	TSB	LS-SHOU, China
<i>Enterobacter cloacae</i> ATCC13047	TSB	Biobw, China
<i>Enterobacter cloacae</i>	LB	LS-SHOU, China
<i>Escherichia coli</i> ATCC8739	TSB	Biobw, China
<i>Escherichia coli</i> K12	TSB	IIM, China
<i>Escherichia coli</i> ATCC25922	LB	ATCC, United States
<i>Enterobacter sakazakii</i> CMCC45401	TSB	Biobw, China
<i>Listeria monocytogenes</i> ATCC19115	BHI	Biobw, China
<i>Pseudomonas aeruginosa</i> ATCC9027	TSB	Biobw, China
<i>Pseudomonas aeruginosa</i> ATCC27853	TSB	Biobw, China
<i>Staphylococcus aureus</i> ATCC25923	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC8095	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC29213	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC6538	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC6538P	TSB	ATCC, United States
<i>Staphylococcus aureus</i>	TSB	LS-SHOU, China
<i>Shigella dysenteriae</i> CMCC51252	TSB	GCCC, China
<i>Salmonella choleraesuis</i> ATCC13312	TSB	ATCC, United States
<i>Shigella flexneri</i> CMCC51572	TSB	GCCC, China
<i>Shigella flexneri</i> ATCC12022	TSB	ATCC, United States
<i>Shigella flexneri</i> CMCC51574	TSB	GCCC, China
<i>Salmonella paratyphi-A</i> CMCC50093	TSB	GCCC, China
<i>Shigella sonnei</i> ATCC25931	TSB	ATCC, United States
<i>Shigella sonnet</i> CMCC51592	TSB	GCCC, China
<i>Salmonella typhimurium</i> ATCC15611	TSB	ATCC, United States
<i>Salmonella</i>	LB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B3-13	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B4-10	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B5-29	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B9-35	TSB	LS-SHOU, China
<i>Vibrio cholerae</i> GIM1.449	TSB	GCCC, China
<i>Vibrio cholerae</i> Q10-54	TSB	LS-SHOU, China
<i>Vibrio cholerae</i> b10-49	TSB	LS-SHOU, China

ATCC: American Type Culture Collection, United States; GCCC, Guangdong Culture Collection Center, Guangzhou, China; IIM, Institute of Industrial Microbiology, Shanghai, China; LS-SHOU, Laboratory stock, Shanghai Ocean University, Shanghai, China.

Table S2. Expression of representative DEGs by RT-qPCR assay.

Sample	Gene	Predicted protein	Fold change	
			RNA-Seq.	RT-PCR
<i>V. alginolyticus</i> ATCC17749	<i>N646_0236</i>	Hydroxylamine reductase	87.807	32.334
	<i>N646_0310</i>	Histidine ammonia-lyase	3.187	2.121
	<i>N646_2909</i>	Cation transport ATPase%2C E1-E2 family protein	0.123	0.142
	<i>N646_4052</i>	Putative acyl-CoA thiolase	5.154	1.288
	<i>N646_4487</i>	Arginine ABC transporter%2C periplasmic arginine-binding protein	4.958	7.863
<i>V. parahaemolyticus</i> ATCC17802	<i>VP_RS01760</i>	Dihydroxyacetone kinase ADP-binding subunit DhaL	0.040	0.111
	<i>VP_RS01755</i>	Dihydroxyacetone kinase subunit DhaK	0.067	0.158
	<i>VP_RS05780</i>	Hydroxylamine reductase	107.754	26.816
	<i>VP_RS09370</i>	Ammonia-forming nitrite reductase cytochrome c552 subunit	19.809	4.141
	<i>VP_RS10480</i>	Type I glyceraldehyde-3-phosphate dehydrogenase	0.168	0.011
	<i>VP_RS10820</i>	Chemotaxis protein CheA	0.386	0.498
	<i>VP_RS16540</i>	Flagellar basal body rod protein FlgB	0.064	0.667
	<i>VP_RS22540</i>	Flagellar biosynthesis protein FliQ	0.055	0.516
	<i>VP_RS22500</i>	Flagellar motor switch protein FliG	0.294	0.629
	<i>VP_RS23260</i>	6-phospho-beta-glucosidase	0.087	0.049
<i>V. parahaemolyticus</i> B4-10	<i>VP_RS05780</i>	Hydroxylamine reductase	107.754	10.740
	<i>VP_RS06180</i>	Histidine ammonia-lyase	6.284	1.860
	<i>VP_RS06185</i>	Urocanate hydratase	10.231	22.860
	<i>VP_RS06190</i>	Formimidoylglutamase	5.106	9.420
	<i>VP_RS06195</i>	Imidazolonepropionase	6.998	6.770
	<i>VP_RS06485</i>	ABC transporter ATP-binding protein	0.310	0.040
	<i>VP_RS06520</i>	ATP-binding cassette domain-containing protein	0.256	0.070
	<i>VP_RS06525</i>	ABC transporter permease subunit	0.265	0.130
	<i>VP_RS20250</i>	BC transporter permease	10.250	3.780
	<i>VP_RS20670</i>	ABC transporter ATP-binding protein	0.3698	0.018
	<i>VP_RS20695</i>	ABC transporter ATP-binding protein	0.455	0.022
<i>B. cereus</i> A1-1	<i>BCN_RS06525</i>	Indole-3-glycerol phosphate synthase TrpC	0.235	0.062
	<i>BCN_RS08605</i>	Flagellin	0.045	0.038
	<i>BCN_RS08640</i>	Flagellar type III secretion system pore protein FliP	0.108	0.557
	<i>BCN_RS10010</i>	Methyl-accepting chemotaxis protein	0.063	0.235
	<i>BCN_RS10875</i>	Hydroxylamine reductase	15.156	1.693
	<i>BCN_RS16540</i>	Respiratory nitrate reductase subunit gamma	150.78	233.631