

Figure S1. Construction of the $\Delta VpaChn25_0713$ mutant by agarose gel electrophoresis analysis.

(A) Amplicons of upstream and downstream of the *VpaChn25_0713*. M, 100 bp DNA Ladder; Line 1, upstream of *VpaChn25_0713*; Line 2, downstream of *VpaChn25_0713*; Line 3–4, blank. (B) Amplicons of upstream& downstream of *VpaChn25_0713*. M, 100 bp DNA Ladder. (C) Amplicons of upstream, downstream of *VpaChn25_0713* in the recombinant plasmids. M, D2000 DNA Ladder. (D) Amplicons of *VpaChn25_0713*-up-F and *VpaChn25_0713*-down-R. M, 100 bp DNA Ladder. (E) Amplicons of *tlh*. M, 100 bp DNA Ladder. (F) Amplicons of *VpaChn25_0713*-up-ex-F and *VpaChn25_0713*-down-ex-R. M, 100 bp DNA Ladder. (G): Amplicons of *tlh*. M, 100 bp DNA Ladder.

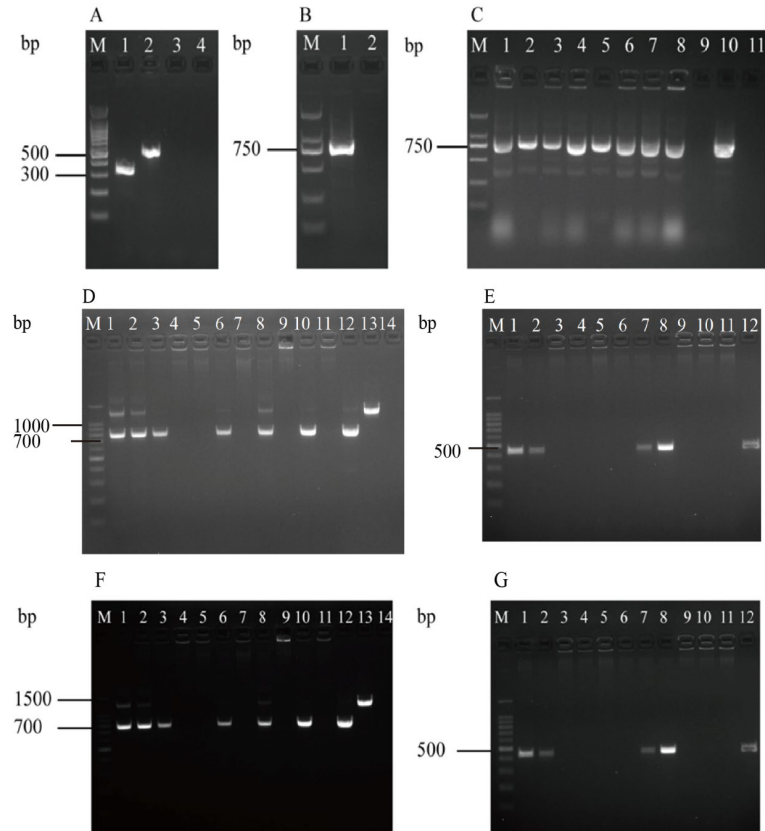


Figure S2. Construction of the $\Delta VpaChn25_0714$ mutant by agarose gel electrophoresis analysis.

(A) amplicons of upstream and downstream of *VpaChn25_0714*. M, 100 bp DNA Ladder; Line 1, upstream of *VpaChn25_0714*; Line 2, downstream of *VpaChn25_0714*; Line 3–4, blank. (B) amplicons of upstream& downstream of *VpaChn25_0714*. M, D2000 bp DNA Ladder. (C) amplicons of upstream& downstream of *VpaChn25_0714* in the recombinant plasmids. M, D2000 bp DNA Ladder. (D) amplicons of *VpaChn25_0714*-up-F and *VpaChn25_0714*-down-R. M, 100 bp DNA Ladder. (E): Amplicons of *tlh*. M, 100 bp DNA Ladder. (F) Amplicons of *VpaChn25_0714*-up-ex-F and *VpaChn25_0714*-down-ex-R. M, 100 bp DNA Ladder. (G) Amplicons of *tlh*. M, 100 bp DNA Ladder.

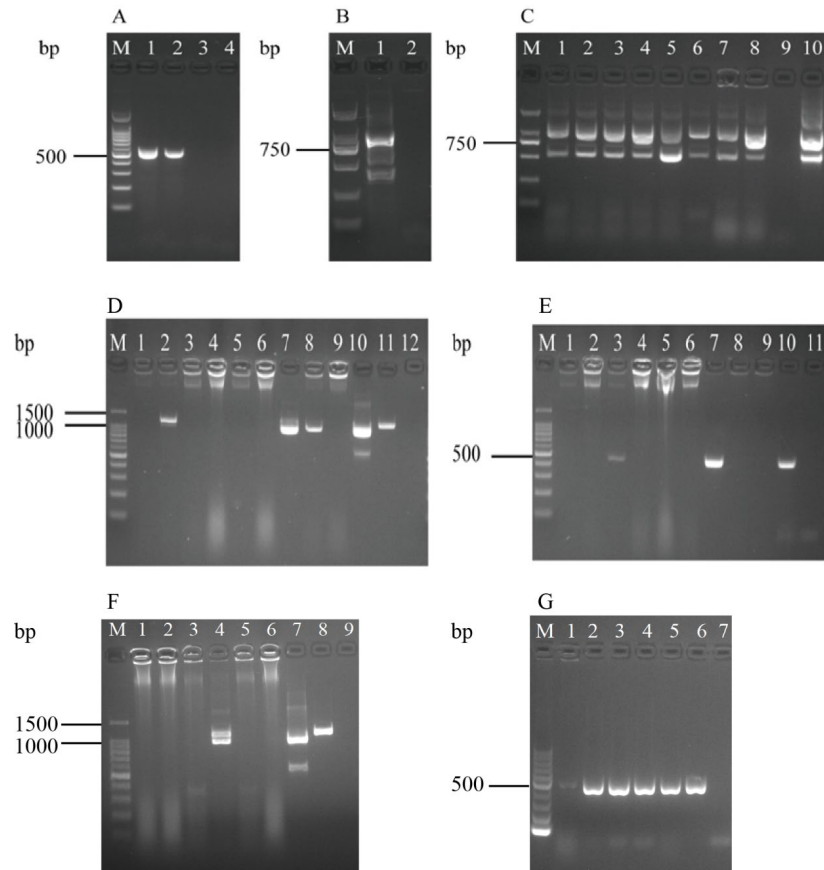


Figure S3. Construction of the $\Delta VpaChn25_RS25055$ mutant by agarose gel electrophoresis analysis.

(A) Amplicons of upstream and downstream of *VpaChn25_RS25055*. M, 100 bp DNA Ladder; Line1, upstream of *VpaChn25_RS25055*; Line2, downstream of *VpaChn25_RS25055*; Line3–4, blank. (B) Amplicons of upstream& downstream of *VpaChn25_RS25055*. M, D2000 bp DNA Ladder. (C) Amplicons of upstream& downstream of *VpaChn25_RS25055* in the recombinant plasmids. M, D2000 bp DNA Ladder. (D) Amplicons of *VpaChn25_RS25055*-up-F and *VpaChn25_RS25055*-down-R. M, 100 bp DNA Ladder. (E) Amplicons of *tlh*. M, 100 bp DNA Ladder. (F) Amplicons of *VpaChn25_RS25055*-up-ex-F and *VpaChn25_RS25055*-down-ex-R. M, 100 bp DNA Ladder. (G) Amplicons of *tlh*. M, 100 bp DNA Ladder.

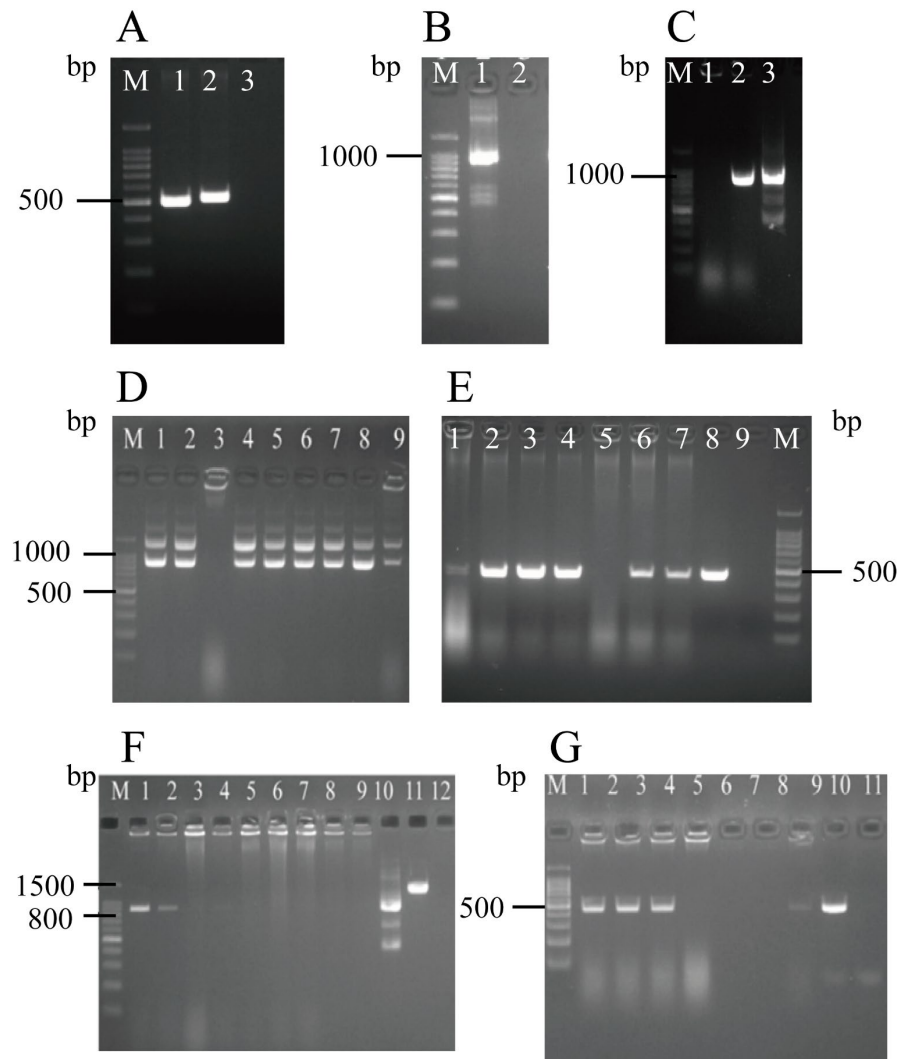


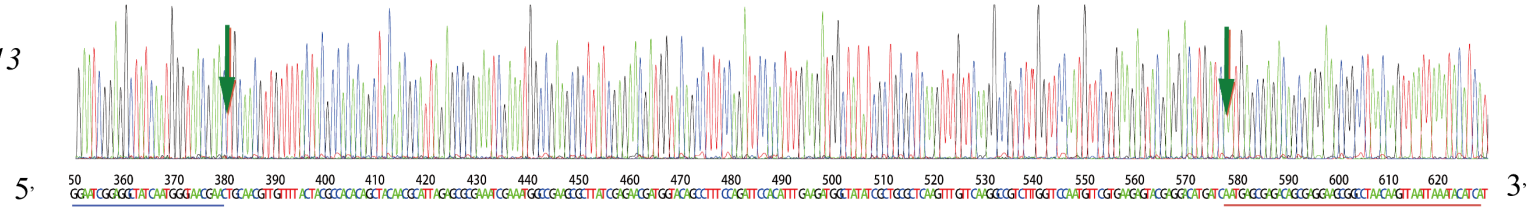
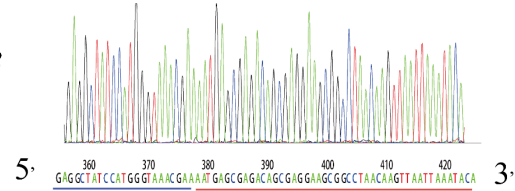
Figure S4. Construction of the $\Delta VpaChn25_RS25055-0713-0714$ mutant by agarose gel electrophoresis analysis.

(A) Amplicons of upstream and downstream of *VpaChn25_RS25055-0713-0714*. M, 100 bp DNA Ladder; Line1, upstream of *VpaChn25_RS25055-0713-08714*; Line2, downstream of *VpaChn25_RS25055-0713-0714*; Line3, blank. (B) Amplicons of upstream& downstream of *VpaChn25_RS25055-0713-0714*. M, 100 bp DNA Ladder. (C) Amplicons of upstream& downstream of *VpaChn25_RS25055-0713-0714* in the recombinant plasmids. M, 100 bp DNA Ladder. (D) Amplicons of *VpaChn25_RS25055-0713-0714*-up-F and *VpaChn25_RS25055-0713-0714*-down-R. M, 100 bp DNA Ladder. (E) Amplicons of *tlh*. M, 100 bp DNA Ladder. (F) Amplicons of *VpaChn25_RS25055-0713-0714*-up-ex-F and *VpaChn25_RS25055-0713-0714*-down-ex-R. M, 100 bp DNA Ladder. (G) Amplicons of *tlh*. M, 100 bp DNA Ladder.

WT

VpaChn25_0713
(234 bp)

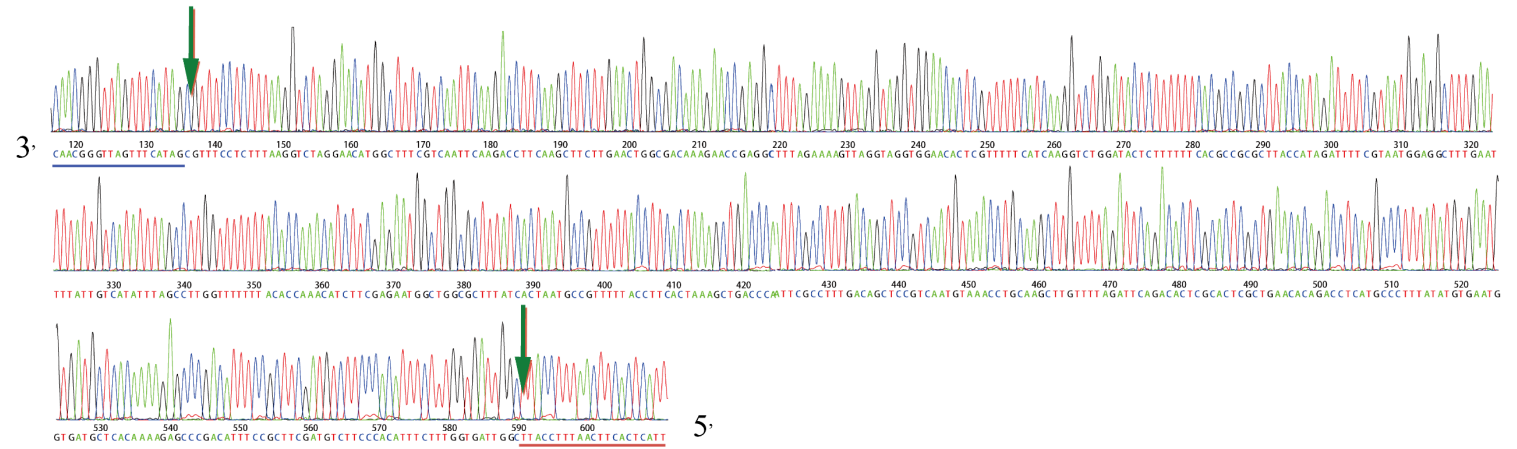
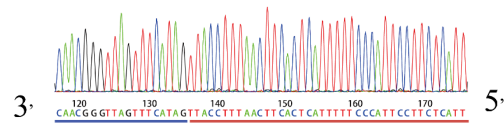
(234 bp)

 $\Delta V_{paChn25_0713}$ 

WT
VpaChn25_0714
(480 bp)

VpaChn25_0714

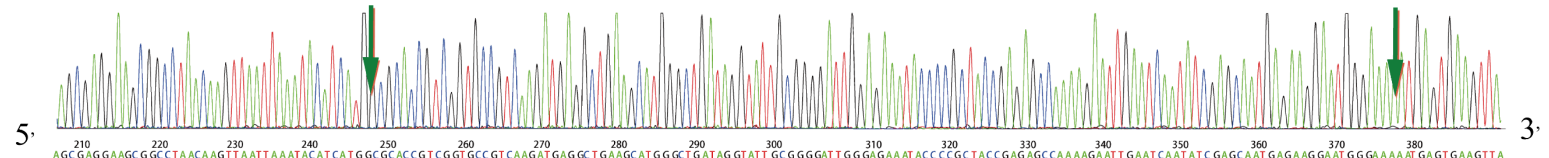
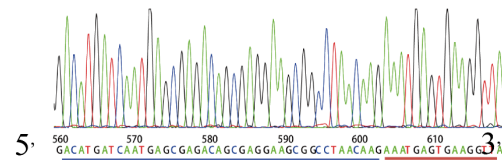
(480 bp)

 $\Delta V_{paChn25_0714}$ 

WT
VpaChn25_RS25055
(186 bp)

VpaChn25_RS25055

(186 bp)

 $\Delta V_{paChn25_RS25055}$ 

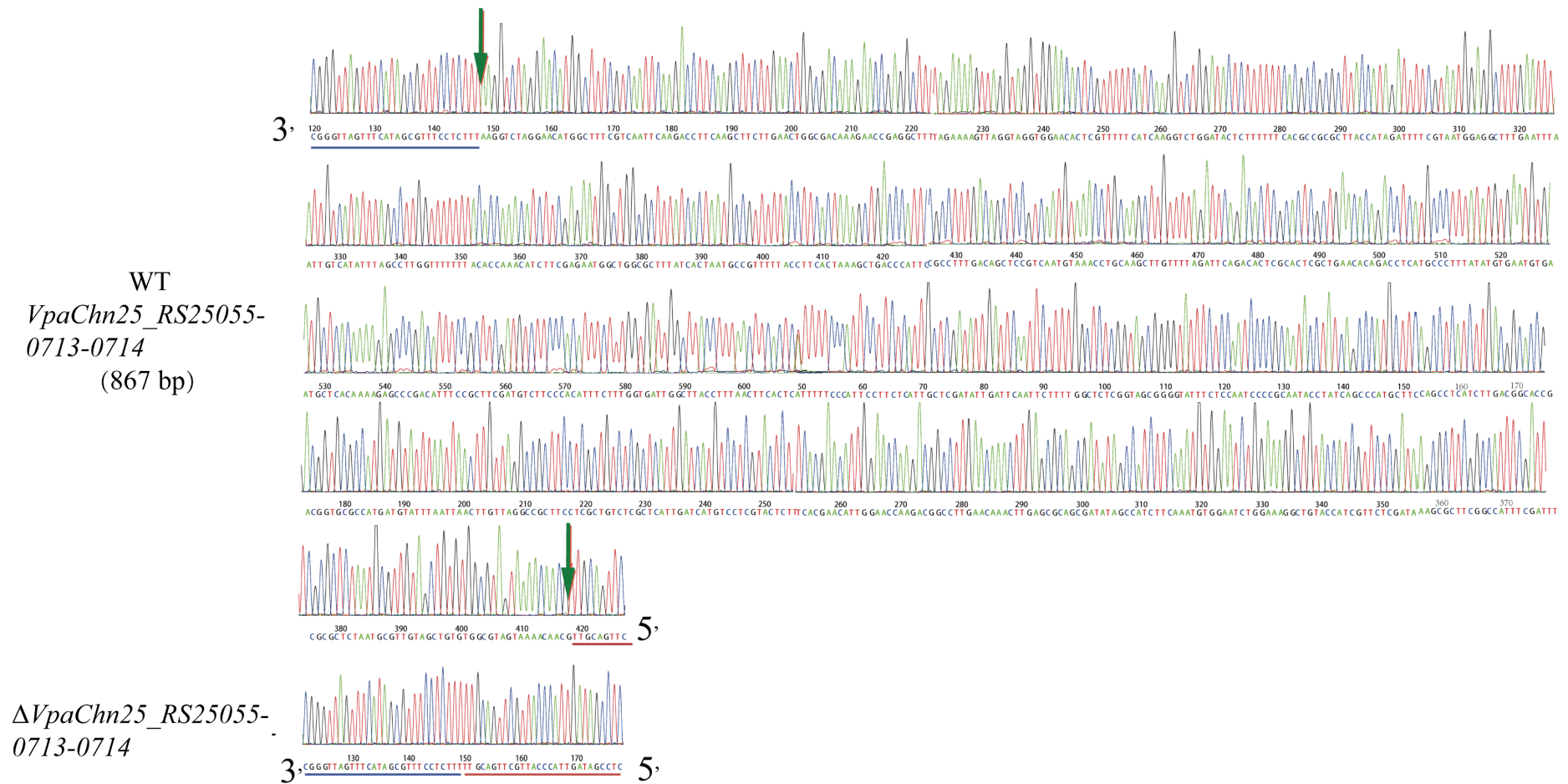


Figure S5. DNA sequencing chromatographs and schematic drawings of the *V. parahaemolyticus* CHN25 WT and $\Delta VpaChn25_{0713}$, $\Delta VpaChn25_{RS25055}$, $\Delta VpaChn25_{0714}$, and $\Delta VpaChn25_{RS25055-0713-0714}$ mutants, respectively. The sequence between the two arrows represents the corresponding prophage gene base sequence

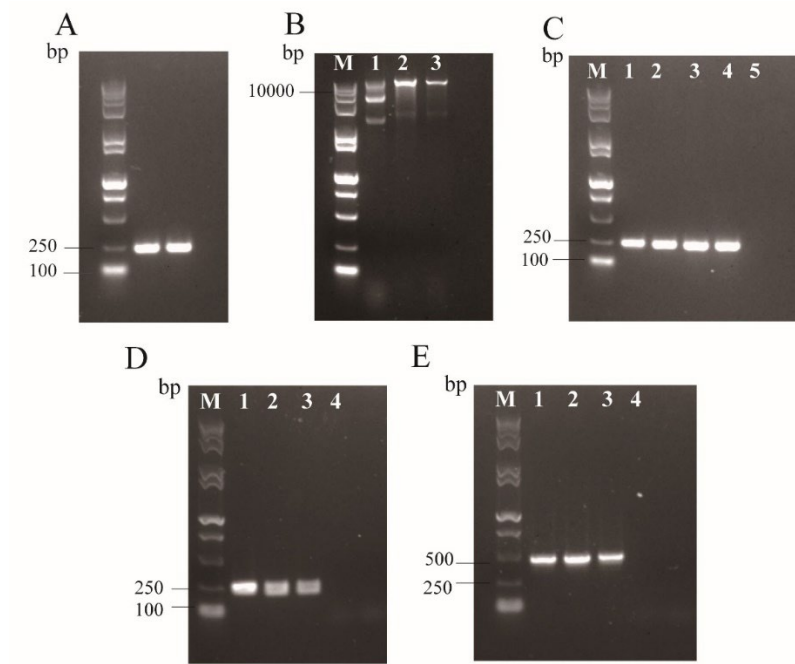


Figure S6. Construction of the $\Delta VpaChn25_0713$ -com by agarose gel electrophoresis analysis.

(A) Amplicons of the *VpaChn25_0713* gene. M, D15000+2000 Ladder; Lines 1–2, positive bands; Line 3, blank control. (B) High-level expression vector pMMB207 plasmid DNA and its double digestion results. M, D15000+2000 Ladder. (C) Double digestion of the recombinant pMMB207+*VpaChn25_0713* plasmid. M, D15000+2000 Ladder. (D) Amplicons of *VpaChn25_0713* from positive transformants. M, D15000+2000 Ladder. (E) Amplicons of *tllh* from $\Delta VpaChn25_0713$ -com mutants. M, D15000+2000 Ladder.

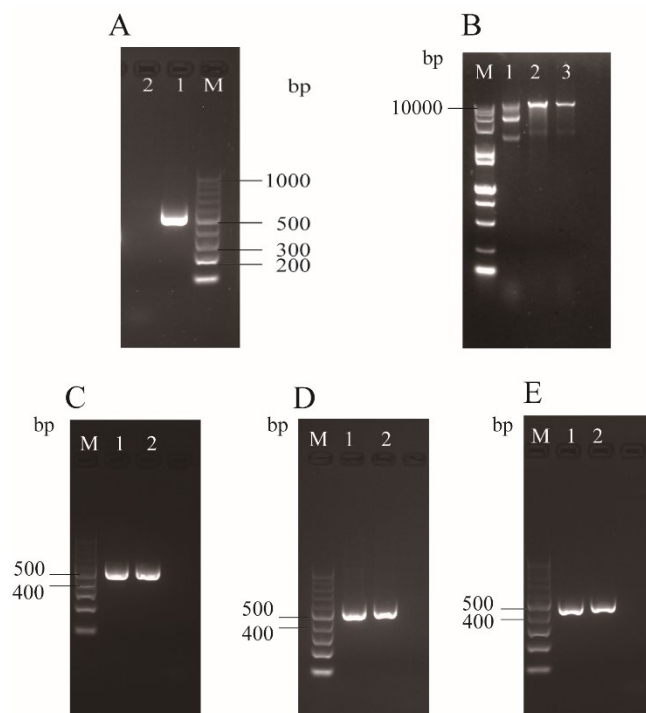


Figure S7. Construction of the $\Delta VpaChn25_0714$ -com by agarose gel electrophoresis analysis.

(A) Amplicons of the *VpaChn25_0714* gene. M, 100 bp DNA Ladder; Lines 1, positive bands; Line 2, blank control. (B) High level expression vector pMMB207 plasmid DNA and its double digestion results. M, D15000+2000 Ladder. (C) Double digestion of the recombinant pMMB207+*VpaChn25_0714* plasmid. M, 100 bp DNA Ladder. (D) Amplicons of *VpaChn25_0714* from positive transformants. M, 100 bp DNA Ladder. (E) Amplicons of *tlh* from $\Delta VpaChn25_0714$ -com mutants. M, 100 bp DNA Ladder.

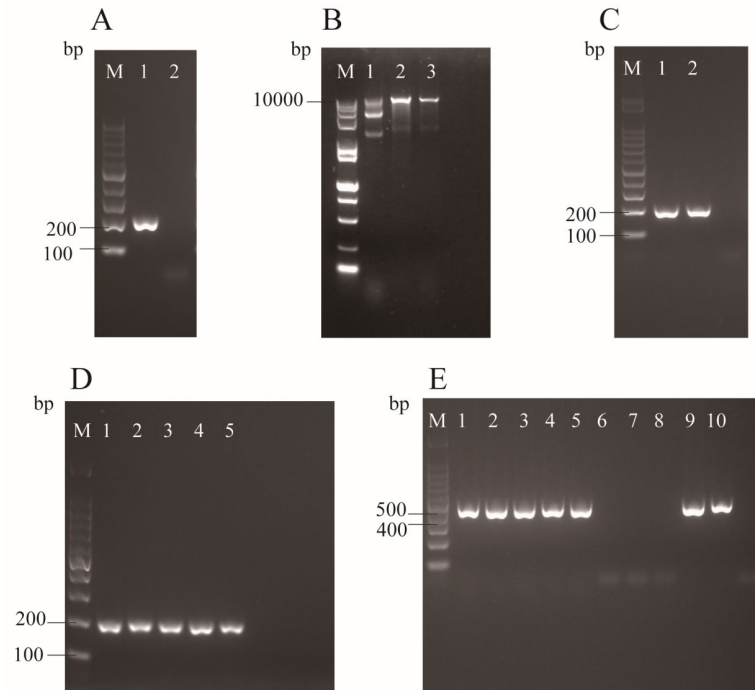


Figure S8. Construction of the $\Delta VpaChn25_RS25055$ -com by agarose gel electrophoresis analysis.

(A) Amplicons of the *VpaChn25_RS25055* gene. M, 100 bp DNA Ladder; Lines 1, positive bands; Line 2, blank control. (B) High level expression vector pMMB207 plasmid DNA and its double digestion results. M, D15000+2000 Ladder. (C) Double digestion of the recombinant pMMB207+*VpaChn25_RS25055* plasmid. M, 100 bp DNA Ladder. (D) Amplicons of *VpaChn25_RS25055* from positive transformants. M, 100 bp DNA Ladder. (E) Amplicons of *tlh* from $\Delta VpaChn25_RS25055$ -com mutants. M, 100 bp DNA Ladder.

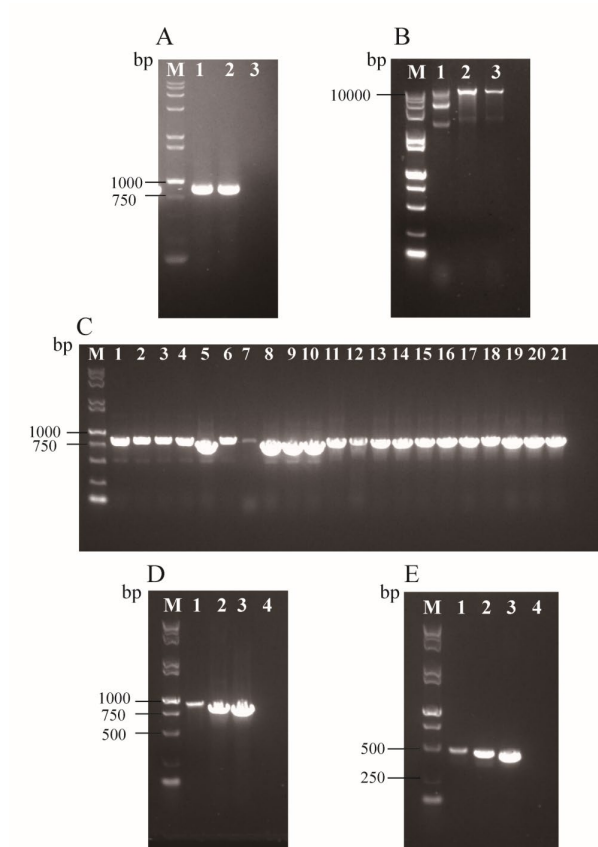


Figure S9. Construction of the $\Delta VpaChn25_RS25055-0713-0714$ -com by agarose gel electrophoresis analysis.

(A) Amplicons of the *VpaChn25_RS25055-0713-0714* gene. M, D15000+2000 Ladder; Lines 1, positive bands; Line 2, blank control. (B) High level expression vector pMMB207 plasmid DNA and its double digestion results. M, D15000+2000 Ladder. (C) Double digestion of the recombinant pMMB207+*VpaChn25_RS25055-0713-0714* plasmid. M, D15000+2000 Ladder. (D) Amplicons of *VpaChn25_RS25055-0713-0714* from positive transformants. M, D15000+2000 Ladder. (E) Amplicons of *tlh* from $\Delta VpaChn25_RS25055-0713-0714$ -com mutants. M, D15000+2000 Ladder

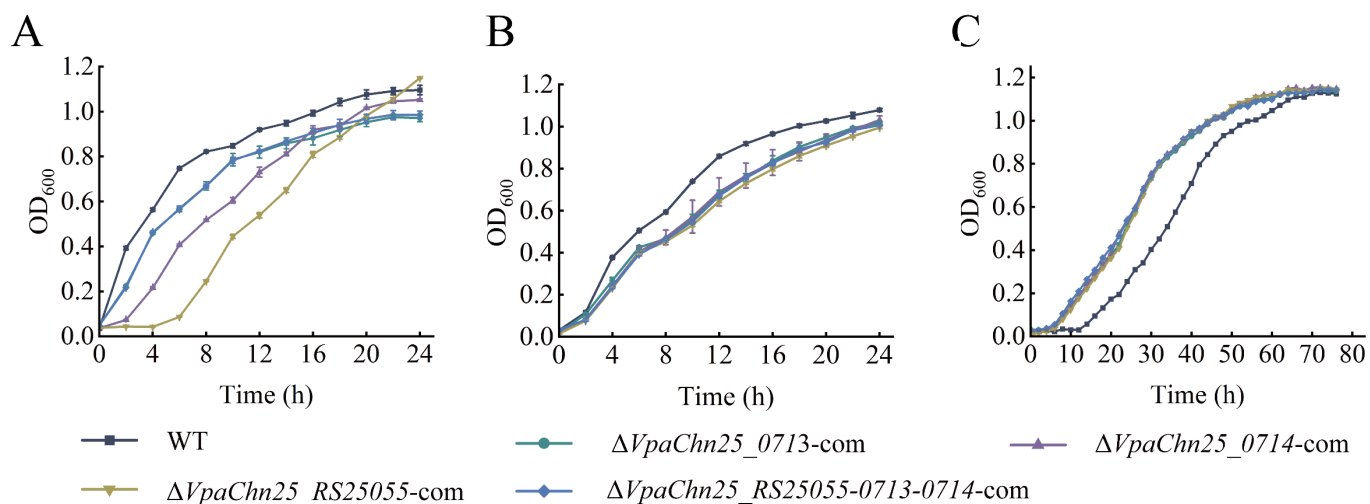


Figure S10. Survival of the *V. parahaemolyticus* CHN25 (WT), $\Delta VpaChn25_RS25055-com$, $\Delta VpaChn25_0713-com$, $\Delta VpaChn25_0714-com$, and $\Delta VpaChn25_RS25055-0713-0714-com$ strains at different temperatures. The strains were individually incubated in the TSB medium (pH 8.5, 3% NaCl) at 37 °C (A), 25 °C (B), and 15 °C (C), respectively.

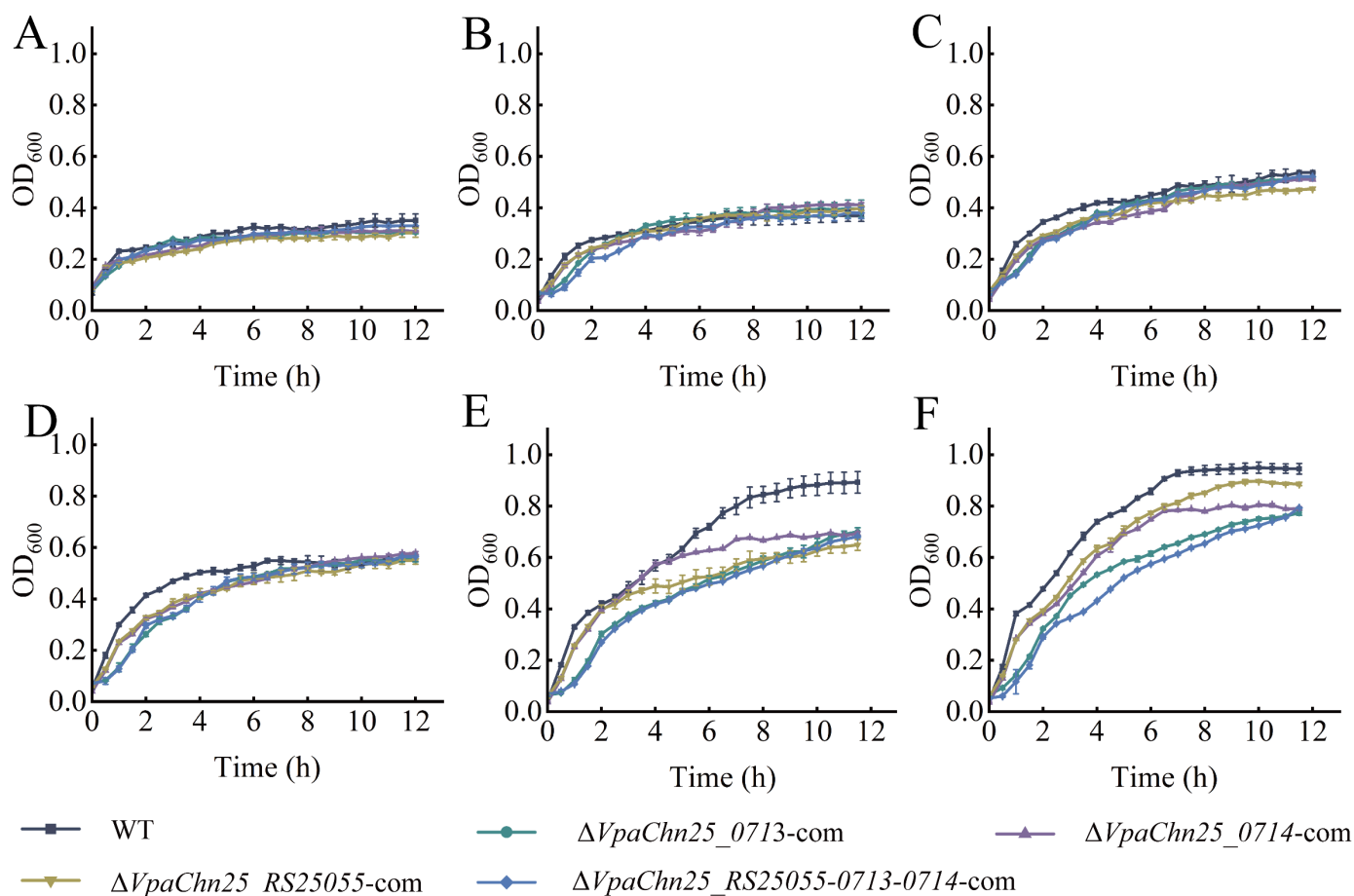


Figure S11. Survival of the *V. parahaemolyticus* CHN25 WT, $\Delta VpaChn25_RS25055-com$, $\Delta VpaChn25_0713-com$, $\Delta VpaChn25_0714-com$, $\Delta VpaChn25_RS25055-0713-0714-com$ strains at different pH conditions. The strains were individually incubated in the TSB medium (pH 8.5, 3% NaCl) at pH 5.5 (A), pH 6.0 (B), pH 6.5 (C), pH 7.0 (D), pH 7.5 (E), and pH 8.0 (F), respectively.

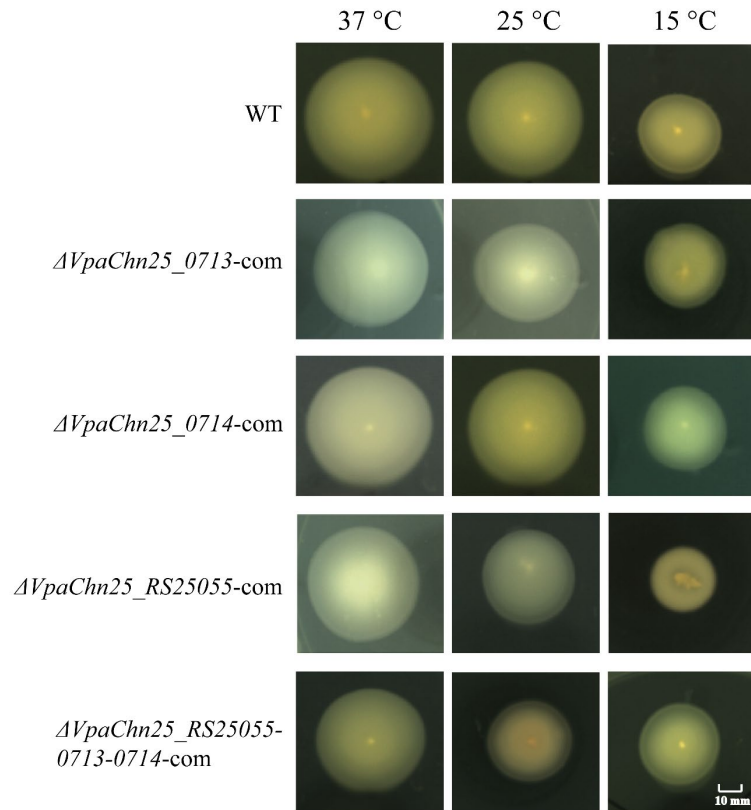


Figure S12 Swimming motility of the *V. parahaemolyticus* CHN25 WT, *ΔVpaChn25_RS25055-com*, *ΔVpaChn25_0713-com*, *ΔVpaChn25_0714-com*, *ΔVpaChn25_RS25055-0713-0714-com* strains at different temperatures. The strains were individually incubated in a semi-solid TSB medium containing 0.25% agar at 37 °C, 25 °C, and 15 °C, respectively.

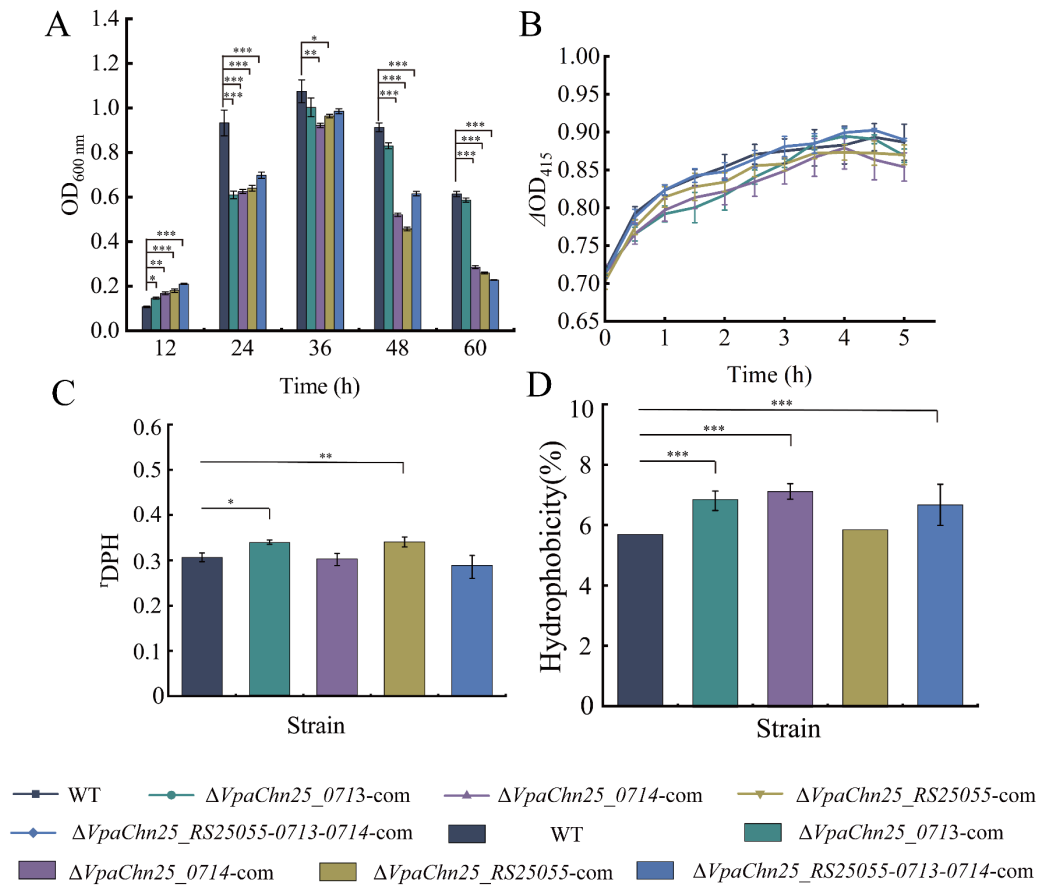


Figure S13. Biofilm formation (A), internal membrane permeability (B), fluidity (C), and hydrophobicity (D) of the *V. parahaemolyticus* CHN25 (WT), $\Delta VpaChn25_RS25055$ -com, $\Delta VpaChn25_0713$ -com, $\Delta VpaChn25_0714$ -com, $\Delta VpaChn25_RS25055$ -0713-0714-com strains. DPH: 1, 6-diphenyl-1,3,5-hexatriene. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

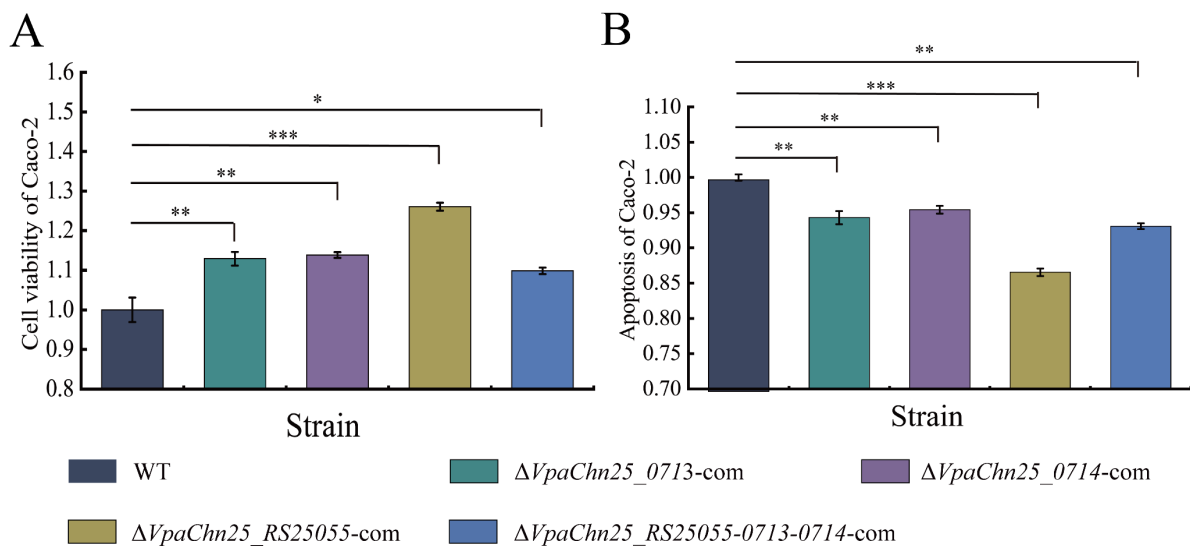


Figure S14. The viability and apoptosis of Caco-2 cells infected by the *V. parahaemolyticus* CHN25 WT, $\Delta VpaChn25_RS25055$ -com, $\Delta VpaChn25_0713$ -com, $\Delta VpaChn25_0714$ -com, and $\Delta VpaChn25_RS25055$ -0713-0714-com strains. The infection was performed at 37 °C for 4 h. (A) Cell viability; (B) cell apoptosis. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

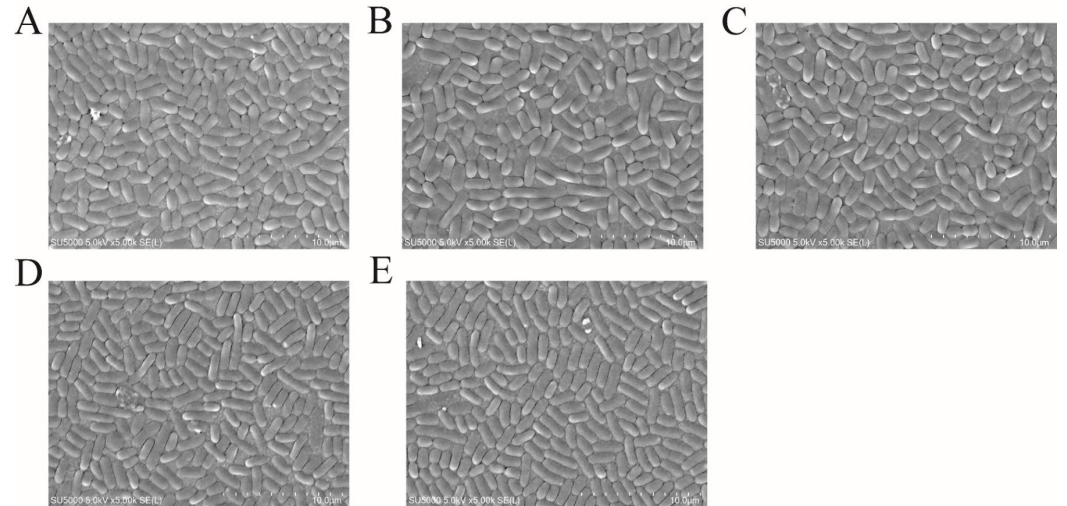


Figure S15. The SEM observation of cell structure of the *V. parahaemolyticus* CHN25 (WT), $\Delta VpaChn25_RS25055$ -com, $\Delta VpaChn25_0713$ -com, $\Delta VpaChn25_0714$ -com, and $\Delta VpaChn25_RS25055$ -0713-0714-com strains. (A) WT; (B) $\Delta VpaChn25_0713$ -com; (C) $\Delta VpaChn25_0714$ -com; (D) $\Delta VpaChn25_RS25055$ -com; (E) $\Delta VpaChn25_RS25055$ -0713-0714-com.

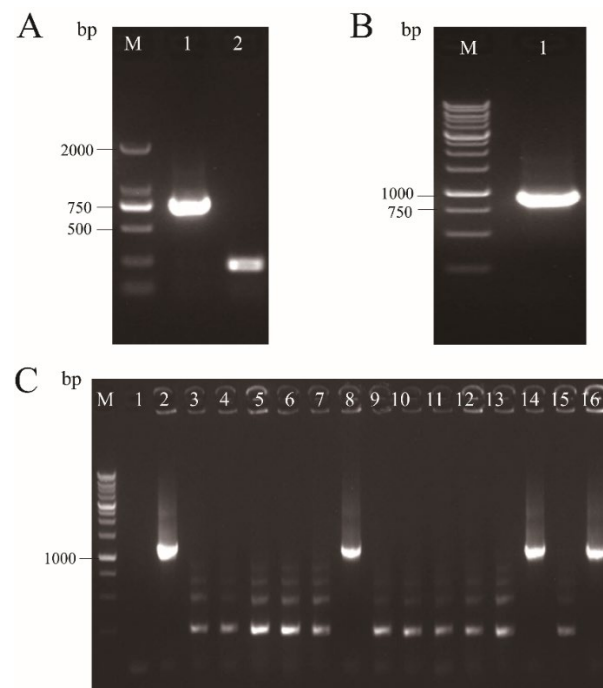


Figure S16. Construction of the $\Delta VpaChn25_RS25055$ (pMMB207+*VpaChn25_RS25055*-sfGFP) by agarose gel electrophoresis analysis.

(A) Amplicons of the *VpaChn25_RS25055* and sfGFP genes. M, 2000 bp DNA Ladder; Lines 1, sfGFP; Line 2, *VpaChn25_RS25055*. (B) PCR fusion product of *VpaChn25_RS25055* and sfGFP genes. M, DL 1000 bp DNA Ladder. (C) Ligation of the high expression vector pMMB207 and *VpaChn25_RS25055*+sfGFP. M, DL 1000 bp DNA Ladder; Line 1–15, amplification results of clones 1–15.

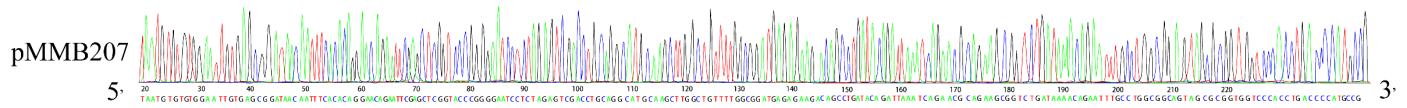


Figure S17. DNA sequencing chromatographs and schematic drawings of $\Delta VpaChn25_RS25055$ (pMMB207)

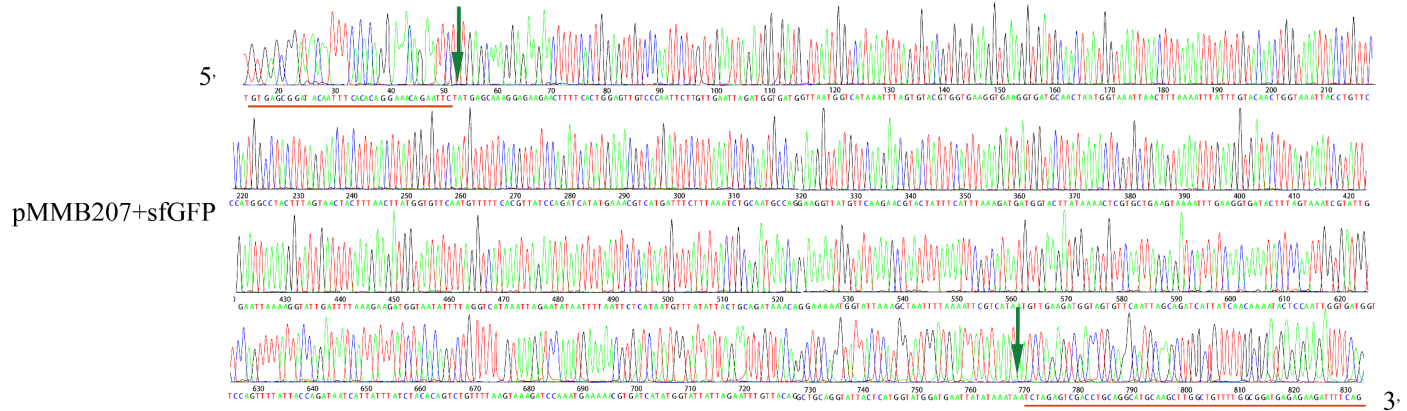


Figure S18. DNA sequencing chromatographs and schematic drawings of $\Delta VpaChn25_RS25055$ (pMMB207+ sfGFP). The sequence between the two green arrows represents sfGFP.

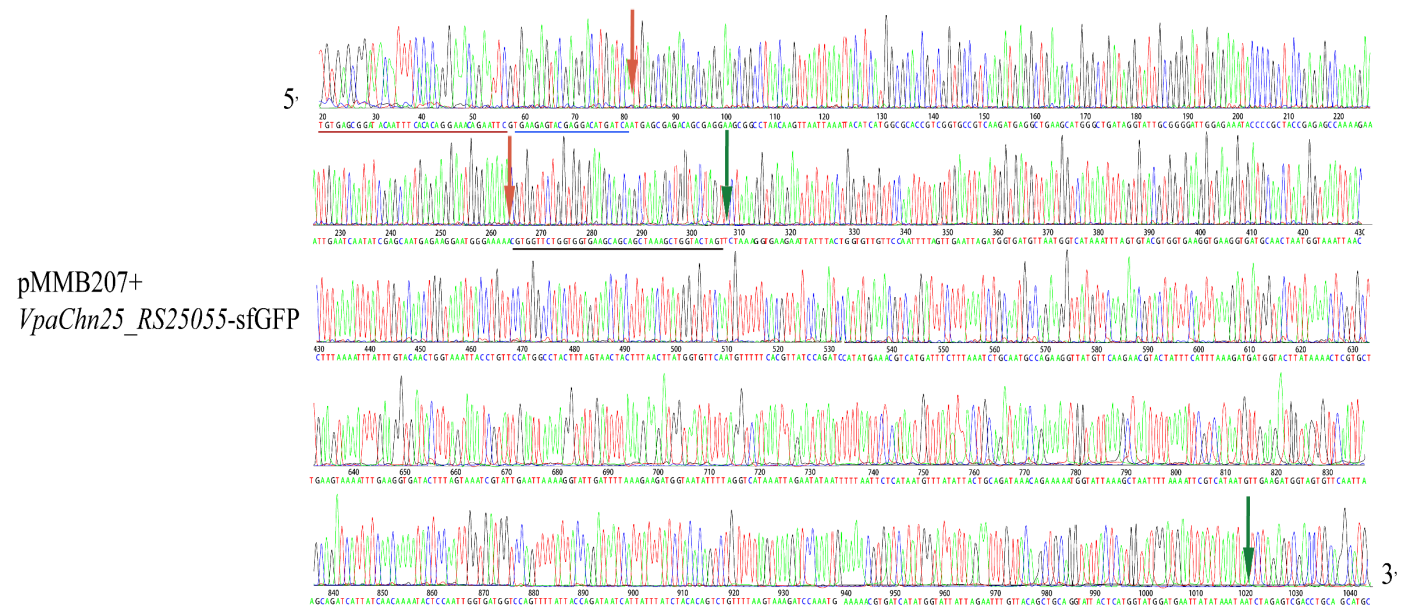


Figure S19. DNA sequencing chromatographs and schematic drawings of $\Delta VpaChn25_RS25055$ (pMMB207+*VpaChn25_RS25055*-sfGFP). The sequence between two red arrows represents *VpaChn25_RS25055* and the sequence between two green arrows represents sfGFP.

Table S1. Oligonucleotide primers used in RT-PCR assay

	Primer	Sequence(5'-3')	Product size (bp)
Δ VpaChn25_0713	VpaChn25_RS05195-F	GCACTAAACGCAATCCACT	283
	VpaChn25_RS05195-R	TGCCCATAAATACAGAAACA	
	VpaChn25_RS11110-F	AACCTAGAAAGGCCGAATG	229
	VpaChn25_RS11110-R	CACGAAATCCAAGACTGCT	
	VpaChn25_RS23525-F	CCAGCAGACTTCACATTCCG	196
	VpaChn25_RS23525-R	TGATGTTGCCTGTTTGGTC	
	VpaChn25_RS22165-F	ACAGTGGCTCACCCAGACG	232
	VpaChn25_RS22165-R	GGGACTCAACCGCAACAGG	
	VpaChn25_RS21450-F	AATCAAGCGAAATCAAAGAG	201
	VpaChn25_RS21450-R	AAGCGTTAAGCATCCACAT	
	VpaChn25_RS23335-F	GTGGTATGGACGGAAGCAA	243
	VpaChn25_RS23335-R	GAACCCAAGCGAAAGAAAC	
Δ VpaChn25_0714	VpaChn25_RS10475-F	TACTTCCGTCGTGGTAGCC	210
	VpaChn25_RS10475-R	CATTTGAGCCGCACCTTTT	
	VpaChn25_RS15965-F	CGCCAACGGAGTTCGGTAA	182
	VpaChn25_RS15965-R	CGCCAGCATCGCAATCTTT	
	VpaChn25_RS05195-F	GCACTAAACGCAATCCACT	283
	VpaChn25_RS05195-R	TGCCCATAAATACAGAAACA	
	VpaChn25_RS11110-F	AACCTAGAAAGGCCGAATG	229
	VpaChn25_RS11110-R	CACGAAATCCAAGACTGCT	
	VpaChn25_RS10585-F	CGTATCGGTCGTTTCGTAT	226
	VpaChn25_RS10585-R	CGTCCCATTAAAGGTCAGC	
	VpaChn25_RS00065-F	CCCAAAGAGTCAGAGTTATT	122
	VpaChn25_RS00065-R	CAACCGTCAAGCCAGTAAG	
Δ VpaChn25_RS25055	VpaChn25_RS02420-F	AACGACGAACTACTAAACTC	256
	VpaChn25_RS02420-R	TAACCAGAAACACGGATTG	
	VpaChn25_RS00565-F	CTTCTATCCGTATCCCAGTG	119
	VpaChn25_RS00565-R	GTCAAGACCAGCCATCAGT	
	VpaChn25_RS18370-F	TCAACATGATGGGAACTGG	106
	VpaChn25_RS18370-R	TAGCGTCTGCTGATAGTAGGA	
	VpaChn25_RS11110-F	AACCTAGAAAGGCCGAATG	229
	VpaChn25_RS11110-R	CACGAAATCCAAGACTGCT	
	VpaChn25_RS05045-F	GCCTACACTTCGCTCCAAT	178
	VpaChn25_RS05045-R	CGCTTCACAACACGACCAG	
	VpaChn25_RS11070-F	AGCGTTTGTCTTCGGGTTA	295
	VpaChn25_RS11070-R	TCAGCGATACGGTTTAGTT	
Δ VpaChn25_RS25055-0713-0714	VpaChn25_RS01880-F	GAATCGCAAACGGATACAG	207
	VpaChn25_RS01880-R	CACCAAAACCGATCACGATTGGGCT	
	VpaChn25_RS01875-F	CATCCCTACGGAAGTTATT	125
	VpaChn25_RS01875-R	TGCTACCGCTGTCTATCAC	
	VpaChn25_RS05195-F	GCACTAAACGCAATCCACT	283
	VpaChn25_RS05195-R	TGCCCATAAATACAGAAACA	

<i>VpaChn25_RS11110</i> -F	AACCTAGAAAGGCCGAATG	229
<i>VpaChn25_RS11110</i> -R	CACGAAATCCAAGACTGCT	
<i>VpaChn25_RS16665</i> -F	GTTACTGTAGATGCGAAAGG	121
<i>VpaChn25_RS16665</i> -R	CAACAACAAGACGACCAAG	
<i>VpaChn25_RS22165</i> -F	ACAGTGGCTCACCCAGACG	232
<i>VpaChn25_RS22165</i> -R	GGGACTCAACCGCAACAGG	

Table S2. Expression of representative DEGs in $\Delta VpaChn25_0713$, $\Delta VpaChn25_0714$, $\Delta VpaChn25_RS25055$, and $\Delta VpaChn25_RS25055$ -0713-0714 mutants by the RT-PCR assay.

strain	Gene	Predicted protein	Fold change	
			RNA-Seq.	RT-PCR
$\Delta VpaChn25_0713$	<i>VpaChn25_RS05195</i>	formate C-acetyltransferase	0.162	0.306
	<i>VpaChn25_RS11110</i>	helix-turn-helix domain-containing protein	0.194	0.113
	<i>VpaChn25_RS23525</i>	alkyl hydroperoxide reductase subunit C	0.262	0.475
	<i>VpaChn25_RS22165</i>	maltose/maltodextrin ABC transporter	4.423	2.156
	<i>VpaChn25_RS21450</i>	DNA starvation/stationary phase protection	0.412	0.578
	<i>VpaChn25_RS23335</i>	maltoporin	3.497	2.986
$\Delta VpaChn25_0714$	<i>VpaChn25_RS10475</i>	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	0.396	0.478
	<i>VpaChn25_RS15965</i>	DUF3081 domain-containing protein	2.462	3.579
	<i>VpaChn25_RS05195</i>	formate C-acetyltransferase	0.172	0.223
	<i>VpaChn25_RS11110</i>	helix-turn-helix domain-containing protein	0.246	0.378
	<i>VpaChn25_RS10585</i>	type I glyceraldehyde-3-phosphate dehydrogenase	0.285	0.872
	<i>VpaChn25_RS00065</i>	hypothetical protein	2.679	1.689
$\Delta VpaChn25_RS25055$	<i>VpaChn25_RS02420</i>	autonomous glycyl radical cofactor GrcA	0.444	0.372
	<i>VpaChn25_RS00565</i>	glutamate--ammonia ligase	6.026	4.358
	<i>VpaChn25_RS18370</i>	hypothetical protein	2.786	2.323
	<i>VpaChn25_RS11110</i>	helix-turn-helix domain-containing protein	0.188	0.372
	<i>VpaChn25_RS05045</i>	uridine phosphorylase	0.317	0.742
	<i>VpaChn25_RS11070</i>	flagellin	0.396	0.562
$\Delta VpaChn25_RS25055$ - 0713-0714	<i>VpaChn25_RS01880</i>	glutamine-fructose-6-phosphate transaminase (isomerizing)	0.237	0.676
	<i>VpaChn25_RS01875</i>	DeoR family transcriptional regulator	0.237	0.242
	<i>VpaChn25_RS05195</i>	formate C-acetyltransferase	0.055	0.469
	<i>VpaChn25_RS11110</i>	helix-turn-helix domain-containing protein	0.129	0.187
	<i>VpaChn25_RS16665</i>	porin	3.477	4.552
	<i>VpaChn25_RS22165</i>	maltose/maltodextrin ABC transporter substrate-binding protein MalE	7.184	8.135

Table S3. Major changed metabolic pathways in the $\Delta VpaChn25_0713$ mutant.

Metabolism Pathway	Gene ID	Fold Change	Gene Description
Phosphotransferase system	<i>VpaChn25_RS19520</i>	0.057	PTS fructose transporter subunit IIBC
	<i>VpaChn25_RS19525</i>	0.080	1-phosphofructokinase
	<i>VpaChn25_RS19530</i>	0.136	Fused PTS fructose transporter subunit IIA/HPr protein
	<i>VpaChn25_RS16970</i>	0.173	PTS sugar transporter subunit IIB
	<i>VpaChn25_RS21735</i>	0.180	PTS sugar transporter subunit IIA

	<i>VpaChn25_RS01935</i>	0.357	PTS mannitol transporter subunit IICBA
	<i>VpaChn25_RS13465</i>	0.370	PTS lactose/cellobiose transporter subunit IIA
	<i>VpaChn25_RS21730</i>	0.451	PTS mannitol transporter subunit IICB
	<i>VpaChn25_RS16965</i>	0.491	PTS ascorbate transporter subunit IIC
	<i>VpaChn25_RS13470</i>	2.022	PTS sugar transporter subunit IIC
	<i>VpaChn25_RS01915</i>	2.370	Phosphoenolpyruvate-protein phosphotransferase
	<i>VpaChn25_RS23450</i>	4.023	Glucose-specific PTS transporter subunit IIBC
Glycolysis/Gluconeogenesis	<i>VpaChn25_RS10585</i>	0.203	Type I glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS10590</i>	0.269	D-hexose-6-phosphate mutarotase
	<i>VpaChn25_RS10475</i>	0.306	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>VpaChn25_RS19575</i>	0.421	Pyruvate kinase
	<i>VpaChn25_RS23575</i>	0.454	6-phospho- β -glucosidase
	<i>VpaChn25_RS01325</i>	0.492	Triose-phosphate isomerase
	<i>VpaChn25_RS17630</i>	0.494	Phosphoenolpyruvate synthase
	<i>VpaChn25_RS00605</i>	2.174	Phosphoenolpyruvate carboxykinase (ATP)
	<i>VpaChn25_RS18050</i>	2.971	Glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS08880</i>	4.278	Aldehyde dehydrogenase
Glycerolipid metabolism	<i>VpaChn25_RS16340</i>	2.077	Glycerate kinase
	<i>VpaChn25_RS01910</i>	2.225	Dihydroxyacetone kinase ADP-binding subunit DhaL
	<i>VpaChn25_RS01905</i>	2.231	Dihydroxyacetone kinase subunit DhaK
	<i>VpaChn25_RS06325</i>	2.240	Triacylglycerol lipase
	<i>VpaChn25_RS01900</i>	3.040	Glycerol dehydrogenase
	<i>VpaChn25_RS17910</i>	3.844	Diacylglycerol kinase
Sulfur metabolism	<i>VpaChn25_RS07520</i>	0.150	Dimethylsulfoxide reductase subunit B
	<i>VpaChn25_RS07525</i>	0.172	Dimethyl sulfoxide reductase anchor subunit
	<i>VpaChn25_RS07515</i>	0.211	Dimethyl sulfoxide reductase subunit A
	<i>VpaChn25_RS01595</i>	0.228	Adenylyl-sulfate kinase
	<i>VpaChn25_RS01585</i>	0.358	Sulfate adenylyltransferase subunit CysN
	<i>VpaChn25_RS07355</i>	0.497	Homoserine O-succinyltransferase
	<i>VpaChn25_RS04200</i>	0.498	Cysteine synthase A
	<i>VpaChn25_RS13920</i>	0.499	Phosphoadenylyl-sulfate reductase
Mannose and fructose metabolism	<i>VpaChn25_RS22285</i>	0.475	Mannose-6-phosphate isomerase, class I
Oxidative phosphorylation	<i>VpaChn25_RS05680</i>	0.266	Cytochrome bd-I oxidase subunit CydX
	<i>VpaChn25_RS20880</i>	0.308	Cytochrome o ubiquinol oxidase subunit IV
	<i>VpaChn25_RS07260</i>	0.493	Manganese-dependent inorganic pyrophosphatase
	<i>VpaChn25_RS21575</i>	2.081	Cytochrome c oxidase subunit II
	<i>VpaChn25_RS21560</i>	2.268	Cytochrome c oxidase subunit 3
	<i>VpaChn25_RS21565</i>	2.276	Cytochrome c oxidase assembly protein
	<i>VpaChn25_RS02145</i>	2.280	Ubiquinol-cytochrome c reductase iron-sulfur subunit
	<i>VpaChn25_RS04445</i>	2.456	Succinate dehydrogenase cytochrome b556 subunit
	<i>VpaChn25_RS04450</i>	2.464	Succinate dehydrogenase, hydrophobic membrane anchor protein
	<i>VpaChn25_RS02155</i>	2.911	Cytochrome c1
	<i>VpaChn25_RS21540</i>	3.411	COX15/CtaA family protein
	<i>VpaChn25_RS02150</i>	4.053	Cytochrome bc complex cytochrome subunit
Histidine metabolism	<i>VpaChn25_RS04675</i>	0.436	Aromatic amino acid ammonia-lyase
	<i>VpaChn25_RS06765</i>	3.843	Histidine ammonia-lyase
	<i>VpaChn25_RS06780</i>	4.142	Imidazolonepropionase
	<i>VpaChn25_RS06770</i>	4.374	Urocanate hydratase
	<i>VpaChn25_RS06775</i>	4.716	Formimidoylglutamase
Nitrogen metabolism	<i>VpaChn25_RS02355</i>	0.096	Glutamate synthase subunit β
	<i>VpaChn25_RS02360</i>	0.112	Glutamate synthase large subunit
	<i>VpaChn25_RS20680</i>	0.231	ABC transporter ATP-binding protein
	<i>VpaChn25_RS16925</i>	0.362	Carbonic anhydrase family protein
	<i>VpaChn25_RS02345</i>	0.473	FAD-dependent oxidoreductase
	<i>VpaChn25_RS22655</i>	0.481	Carbonic anhydrase
	<i>VpaChn25_RS09500</i>	3.477	Ammonia-forming nitrite reductase cytochrome c552 subunit
Amino sugar and nucleotide sugar	<i>VpaChn25_RS21110</i>	0.001	UDP-glucose 4-epimerase GalE

metabolism	<i>VpaChn25_RS21105</i>	0.001	UDP-glucose-hexose-1-phosphate uridylyltransferase
	<i>VpaChn25_RS21100</i>	0.001	Galactokinase
	<i>VpaChn25_RS23815</i>	0.164	N-acetylmuramic acid 6-phosphate etherase
	<i>VpaChn25_RS07740</i>	2.008	N-acetylglucosamine kinase
	<i>VpaChn25_RS10005</i>	2.279	NAD-dependent epimerase
	<i>VpaChn25_RS12610</i>	3.364	N, N'-diacetylchitobiose phosphorylase
	<i>VpaChn25_RS12600</i>	3.554	N-acetylglucosamine kinase
	<i>VpaChn25_RS12605</i>	5.481	Family 20 glycosylhydrolase
Nitrotoluene degradation	<i>VpaChn25_RS21015</i>	0.009	Alkene reductase
	<i>VpaChn25_RS21020</i>	0.021	Alkene reductase
	<i>VpaChn25_RS23085</i>	0.274	Oxygen-insensitive NAD(P)H nitroreductase
Taurine and hypotaurine metabolism	<i>VpaChn25_RS15390</i>	2.136	γ -glutamyltransferase
Propanoate metabolism	<i>VpaChn25_RS21225</i>	0.216	Acetate/propionate family kinase
	<i>VpaChn25_RS10295</i>	0.418	Phosphate acetyltransferase
	<i>VpaChn25_RS20810</i>	2.677	Pyruvate dehydrogenase (acetyl-transferring) E1 component subunit α
	<i>VpaChn25_RS20820</i>	2.715	2-oxo acid dehydrogenase subunit E2
	<i>VpaChn25_RS20815</i>	3.263	α -ketoacid dehydrogenase subunit β
Pyruvate metabolism	<i>VpaChn25_RS05195</i>	0.162	Formate C-acetyltransferase
	<i>VpaChn25_RS14110</i>	0.342	Phosphoenolpyruvate carboxylase
	<i>VpaChn25_RS19425</i>	0.377	Acetyl-CoA carboxylase, carboxyltransferase subunit β
	<i>VpaChn25_RS12745</i>	0.379	Pyruvate dehydrogenase complex dihydrolipoyllysine-residue acetyltransferase
	<i>VpaChn25_RS18565</i>	0.421	Thiolase family protein
Longevity regulating pathway	<i>VpaChn25_RS14590</i>	0.155	Chaperonin GroEL
	<i>VpaChn25_RS03265</i>	0.269	Molecular chaperone DnaK
	<i>VpaChn25_RS17350</i>	0.433	Catalase
	<i>VpaChn25_RS17235</i>	0.455	Chaperonin GroEL

Table S4. Major changed metabolic pathways in the $\Delta VpaChn25_0714$ mutant.

Metabolism Pathway	Gene ID	Fold Change	Gene Description
Propanoate metabolism	<i>VpaChn25_RS21225</i>	0.233	Acetate/propionate family kinase
	<i>VpaChn25_RS07255</i>	0.312	4-aminobutyrate-2-oxoglutarate transaminase
	<i>VpaChn25_RS18570</i>	0.373	CoA-acylating methylmalonate-semialdehyde dehydrogenase
	<i>VpaChn25_RS10295</i>	0.433	Phosphate acetyltransferase
	<i>VpaChn25_RS19605</i>	0.435	Iron-containing alcohol dehydrogenase
	<i>VpaChn25_RS04475</i>	2.019	ADP-forming succinate-CoA ligase subunit β
Mannose and fructose metabolism	<i>VpaChn25_RS19525</i>	0.080	1-phosphofructokinase
	<i>VpaChn25_RS21725</i>	0.426	Zinc-binding dehydrogenase
	<i>VpaChn25_RS20215</i>	3.217	Mannose-6-phosphate isomerase, class I
Nitrotoluene degradation	<i>VpaChn25_RS17690</i>	0.325	Alkene reductase
	<i>VpaChn25_RS18635</i>	0.374	NAD(P)H-dependent oxidoreductase
	<i>VpaChn25_RS23085</i>	0.416	Oxygen-insensitive NAD(P)H nitroreductase
	<i>VpaChn25_RS19315</i>	0.439	Alkene reductase
Phosphotransferase system (PTS)	<i>VpaChn25_RS19520</i>	0.047	PTS fructose transporter subunit IIBC
	<i>VpaChn25_RS19530</i>	0.134	Fused PTS fructose transporter subunit IIA / HPr protein
	<i>VpaChn25_RS17315</i>	0.187	PTS sugar transporter subunit IIA
	<i>VpaChn25_RS21730</i>	0.265	PTS mannitol transporter subunit IICB
	<i>VpaChn25_RS16970</i>	0.343	PTS sugar transporter subunit IIB
	<i>VpaChn25_RS16965</i>	0.351	PTS ascorbate transporter subunit IIC
	<i>VpaChn25_RS21735</i>	0.357	PTS sugar transporter subunit IIA

	<i>VpaChn25_RS23820</i>	0.496	PTS N-acetylmuramic acid transporter subunit IIBC
	<i>VpaChn25_RS23450</i>	2.823	Glucose-specific PTS transporter subunit IIBC
Lysine degradation	<i>VpaChn25_RS14795</i>	0.052	Lysine decarboxylase CadA
	<i>VpaChn25_RS07250</i>	0.205	NAD-dependent succinate-semialdehyde Dehydrogenase
Glycolysis/Gluconeogenesis	<i>VpaChn25_RS10590</i>	0.228	D-hexose-6-phosphate mutarotase
	<i>VpaChn25_RS23575</i>	0.237	6-phospho- β -glucosidase
	<i>VpaChn25_RS10585</i>	0.285	Type I glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS10475</i>	0.396	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>VpaChn25_RS19575</i>	0.406	Pyruvate kinase
	<i>VpaChn25_RS01325</i>	0.483	Triose-phosphate isomerase
	<i>VpaChn25_RS00605</i>	2.022	Phosphoenolpyruvate carboxykinase (ATP)
	<i>VpaChn25_RS08880</i>	2.211	Aldehyde dehydrogenase
Benzoate degradation	<i>VpaChn25_RS18050</i>	2.964	Glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS18485</i>	0.463	Carboxymuconolactone decarboxylase family protein
Pyruvate metabolism	<i>VpaChn25_RS19425</i>	0.166	Acetyl-CoA carboxylase, carboxyltransferase subunit β
	<i>VpaChn25_RS05195</i>	0.172	Formate C-acetyltransferase
	<i>VpaChn25_RS19320</i>	0.298	Lactoylglutathione lyase
	<i>VpaChn25_RS01820</i>	0.405	2-isopropylmalate synthase
	<i>VpaChn25_RS14110</i>	0.490	Phosphoenolpyruvate carboxylase
	<i>VpaChn25_RS18565</i>	0.494	Thiolase family protein
	<i>VpaChn25_RS08505</i>	2.146	Acylphosphatase
	<i>VpaChn25_RS14715</i>	2.204	Acetate-CoA ligase
Ascorbate and aldarate metabolism	<i>VpaChn25_RS07015</i>	0.151	Aldehyde dehydrogenase (NADP ⁺)
	<i>VpaChn25_RS10005</i>	2.710	NAD-dependent epimerase
Butanoate metabolism	<i>VpaChn25_RS17675</i>	0.268	SDR family oxidoreductase
	<i>VpaChn25_RS15645</i>	0.445	Acetolactate synthase 2 catalytic subunit
	<i>VpaChn25_RS18170</i>	2.017	SDR family oxidoreductase
Fatty acid degradation	<i>VpaChn25_RS18430</i>	0.470	Long-chain fatty acid-CoA ligase
	<i>VpaChn25_RS10820</i>	2.100	Fatty acid oxidation complex subunit α FadJ
	<i>VpaChn25_RS10825</i>	2.324	Acetyl-CoA C-acyltransferase FadI
	<i>VpaChn25_RS18175</i>	2.425	Acetyl-CoA C-acetyltransferase
Histidine metabolism	<i>VpaChn25_RS04675</i>	0.307	Aromatic amino acid ammonia-lyase
	<i>VpaChn25_RS06765</i>	3.400	Histidine ammonia-lyase
	<i>VpaChn25_RS06780</i>	3.435	Imidazolonepropionase
	<i>VpaChn25_RS06770</i>	4.504	Urocanate hydratase
	<i>VpaChn25_RS06775</i>	4.629	Formimidoylglutamate
β -lactam resistance	<i>VpaChn25_RS07075</i>	0.119	ATP-binding cassette domain-containing protein
	<i>VpaChn25_RS07085</i>	0.214	ABC transporter permease subunit
	<i>VpaChn25_RS07090</i>	0.306	Oligopeptide ABC transporter permease OppB
	<i>VpaChn25_RS12510</i>	0.357	Porin
	<i>VpaChn25_RS07080</i>	0.417	ATP-binding cassette domain-containing protein
	<i>VpaChn25_RS07095</i>	0.426	Peptide ABC transporter substrate-binding protein
	<i>VpaChn25_RS21835</i>	0.432	Carbenicillin-hydrolyzing class A β -lactamase CARB-18
	<i>VpaChn25_RS18245</i>	0.462	Multidrug efflux RND transporter periplasmic adaptor subunit VmeY

Table S5. Major changed metabolic pathways in the $\Delta VpaChn25_RS25055$ mutant.

Metabolism Pathway	Gene ID	Fold Change	Gene Description
Sulfur metabolism	<i>VpaChn25_RS07520</i>	0.298	Dimethylsulfoxide reductase subunit B
	<i>VpaChn25_RS07525</i>	0.319	Dimethyl sulfoxide reductase anchor subunit
	<i>VpaChn25_RS07515</i>	0.343	Dimethyl sulfoxide reductase subunit A
	<i>VpaChn25_RS04975</i>	0.396	PLP-dependent cysteine synthase family protein
	<i>VpaChn25_RS06515</i>	0.487	C-type cytochrome
	<i>VpaChn25_RS09955</i>	2.050	Polysulfide reductase NrfD
	<i>VpaChn25_RS01585</i>	2.714	Sulfate adenyltransferase subunit CysN

Glyoxylate and dicarboxylate metabolism	<i>VpaChn25_RS01580</i>	3.078	Sulfate adenylyltransferase subunit CysD
	<i>VpaChn25_RS17350</i>	0.436	Catalase
	<i>VpaChn25_RS21805</i>	2.591	Formate dehydrogenase subunit α
	<i>VpaChn25_RS07825</i>	3.661	Formate dehydrogenase FDH3 subunit β
	<i>VpaChn25_RS07820</i>	3.982	Formate dehydrogenase subunit α
Arginine biosynthesis	<i>VpaChn25_RS07830</i>	4.105	Formate dehydrogenase subunit γ
	<i>VpaChn25_RS00565</i>	6.026	Glutamate-ammonia ligase
	<i>VpaChn25_RS11620</i>	0.084	Amino-acid N-acetyltransferase
	<i>VpaChn25_RS14100</i>	0.100	N-acetyl- γ -glutamyl-phosphate reductase
	<i>VpaChn25_RS14095</i>	0.107	Acetylglutamate kinase
Longevity regulating pathway	<i>VpaChn25_RS13555</i>	0.302	Ornithine carbamoyltransferase
	<i>VpaChn25_RS14090</i>	0.305	Argininosuccinate synthase
	<i>VpaChn25_RS14590</i>	0.290	Chaperonin GroEL
	<i>VpaChn25_RS17235</i>	0.313	Chaperonin GroEL
	<i>VpaChn25_RS03265</i>	0.373	Molecular chaperone DnaK
Glycolysis/Gluconeogenesis	<i>VpaChn25_RS20830</i>	0.472	Glutathione S-transferase family protein
	<i>VpaChn25_RS10590</i>	0.215	D-hexose-6-phosphate mutarotase
	<i>VpaChn25_RS10585</i>	0.363	Type I glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS08880</i>	0.368	Aldehyde dehydrogenase
	<i>VpaChn25_RS21435</i>	0.420	L-threonine dehydrogenase
NOD-like receptor signaling pathway	<i>VpaChn25_RS23575</i>	0.426	6-phospho- β -glucosidase
	<i>VpaChn25_RS10475</i>	0.449	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>VpaChn25_RS18050</i>	2.379	Glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS01350</i>	2.553	Class II fructose-bisphosphatase
	<i>VpaChn25_RS04175</i>	0.317	Flagellin
Ribosome	<i>VpaChn25_RS04340</i>	0.389	Molecular chaperone HtpG
	<i>VpaChn25_RS11070</i>	0.396	Flagellin
	<i>VpaChn25_RS11075</i>	0.451	Flagellin
	<i>VpaChn25_RS01405</i>	2.006	50S ribosomal protein L3
	<i>VpaChn25_RS01475</i>	2.016	30S ribosomal protein S8
Monobactam biosynthesis	<i>VpaChn25_RS14000</i>	2.028	30S ribosomal protein S18
	<i>VpaChn25_RS01415</i>	2.052	50S ribosomal protein L23
	<i>VpaChn25_RS01520</i>	2.054	30S ribosomal protein S11
	<i>VpaChn25_RS01465</i>	2.094	50S ribosomal protein L5
	<i>VpaChn25_RS01735</i>	2.100	50S ribosomal protein L21
	<i>VpaChn25_RS02135</i>	2.191	50S ribosomal protein L13
	<i>VpaChn25_RS01450</i>	2.206	30S ribosomal protein S17
	<i>VpaChn25_RS14165</i>	2.253	30S ribosomal protein S7
	<i>VpaChn25_RS01460</i>	2.357	50S ribosomal protein L24
	<i>VpaChn25_RS02140</i>	2.478	30S ribosomal protein S9
	<i>VpaChn25_RS01740</i>	2.705	50S ribosomal protein L27
	<i>VpaChn25_RS02405</i>	0.288	Bifunctional a spartate kinase/homoserine dehydrogenase I
	<i>VpaChn25_RS13865</i>	2.289	Lysine-sensitive a spartokinase 3

Table S6. Major changed metabolic pathways in the $\Delta VpaChn25_RS25055-0713-0714$ mutant.

Metabolism Pathway	Gene ID	Fold Change	Gene Description
Mannose and fructose metabolism	<i>VpaChn25_RS19525</i>	0.095	1-phosphofructokinase
	<i>VpaChn25_RS22285</i>	0.456	Mannose-6-phosphate isomerase, class I
	<i>VpaChn25_RS01930</i>	0.499	Mannitol-1-phosphate 5-dehydrogenase
Propanoate metabolism	<i>VpaChn25_RS05195</i>	0.055	Formate C-acetyltransferase
	<i>VpaChn25_RS21225</i>	0.170	Acetate/propionate family kinase
	<i>VpaChn25_RS10295</i>	0.234	Phosphate acetyltransferase
	<i>VpaChn25_RS10290</i>	0.457	Acetate kinase

	<i>VpaChn25_RS04475</i>	2.407	ADP-forming succinate-CoA ligase subunit β
	<i>VpaChn25_RS20820</i>	2.637	2-oxo acid dehydrogenase subunit E2
	<i>VpaChn25_RS20810</i>	2.744	Pyruvate dehydrogenase (acetyl-transferring) E1 component subunit α
	<i>VpaChn25_RS20815</i>	3.264	α -ketoacid dehydrogenase subunit β
Alanine, aspartate and glutamate metabolism	<i>VpaChn25_RS02355</i>	0.098	Glutamate synthase subunit β
	<i>VpaChn25_RS02360</i>	0.100	Glutamate synthase large subunit
	<i>VpaChn25_RS16990</i>	0.160	Aspartate aminotransferase family protein
	<i>VpaChn25_RS01880</i>	0.237	Glutamine-fructose-6-phosphate transaminase (isomerizing)
	<i>VpaChn25_RS13400</i>	0.476	NAD-dependent succinate-semialdehyde dehydrogenase
	<i>VpaChn25_RS04365</i>	0.480	Asparagine synthase B
	<i>VpaChn25_RS13565</i>	2.013	Aspartate carbamoyltransferase regulatory subunit
	<i>VpaChn25_RS02295</i>	2.104	Carbamoyl-phosphate synthase large subunit
	<i>VpaChn25_RS02290</i>	2.208	Glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit
	<i>VpaChn25_RS17645</i>	2.878	Adenylosuccinate synthase
NOD-like receptor signaling pathway	<i>VpaChn25_RS11075</i>	0.331	Flagellin
	<i>VpaChn25_RS11070</i>	0.340	Flagellin
	<i>VpaChn25_RS04170</i>	0.417	Flagellin
	<i>VpaChn25_RS04340</i>	0.419	Molecular chaperone HtpG
	<i>VpaChn25_RS11085</i>	0.419	Flagellin
	<i>VpaChn25_RS04175</i>	0.425	Flagellin
PTS	<i>VpaChn25_RS19520</i>	0.056	PTS fructose transporter subunit IIBC
	<i>VpaChn25_RS19530</i>	0.122	Fused PTS fructose transporter subunit IIA/HPr protein
	<i>VpaChn25_RS22280</i>	0.162	Fructose-specific PTS transporter subunit EIIC
	<i>VpaChn25_RS17315</i>	0.192	PTS sugar transporter subunit IIA
	<i>VpaChn25_RS21735</i>	0.346	PTS sugar transporter subunit IIA
	<i>VpaChn25_RS21730</i>	0.374	PTS mannitol transporter subunit IICB
	<i>VpaChn25_RS01935</i>	0.392	PTS mannitol transporter subunit IICBA
	<i>VpaChn25_RS04195</i>	0.405	HPr family phosphocarrier protein
	<i>VpaChn25_RS23450</i>	2.104	Glucose-specific PTS transporter subunit IIBC
	<i>VpaChn25_RS13475</i>	2.207	PTS sugar transporter subunit IIB
	<i>VpaChn25_RS13470</i>	2.814	PTS sugar transporter subunit IIC
Amino sugar and nucleotide sugar metabolism	<i>VpaChn25_RS11760</i>	0.427	UDP-glucose 4-epimerase GalE
	<i>VpaChn25_RS11755</i>	0.435	UDP-glucose-hexose-1-phosphate uridylyltransferase
	<i>VpaChn25_RS12480</i>	0.441	Phosphoglucosamine mutase
	<i>VpaChn25_RS21110</i>	0.452	UDP-glucose 4-epimerase GalE
	<i>VpaChn25_RS21100</i>	0.472	Galactokinase
	<i>VpaChn25_RS21105</i>	0.498	UDP-glucose-hexose-1-phosphate uridylyltransferase
	<i>VpaChn25_RS11455</i>	2.100	Ig-like domain-containing protein
	<i>VpaChn25_RS10005</i>	2.435	NAD-dependent epimerase
	<i>VpaChn25_RS12610</i>	3.486	N, N'-diacetylchitobiose phosphorylase
	<i>VpaChn25_RS12600</i>	5.279	N-acetylglucosamine kinase
	<i>VpaChn25_RS12605</i>	5.692	Family 20 glycosylhydrolase
Arginine and proline metabolism	<i>VpaChn25_RS07035</i>	0.189	Ornithine cyclodeaminase family protein
	<i>VpaChn25_RS23295</i>	0.310	Ornithine decarboxylase SpeF
	<i>VpaChn25_RS07215</i>	0.393	Glutamine synthetase family protein
	<i>VpaChn25_RS16685</i>	2.105	Arginine decarboxylase
	<i>VpaChn25_RS09600</i>	2.229	Carboxynorspermidine decarboxylase
	<i>VpaChn25_RS14270</i>	2.285	Succinylglutamate-semialdehyde dehydrogenase
	<i>VpaChn25_RS14275</i>	2.301	Arginine N-succinyltransferase
	<i>VpaChn25_RS09605</i>	2.957	Saccharopine dehydrogenase family protein
	<i>VpaChn25_RS23720</i>	3.110	Bifunctional proline dehydrogenase/L-glutamate γ -semialdehyde dehydrogenase PutA
Oxidative phosphorylation	<i>VpaChn25_RS02155</i>	2.218	Cytochrome c1

	<i>VpaChn25_RS20880</i>	2.544	Cytochrome o ubiquinol oxidase subunit IV
	<i>VpaChn25_RS07945</i>	2.564	CcoQ/FixQ family Cbb3-type cytochrome c oxidase assembly chaperone
	<i>VpaChn25_RS20890</i>	2.569	Cytochrome o ubiquinol oxidase subunit I
	<i>VpaChn25_RS21570</i>	2.638	Cytochrome c oxidase subunit I
	<i>VpaChn25_RS21575</i>	2.724	Cytochrome c oxidase subunit II
	<i>VpaChn25_RS02150</i>	2.740	Cytochrome bc complex cytochrome b subunit
	<i>VpaChn25_RS21535</i>	2.849	Heme o synthase
	<i>VpaChn25_RS21560</i>	2.981	Cytochrome c oxidase subunit 3
	<i>VpaChn25_RS21540</i>	3.028	COX15/CtaA family protein
	<i>VpaChn25_RS20875</i>	3.328	Heme o synthase
	<i>VpaChn25_RS20885</i>	4.543	Cytochrome o ubiquinol oxidase subunit III
	<i>VpaChn25_RS21565</i>	5.684	Cytochrome c oxidase assembly protein
Glycolysis/Gluconeogenesis	<i>VpaChn25_RS10590</i>	0.166	D-hexose-6-phosphate mutarotase
	<i>VpaChn25_RS10585</i>	0.186	Type I glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS23575</i>	0.228	6-phospho- β -glucosidase
	<i>VpaChn25_RS10475</i>	0.286	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>VpaChn25_RS14485</i>	0.382	2, 3-bisphosphoglycerate-independent phosphoglycerate mutase
	<i>VpaChn25_RS01325</i>	0.457	Triose-phosphate isomerase
	<i>VpaChn25_RS19575</i>	0.467	Pyruvate kinase
	<i>VpaChn25_RS18050</i>	4.409	Glyceraldehyde-3-phosphate dehydrogenase
	<i>VpaChn25_RS08880</i>	7.179	Aldehyde dehydrogenase
Thiamine metabolism	<i>VpaChn25_RS15440</i>	2.127	2-iminoacetate synthase ThiH
	<i>VpaChn25_RS16405</i>	2.192	Thiamine phosphate synthase
	<i>VpaChn25_RS15445</i>	2.476	Thiazole synthase
	<i>VpaChn25_RS16410</i>	2.520	Hydroxyethylthiazole kinase
	<i>VpaChn25_RS15455</i>	2.602	Thiazole biosynthesis adenyltransferase ThiF
	<i>VpaChn25_RS15460</i>	2.623	Thiamine phosphate synthase
	<i>VpaChn25_RS16415</i>	3.115	Thiaminase II
Arginine biosynthesis	<i>VpaChn25_RS11620</i>	0.101	Amino-acid N-acetyltransferase
	<i>VpaChn25_RS14100</i>	0.158	N-acetyl- γ -glutamyl-phosphate reductase
	<i>VpaChn25_RS14095</i>	0.204	Acetylglutamate kinase
	<i>VpaChn25_RS14090</i>	0.329	Argininosuccinate synthase
	<i>VpaChn25_RS13555</i>	0.340	Ornithine carbamoyltransferase
	<i>VpaChn25_RS14085</i>	0.376	Argininosuccinate lyase
