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Supplementary Materials

Effect of *fliL* gene on the virulence of *Pseudomonas plecoglossicida*

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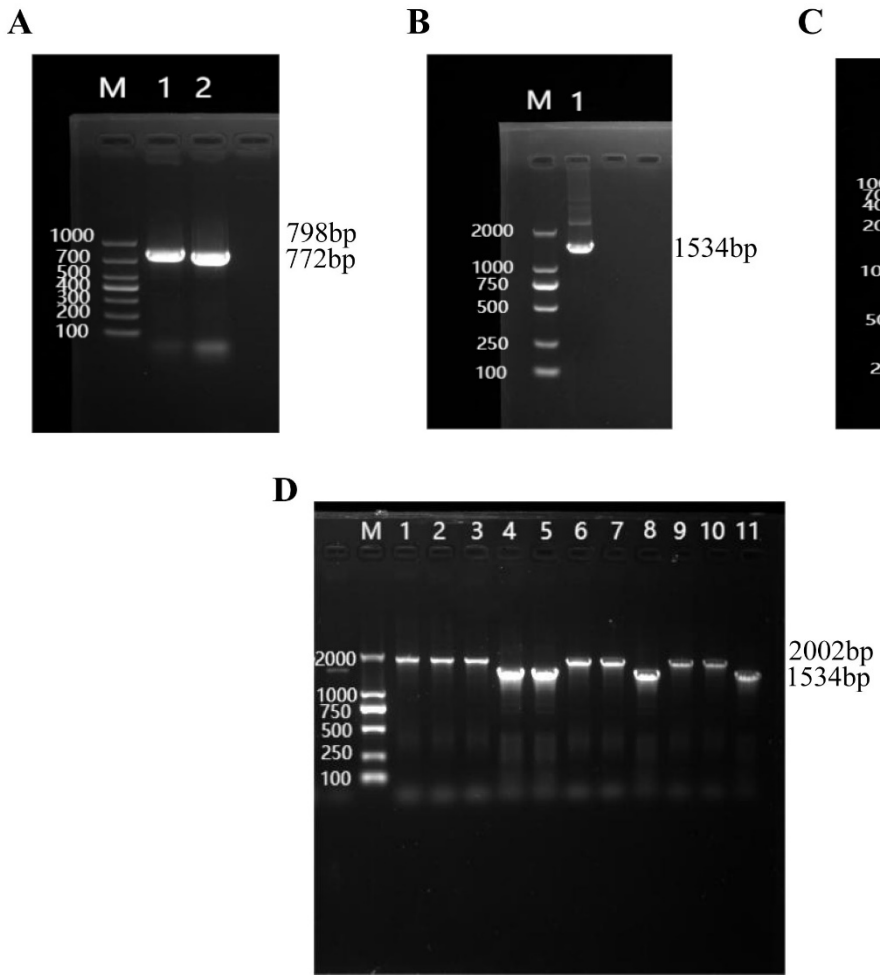

Figure S1. Electrophoretic diagram of the construction of the knockout strain. A. Electrophoresis of the left and right homologous arm segment of *fliL* gene in *P.plecoglossicida*; B. Electrophoretic map of gene deletion fragment (Δ*fliL*); C. Electrophoretic map of recombinant plasmid pK18mobsacB-Δ*fliL*; D. Sucrose screening electrophoresis diagram：Lane 4, 5, 10 and 11 were the mutant that had been successfully knocked out；Lane 1, 2, 3, 6, 7, 9, 10 were the revert mutant (wild type).

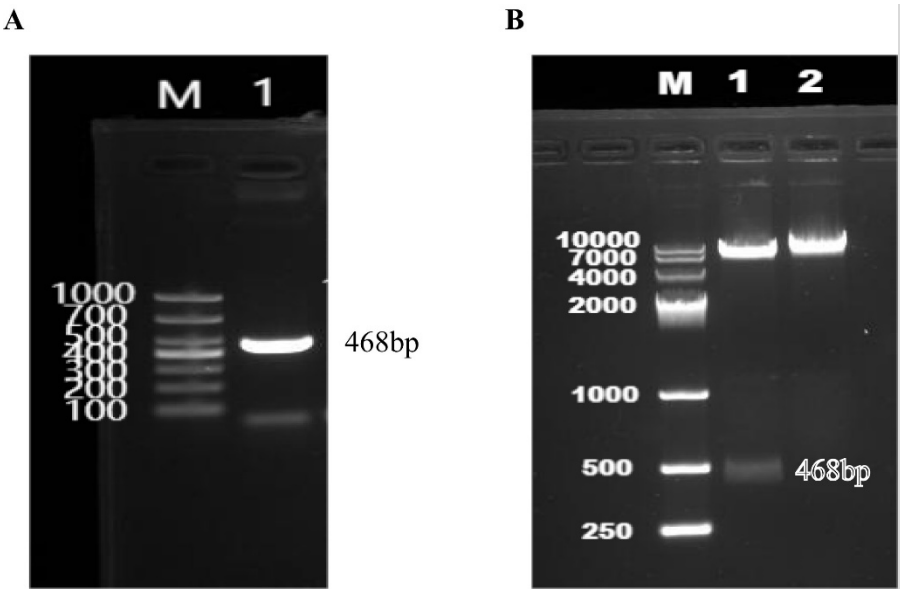

Figure S2. Electrophoretic diagram of the construction of the complement strain. A. Electrophoresis of amplification of fliL gene complement fragments; B. electrophoretic map of recombinant plasmid pCM130/tac-*fliL*.

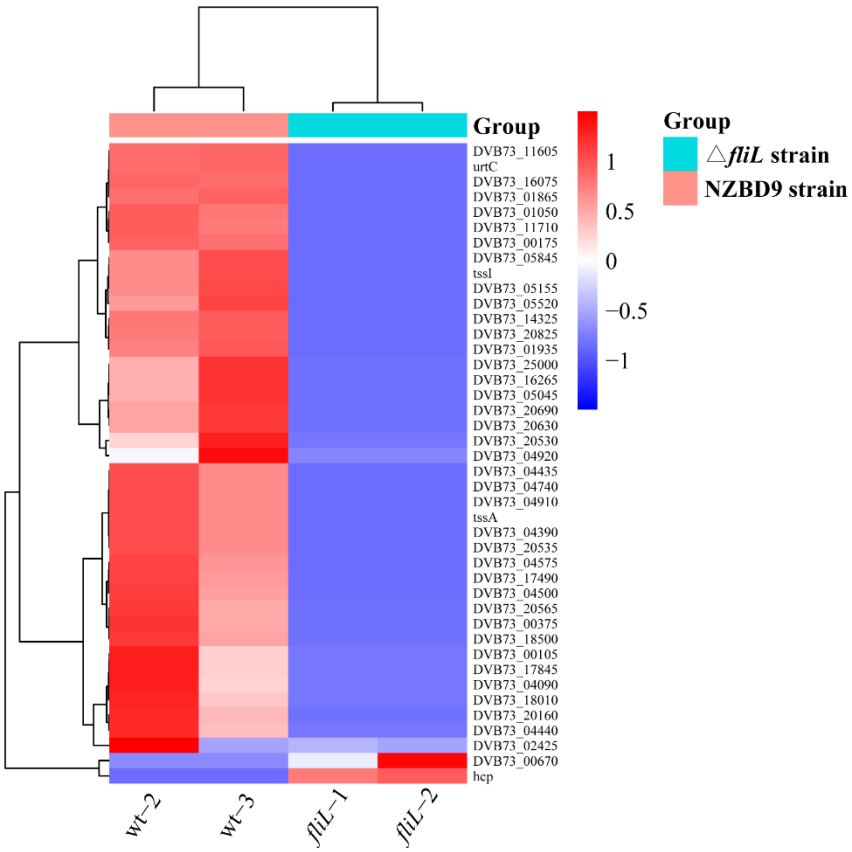

Figure S3. Cluster analysis of differentially expressed genes.

Table S1. The primers used to construct strains.

Primers	Sequences（5′-3′）	Size/bp	Restriction site
P_1	CGGAATTCCCCAGCTTGAAACAACG	25	EcoRI
P_2	TAGCCACTTGCTGACCAGATGACACGCGATATTGAC	36	
P_3	GTCAATATCGCGTGTCATCTGGTCAGCAAGTGGCTA	36	
P_4	GCTCTAGACACAAGCCTTTTCGATG	25	XbaI
P_5	ATGTCAATATCGCGTGTC	18	
P_6	TTACTGCGCTAGCCACTT	18	
C-Δ*fliL* -F	GCCAATGCATATGTCAATATCGCGTGTC	28	NsiI
C-Δ*fliL* -R	GCTGTACATTACTGCGCTAGCCACT	25	BsrGI
fliL-qRT-F	CAGGTGGACAAGAACGAGCA	20	
fliL-qRT-R	TATCTGCATTCCCTTGGCGG	20	
16S-qRT-F	TTCATCGCCACTGCACCTG	19	
16S-qRT-R	GTTCTTGCCCTTCTCCCAC	19	

Table S2. Primer sequence for transcriptome validation.

Gene name	Primer sequences（5′-3′）	PCR fragment size(bp)
DVB73_12420	F-AACCTGCCCTACATCACTGC R-CGGCAACTTCTTTCTGCACC	220
DVB73_07040	F-GCTTCTACCACGATTTCCGC R-GCCAGTTGCTCACGCAGTT	121
hcp	F-TTCCCAGCGTCAGCATAAGG R-ACCTCCTCTACGCCCTTCTT	147
tssE	F-ATGGTCGCACGCTATGA R-TCGGGTGGCAAGATGTA	144
DVB73_22160	TCCGTTTCTCGACCTATGCG GTTCGTGGTCGAGCTTCTGA	159
DVB73_25305	F-GACCCAGCTTGAAACAAC R-CTGAATGGACACTGATGAC	151
tssA	F-GGCGGTGCCAAAAGATAT R-TGGTAGACGGGTGACGAAT	217
tssI	F-ATGGCTCTCACTGTTGGG R-GGTAGGTGTGGCGTTTTT	149
DVB73_04090	F-CTTCTTGTTCCTTTTCCGTC R-CCACTCCATCACATCGCT	120
DVB73_19810	F-GGCCAACGAAAGTCTCCT R-ACCAATACCTTCCACCGC	154