

Table S1. Oligonucleotide primers used in this study

Target	Primers (forward/reverse, 5'-3')
Construction of mutants	
<i>fur</i>	CGGGATCCTTCGTGTAAGGCAGCAGTAATC/CAGAGCGTAAAGCCTATG GATACTTTCTGTTGATGTTC
	GAACATCAACAGGAAAGTATCCATAGGCTTTACGCTCTG/GGACTAGTAG ATGAAGATGGTGTGGGAAAC
	CGGGATCCTTCGTGTAAGGCAGCAGTAATC/GGACTAGTAGATGAAGAT GGTGTGGGAAAC
Construction of complemented mutants	
<i>fur</i>	GATTCTAGAAGGAGGAATTCACCATGTCAGACAATAACCAAG/GCGAAG CTTTTATTTCTTCGGCTTGTGAG
Protein expression	
<i>fur</i>	GCGGGATCCATGTCAGACAATAACCAAG/GCGAAGCTTTTATTTCTTCGG CTTGTGAG
qPCR	
<i>vieS</i>	AAGCAGCGAAAGCCAACCT/CTTCAAATCCACGCAATAA
<i>cdgD</i>	GATTTACGATGGGCACCA/TTCACCGTCACGACAAGA
<i>vpsA</i>	TGATGCGTTGTTGGCTGTG/TGCTGCTCTGCGGTAGTG
<i>vpsU</i>	CACGCTAAAGACAGGAAA/TGCTCAGCAGGACAAATA
<i>recA</i>	AAGATTGGTGTGATGTTGGTA/CACTTCTTCGCCTTCTTTGA
Primer extension	
<i>cdgD</i>	/AACCAAGTACAAACGCAAC-HEX

Luminescence assay	
<i>vieS</i>	GCGGAGCTCCGCCTAACGAGATGCTGT/GCGACTAGTCCTATCGGCTCCT GACCT
<i>cdgD</i>	GCGGAGCTCATCTCAGGTTTGGCTTCG/GCGGGATCCATGAGATTTTCGCT TCCAG
<i>vpsA</i>	GCGGAGCTCCAATGGATAGGACCAATC/GCGGGATCCCCAAATACGATG AGAAC
<i>vpsU</i>	GCGACTAGTTGTATCGCTTGATTTCCG/GCGGGATCCACCCTAACTACGC ACATG
EMSA	
<i>vieS</i>	GATGATTATGCACTCGATG/ATACCCTAACTACGCACATG
<i>cdgD</i>	TGGCTCTTTTTCTTAGCAAG/TTCGTCGTTATAAACAATC
<i>vpsA</i>	ATCTCAGGTTTGGCTTCG/AGCATGAAGTGTGCCTTTAC
<i>vpsU</i>	CTTCTGTAGGAATTTTCTCTC/CCTATCGGCTCCTGACCT
<i>recA</i>	AAGATTGGTGTGATGTTTGGTA/CACTTCTTCGCCTTCTTTGA
DNase I footprinting	
<i>vieS</i>	GTAAAACGACGGCCAGTCTTCTGTAGGAATTTTCTCTC/CAGGAAACAGC TATGACCCTATCGGCTCCTGACCT
<i>cdgD</i>	GTAAAACGACGGCCAGTATCTCAGGTTTGGCTTCG/CAGGAAACAGCTAT GACAGCATGAAGTGTGCCTTTAC
<i>vpsA</i>	GTAAAACGACGGCCAGTTGGCTCTTTTTCTTAGCAAG/CAGGAAACAGCT ATGACTTCGTCGTTATAAACAATC
<i>vpsU</i>	GTAAAACGACGGCCAGTGATGATTATGCACTCGATG/CAGGAAACAGCT ATGACATAACCCTAACTACGCACATG

M13	FAM-GTAAAACGACGGCCAGT/CAGGAAACAGCTATGAC-HEX
5'-RACE	
<i>vpsA</i>	/GGTGCAAAGTGGTACTGCGTGAGTGC
	/GTATCTGTAGGTGCAAAGTGGTACTG
<i>vpsU</i>	/CACTACTACGCCGATAAGGATCGG
	/GCCACCGCTCCAGATTCAATCAAC
UPM-Long	CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT
UPM-Short	CTAATACGACTCACTATAGGGC

Table S2. Predicted Fur box-like sequences within target promoters

Operon	First gene	Fur box-like sequence		
		Position ^{&}	Sequene	Score
<i>vieSAB</i>	<i>vieS</i>	D-135...-117	AACGATATTTCTTTACATT	9.3
	<i>cdgD</i>	D-376...-358	CATGAGTATTTTTTTCATT	8.5
<i>vpsA-K</i>	<i>vpsA</i>	D-334...-316	AACGAAAATTTATCTCAAT	9.9
	<i>vpsU</i>	D-150...-132	AAATAAACTACTTTCATT	7.2

&, 'D' indicates the direct sequence; minus numbers denote the nucleotide positions upstream of the translation start sites of indicated genes.