

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

Strains or plasmids	Genotypes	Sources
Strains		
<i>E. coli</i>		
DH5 α	λ φ80dlacZΔM15Δ(lacZYA-argF)U169 <i>recA1 endA1 hsdR17</i> (r _K ⁻ m _K ⁻) <i>supE44 thi-1 gyrA relA1</i>	Our collection
S17-1	[C600::RP4-2 (Tc::Mu)(Km::Tn7) <i>thi pro hsdRM⁺ recA</i>	1
S17-1 λ <i>pir</i>	S17-1 with λ <i>pir</i> lysogen	1
BL21(DE3)	F ⁻ <i>ompT hsdSB</i> (r _B ⁻ , m _B ⁻) <i>gal dcm</i> (DE3)	Novagen
GI698	F ⁻ λ ⁻ <i>lacIqlacPL8 ampC::Ptrp cI</i>	2
<i>V. vulnificus</i>		
MO6-24/O	Pathogenic clinical isolate	3
Δ <i>leuO</i>	Derivative of MO6-24/O with a deletion in <i>leuO</i>	This study
Δ <i>hns</i>	Derivative of MO6-24/O with a deletion in <i>hns</i>	This study
Δ <i>leuOΔ<i>hns</i></i>	Derivative of MO6-24/O with double deletions in <i>leuO</i> and <i>hns</i>	This study
Δ <i>toxRSΔ<i>hns</i></i>	Derivative of MO6-24/O with triple deletions in <i>toxRS</i> and <i>hns</i>	This study
Plasmids		

pGEM-T easy	TA cloning vector, <i>lacZ</i> , f1 origin, Ap ^r	Promega
pGEM-hns-up	pGEM-T easy vector containing <i>leuO</i> upstream region	This study
pGEM-hns-down	pGEM-T easy vector containing <i>leuO</i> downstream region	This study
pDM4	Suicide vector for an allelic exchange, <i>sacB</i> , Cm ^r	4
pDM4- <i>dhns</i>	pDM4 with a deletion in <i>hns</i> of <i>V. vulnificus</i>	This study
pDM4- <i>dleuO</i>	pDM4 with a deletion in <i>leuO</i> of <i>V. vulnificus</i>	This study
pMZtc- <i>leuO</i>	pMZtc with a promoter region of <i>leuO</i>	5
pET21a	Expression vector, C-terminal His-tag, Ap ^r	Novagen
pET-HNS	pET21a vector with <i>V. vulnificus</i> H-NS	This study
pET-ToxR-N	pET21a vector with <i>V. vulnificus</i> N-terminal domain of ToxR	5
pRE1- <i>leuO</i>	<i>leuO</i> expression vector	6
pBBR12- <i>leuO</i> -ara	pBBR-MCS2 vector with the <i>V. vulnificus leuO</i> under the <i>araC</i> promoter	5
pBAD-TOPO	Arabinose-regulated expression plasmid, Ap ^r	Invitrogen
pBBR12-hns-ara	pBBR-MCS2 vector with the <i>V. vulnificus hns</i> under the <i>araC</i> promoter	This study

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6. Kim JA, Park JH, Lee MA, Lee HJ, Park SJ, Kim KS, *et al.* 2015. Stationary-phase induction of *vvpS* expression by three transcription factors: repression by LeuO and activation by SmcR and CRP. *Mol. Microbiol.* **97**: 330-346

Table S2. Primers used in this study.

Function and Name	Nucleotide sequence (5' → 3')
Construction of a <i>leuO</i>-deletion mutation	
dleuO-up-F	AATCCCGGGAGAGCTCTTGGCTTAGCGACGGTGA
dleuO-up-R	CAACCACTTCGCCACAGCTCATCGCATCTTTTTTATC
dleuO-down-F	AAAAGATGCGATGAGCTGTGGCGAAGTGGTTGCTGCG
dleuO-down-R	CGGGTAACTGAGCTCATCGAAGATTTTCACTGC
Construction of a <i>hns</i>-deletion mutation, a <i>leuO/hns</i> deletion mutation, and <i>toxRS/leuO</i> double mutations	
dhns-up-F	CCTGAGCATGCGGATGTCCGTTACTTATG
dhns-up-R	TCAGGATCCCAACAGAGTTTTTGTTAG
dhns-down-F	GTCGGATCCGCGGGTAAATCTCTAGAAGAT
dhns-down-R	TACCTCGAGGTTGTTTTGACGCTTGGC
Construction of an arabinose-inducible H-NS expression system	
BAD-hns-F	ATGTCTGAACTAACAAAACTC
BAD-hns-R	TTAGATTTTCGAAATCTTC
pBAD-F	ATGCCATAGCATTTTTATCC
pBAD-R	GATTTAATCTGTATCAGG
qRT-PCR for quantitative analysis of <i>leuO</i> and <i>hns</i> transcripts	
leuO_qPCR_F	TCAAACCTGGCGATTTGCAGC
leuO_qPCR_R	AGGATGCTGCTTAGACGTCAC
HNS_qPCR_F	GGAAGCAGAAGAACGTGCAG

HNS_qPCR_R AGCTTGGATTGCAGAAGGTGT

ChIP analysis

leuO-chIP-F CGGAGTGGATCTCAACCTACTGAC

leuO-chIP-R ACGCATGAAAAGCTCATCATTA

Expression of a recombinant H-NS

Pet-hns-F GGATCCATGTCTGAACTAACAAAAC

Pet-hns-R GTCGACGATTTCGAAATCTTCTAG

DNaseI footprinting

FP-leuO-F CGCTAATATTGACGAGATTG

FP-leuO-F2 GGTACCCGCTAATATTGACGA

FP-leuO-F3 GTGGTGAAACAATAGTTAG

FP-leuO-R GTCAGGAATAGATAACCTG

FP-leuO-R2 TTTGTTGATTA AAAACAT

Nucleotides modified for the generation of restriction sites are underlined.