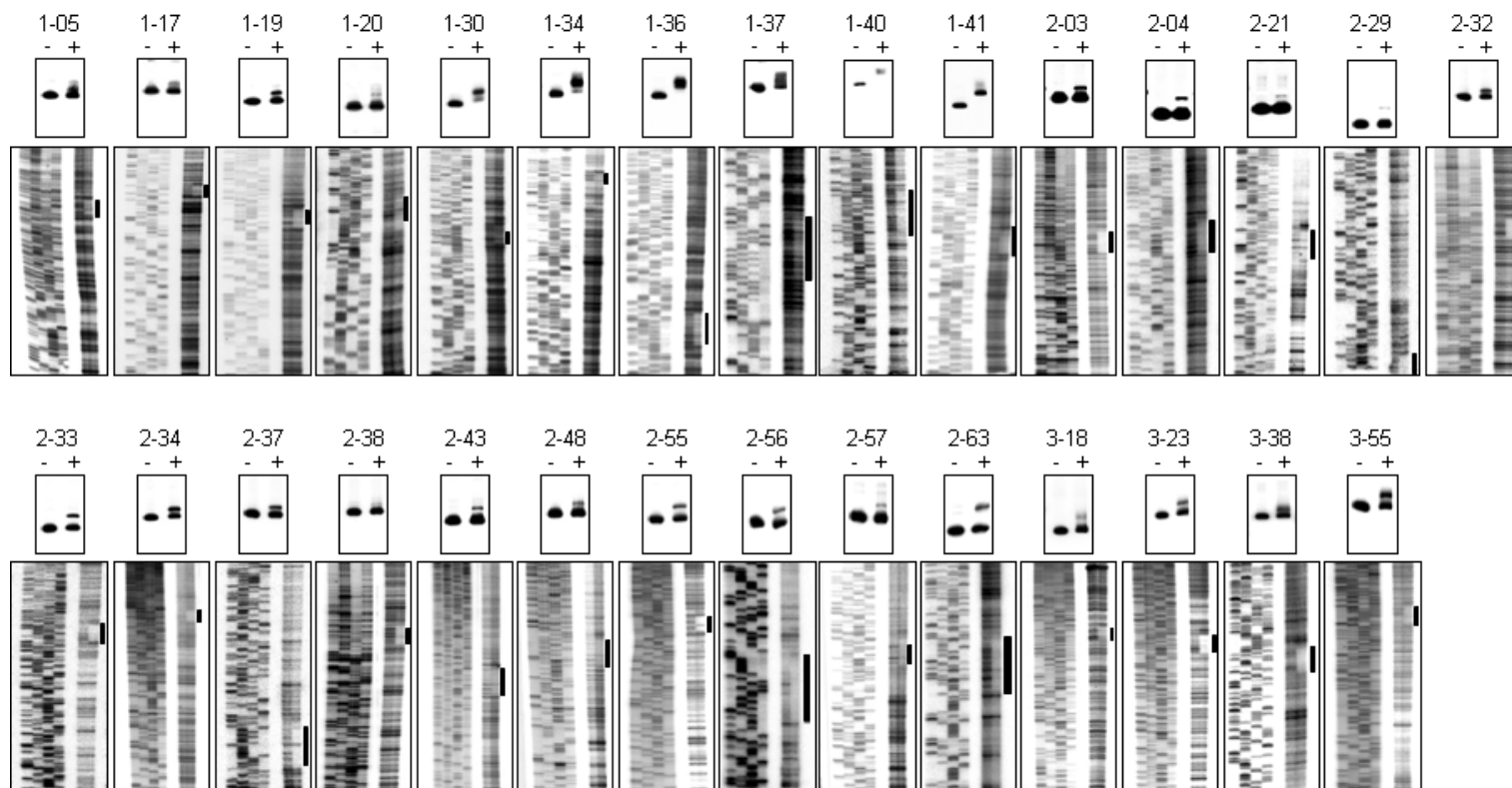


Supplemental Figure 1.



Supplemental Figure 1. EMSA for binding of SmcR to *V. vulnificus* genomic DNA fragments and determination of SmcR-binding sequences. Each of the 29 radiolabeled DNA fragments (about 30 ng for each) was mixed with 200 nM of SmcR and then resolved on a 4% polyacrylamide gel. EMSAs were performed in the presence of 0.1 μ g of poly(dI-dC) as a nonspecific competitor. The same labeled DNA fragments were incubated with 400 nM of SmcR and then digested with DNase I. Protection by SmcR is indicated by filled bars. For each panel, lanes G, A, T, and C (from the left) represent the nucleotide sequencing ladders of the individual clones containing the DNA fragments that were gel-shifted. Details are in the text. -, without SmcR; +, with SmcR. Same isolate numbers appeared in Fig. 2A are on the top of each panel.

Supplemental TABLE 1. Genes and their products of the *V. vulnificus* SmcR regulon identified using the consensus SmcR-binding sequence*

Functional Category	Locus tag	Gene	Product
Amino acid transport and metabolism	VV1_1370 [‡]	— [†]	Acetylornithine deacetylase
	VV1_1371	—	N-acetyl-gamma-glutamyl-phosphate reductase
	VV1_1372	—	Acetylglutamate kinase
	VV1_1373	—	Argininosuccinate synthase
	VV1_1374	—	Argininosuccinate lyase
Carbohydrate transport and metabolism	VV2_1326	—	ABC-type sugar transport system, periplasmic component
Cell motility	VV1_1950[‡]	—	Flagellar biosynthesis protein
	VV1_1951	—	Flagellar biosynthesis MinD-related protein
	VV1_1952	—	Flagellar biosynthesis sigma factor FliA
Cell wall/membrane biogenesis	VV1_1103	—	Membrane protein
	VV2_0929	—	Membrane-fusion protein
	VV2_0928	—	Cation/multidrug efflux pump
Coenzyme transport and metabolism	VV1_2257	—	6-pyruvoyl tetrahydrobiopterin synthase
Defense mechanisms	VV2_1089 [‡]	—	ABC-type multidrug transport system, ATPase and permease component
Function unknown	VV1_1265	—	Hypothetical protein
	VV1_1471	—	Predicted membrane protein
	VV2_0057	—	Hypothetical protein
	VV2_0058	—	Predicted membrane protein
	VV2_0279	—	Hypothetical protein
	VV2_0517	—	Hypothetical protein
	VV2_1111	—	Hypothetical protein
	VV2_1541	—	Hypothetical protein
	VV2_1542	—	Transcriptional regulator, MerR family
	VV2_1543	—	Deoxyribodipyrimidine photolyase
	VV2_1544	—	Hypothetical protein
	General function prediction only	VV1_0300	—
VV1_0840		—	ABC-type transport system, permease component
VV1_0839		—	ABC-type oligopeptide transport system, periplasmic component
VV1_0838		—	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component
VV1_0837		—	ABC-type oligopeptide transport system, ATPase component
VV1_1085		—	Peptide ABC transporter, ATP-binding protein
VV1_1456		—	Predicted Zn-dependent protease and their inactivated homologs
VV1_1455		—	Predicted amidohydrolase
VV1_1454		—	Predicted membrane protein
VV1_1453		—	Ribonuclease G and E

	VV1_1452	<i>maf</i>	Maf-like protein
	VV1_1451	—	Cell shape-determining protein
	VV1_1450	—	Cell shape-determining protein
	VV1_2358	—	Probable hydrolase
	VV1_2976 [‡]	—	ABC-type uncharacterized transport system, permease component
	VV1_2975	—	ABC-type uncharacterized transport system, permease component
	VV1_2974	—	ABC-type dipeptide transport system, periplasmic component
	VV1_2973	—	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component
	VV1_2972	—	ABC-type oligopeptide transport system, ATPase component
	VV2_0856	—	ATPase component of ABC transporter with duplicated ATPase domains
	VV2_0970	—	Predicted hydrolase/acyltransferase
	VV2_1270	—	Predicted Zn-dependent peptidase
	VV2_1527	—	Predicted acetyltransferase
Inorganic ion transport and metabolism	VV1_0842 [‡]	—	Outer membrane receptor protein
	VV1_0843	—	Hypothetical protein
	VV1_0844	—	TolR
	VV1_0845	—	TonB system transport protein ExbB2
	VV1_2805	—	Di- and tricarboxylate transporter
	VV2_1106	—	Arylsulfatase A
Intracellular trafficking and secretion	VV1_3112	—	Multiple antibiotic transporter
Nucleotide transport and metabolism	VV1_0302	—	DNA/RNA endonuclease G
	VV1_1635	—	Hypoxanthine phosphoribosyltransferase
	VV1_1636	—	Hypoxanthine phosphoribosyltransferase
Posttranslational modification, protein turnover, chaperones	VV1_0453	—	Peroxiredoxin
	VV2_0020 [‡]	—	Molecular chaperone
	VV2_1650	—	Predicted redox protein, regulator of disulfide bond formation
Replication, recombination and repair	VV1_1702	—	Superfamily II DNA helicase
	VV2_1406 [‡]	—	Endonuclease I
	VV2_1643	—	Alkylated DNA repair protein
Signal transduction mechanisms	VV1_1489	—	HD-GYP domain
	VV1_1931	—	FlaK protein
	VV1_2096 [‡]	—	Methyl-accepting chemotaxis protein
	VV1_2211	—	Hypothetical protein
	VV1_2868	—	Methyl-accepting chemotaxis protein
	VV1_2867	—	Pseudouridylate synthase, 23S RNA-specific
	VV1_2866	—	Predicted SAM-dependent methyltransferase
	VV1_2911	—	Predicted signal transduction protein
	VV2_0528	—	Methyl-accepting chemotaxis protein
	VV2_0823	—	ABC-type amino acid transport/signal transduction systems
	VV2_0825	—	Methyl-accepting chemotaxis protein

Transcription	VV1_0829	<i>slmA</i>	Nucleoid occlusion protein
	VV1_0830	—	Lipid A biosynthesis lauroyl acyltransferase
	VV1_1687	<i>greA</i>	Transcription elongation factor GreA
	VV2_0446	—	Serine/threonine protein kinase
	VV2_0981	—	Response regulator
	VV2_1391 [†]	—	Transcriptional regulator
Translation	VV1_1270	—	Lysyl-tRNA synthetase
	VV1_1271	—	Hypothetical protein
	VV1_2397	—	Threonyl-tRNA synthetase
	VV1_3016	—	Ribosomal large subunit pseudouridine synthase C
Not in COGs	VV1_0464	—	Polyphosphate kinase
	VV1_0522	—	Hypothetical protein
	VV1_0644	—	Pyruvate kinase
	VV1_1215	—	Hypothetical protein
	VV1_1216	—	Hypothetical protein
	VV1_1401	—	Thymidylate kinase
	VV1_1472	—	Predicted membrane protein
	VV1_1473	—	Zn-dependent protease with chaperone function
	VV1_1720	—	GGDEF family protein
	VV1_2362	—	Hypothetical protein
	VV1_2380	—	Hypothetical protein
	VV1_2430	—	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase
	VV1_2726	—	Histone acetyltransferase HPA2
	VV1_2957	—	Hypothetical protein
	VV1_2958	—	ISSod7
	VV2_0067	—	Hypothetical protein
	VV2_0133	—	Decaheme cytochrome c related protein
	VV2_0250 [†]	—	Zn-dependent protease
	VV2_0364	—	Chromosome segregation ATPase
	VV2_0363	—	Biopolymer transport protein
	VV2_0362	—	Biopolymer transport protein
	VV2_0361	—	Biopolymer transport protein
	VV2_0360	—	Periplasmic protein TonB
	VV2_0359	—	FOG: TPR repeat protein
	VV2_0400	—	Glycosidase
	VV2_0414	—	Succinyl-CoA synthetase, alpha subunit
	VV2_0429	—	Hemolysin-coregulated protein
	VV2_0658	—	Hypothetical protein
	VV2_1035	—	Uncharacterized ABC-type transport system, permease component
	VV2_1046	—	AraC-type DNA-binding domain-containing protein
	VV2_1147	—	Hypothetical protein
	VV2_1179	—	Hypothetical protein
	VV2_1201	—	Hypothetical protein
VV2_1281	—	Maltoporin	
VV2_1371	—	Hypothetical protein	
VV2_1398	—	Hypothetical protein	

*Functional categories, gene names, locus tag numbers, and annotation of gene products are based on the database of the *V. vulnificus* CMCP6 genome. Locus tags likely in an operon are indicated in boldface.

[†]Locus tags without gene name.

‡Binding of SmcR to their upstream region was experimentally verified by EMSA.

§Clusters of orthologous group.

Supplemental TABLE 2. Oligonucleotides used for EMSA, ChIP, and quantitative RT-PCR analysis of the ten genes randomly selected from the pool of the newly predicted SmcR-regulon

Locus tag*	Oligonucleotide sequence, 5'-3'	
	Forward	Reverse
EMSA and ChIP assay		
VV1_0842	AGATCCACCCTCCAACACATACC	GAACGACGACCAAATGTGACG
VV1_1370	ACTTCCCCTGTTGACAGTTGGG	AGTTGAGAAATGCACTTGCCCG
VV1_1950	AGCAGTCTTACTCACCTCCGGC	GACATGATGACAGCATCAACGC
VV1_2096	GACCCGTTGTTGTCATGTCTAGC	ACGTTTCTGAGAGAGCGCAAGC
VV1_2976	TAATGCCAAGAAACGTCGGC	CCACACTTTCATACGTTTTACCG
VV2_0020	ACTTGCCATTTGGATTGCTCC	CGTGGCAATCAATAAACACCG
VV2_0250	CCTCCTAGGGTGTGTGATTGTGG	AACAGATAGCAGCTATTTCCCC
VV2_1089	ACCACACAGTCTGCATTTTGGG	CCAGTTGGTTATCACTTTGCGG
VV2_1391	CTGTGCCAATTGCTCAGATCG	GTTCTGCAATAGCCACAAAGGC
VV2_1406	AATCGCCATTGAGTAGCTGTGC	CTCAAACACCACAAAACACCCG
Quantitative RT-PCR		
VV1_0842	TCGCAGAAGAGCAGCAAGTCG	TGGTAATGACGGTGACAGGAGAAG
VV1_1370	GCTATCCCATCTCCCCTCTTAACC	CCCACGCAACAGATTATCCAAACC
VV1_1950	ACCGCCGTAAGCCTCAAACCTG	TCCTGCCACAATAAACCCGATACC
VV1_2096	CTCGGCGGCTGGACACATC	GCACGGGCGGCTTCTATGG
VV1_2976	CCTTTCCGAAGATCAAATGGCAGAG	GACAAGAAGACGAGTCAACCAATCC
VV2_0020	AAGATGTGGTGTGGTCAAGCG	GTGCCGAATGTTCTGCGTTGG
VV2_0250	ATACCCGTTGGCAGGATGTGG	AAAGCCTCGCCCGTCAGC
VV2_1089	TCCAGATGCCAGTGAAGAAGAGC	GCCAAACGGGTCGGTGAGG
VV2_1391	GAACAAGGCAGTTTGTCTGGCG	ATCCGTGAGACTTTGTTTGCGG
VV2_1406	GGCACACAAGGCAACACTGAC	CACCGACACCGAGAAGTATAGG

*Locus tag numbers are based on the database of the *V. vulnificus* CMCP6 genome which was retrieved from GenBank (AE016795; AE016796).