

Table S5

Bacterial strains used in this study

Genotype		References
<i>E. coli</i>		
β2163	<i>E. coli</i> K12 Δ dapA::erm pir RP4-2 Tc::Mu [Km]	(1)
MFDpir	<i>E. coli</i> K12 Δ dapA::erm pir RP4-2 Δ recA	(2)
GEB882	β2163-pGEB53	
GEB883	<i>E. coli</i> K12 Δ dapA::erm pir RP4-2 Δ recA gyrA462, zei298 ::Tn10	This study
<i>V. cholerae</i>		
MM227	El Tor strain C6706str2 derivative	(3)
DL3232	MM227- Δ csrBCD	
VC1	MM227-pBB1	
VC2	DL3232-pBB1	This study
VC4	DL3232-pBB1-pGEB53	
<i>V. tasmaniensis</i>		
LGP32	Pathogen of oyster <i>C. gigas</i>	(4)
VS4	LGP32 Δ varS	
VS5	LGP32 Δ varA	
VS16	LGP32 Δ csrB123	
VS17	LGP32 Δ csrB124	
VS18	LGP32 Δ csrB234	This study
VS19	LGP32 Δ csrB134	
VS25	LGP32 Δ csrB1234	
VS22	LGP32 Δ varSvarA	

VS23	LGP32 $\Delta varSvarAcsrB1$	
VS41	LGP32 $\Delta rpoS$	
VS44 & VS45	LGP32 $\Delta luxO$	
VS46	VS23 $\Delta luxO$	
VS50	VS23 $\Delta rpoS$	
VS82	VS22 $\Delta rpoS$	
VS83	VS24 $\Delta rpoS$	
VS84	VS22 $\Delta luxO$	
VS85	VS24 $\Delta luxO$	
Δvsm	LGP32 Δvsm	(5)
$\Delta 1062$	LGP32 $\Delta prtV$	(6)

References

1. Demarre G, Guerout AM, Matsumoto-Mashimo C, Rowe-Magnus DA, Marliere P, Mazel D. 2005. A new family of mobilizable suicide plasmids based on broad host range R388 plasmid (IncW) and RP4 plasmid (IncPalpha) conjugative machineries and their cognate *Escherichia coli* host strains. Res Microbiol 156:245-55.
2. Ferrieres L, Hemery G, Nham T, Guerout AM, Mazel D, Beloin C, Ghigo JM. 2010. Silent mischief: bacteriophage Mu insertions contaminate products of *Escherichia coli* random mutagenesis performed using suicidal transposon delivery plasmids mobilized by broad-host-range RP4 conjugative machinery. J Bacteriol 192:6418-27.
3. Lenz DH, Mok KC, Lilley BN, Kulkarni RV, Wingreen NS, Bassler BL. 2004. The small RNA chaperone Hfq and multiple small RNAs control quorum sensing in *Vibrio harveyi* and *Vibrio cholerae*. Cell 118:69-82.

4. Le Roux F, Zouine M, Chakroun N, Binesse J, Saulnier D, Bouchier C, Zidane N, Ma L, Rusniok C, Lajus A, Buchrieser C, Medigue C, Polz MF, Mazel D. 2009. Genome sequence of *Vibrio splendidus*: an abundant planctonic marine species with a large genotypic diversity. *Environ Microbiol* 11:1959-70.
5. Le Roux F, Binesse J, Saulnier D, Mazel D. 2007. Construction of a *Vibrio splendidus* mutant lacking the metalloprotease gene *vsm* by use of a novel counterselectable suicide vector. *Appl Environ Microbiol* 73:777-84.
6. Binesse J, Delsert C, Saulnier D, Champomier-Verges MC, Zagorec M, Munier-Lehmann H, Mazel D, Le Roux F. 2008. Metalloprotease *vsm* is the major determinant of toxicity for extracellular products of *Vibrio splendidus*. *Appl Environ Microbiol* 74:7108-17.