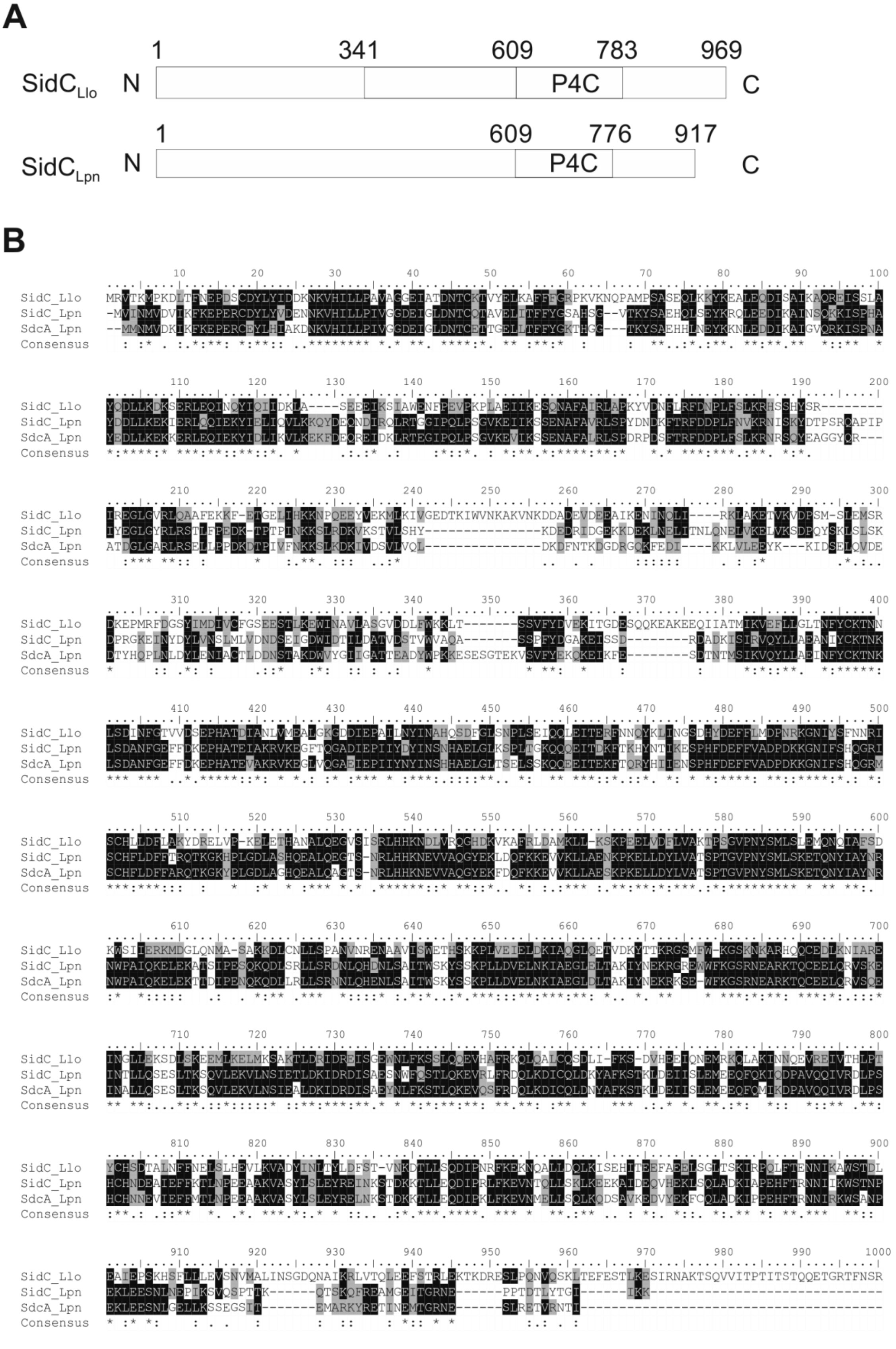

FIG S1 Alignment of SidC$_{Llo}$, SidC$_{Lpn}$ and SdcA$_{Lpn}$. (A) Domain analysis of 111 kDa SidC$_{Llo}$ and 106 kDa SidC$_{Lpn}$. (B) Amino acid sequence alignment of SidC$_{Llo}$, SidC$_{Lpn}$ and SdcA$_{Lpn}$ using the Clustal Omega algorithm. Full-length SidC$_{Llo}$/SidC$_{Lpn}$ or the corresponding P4C domains share 40% or 45% identity, respectively. Identical or similar amino acids are marked in black or in gray.

TABLE S1. Bacterial strains and plasmids.

Strain/plasmid	**Properties**	**Reference**
E. coli		
BL21(DE3)		Novagen
TOP10		Invitrogen
ST18	S17 λ*pir* Δ*hemA*	(1)
L. longbeachae		
NSW150	*L. longbeachae* strain NSW150, serogroup 1	(2)
Δ*dotA*	NSW150 *dotA*::Kan^R (Δ*dotA*)	(2)
IH02	NSW150 *llo3098*::Kan^R (Δ*sidC*)	This study
L. pneumophila		
JR32	*L. pneumophila* strain Philadelphia-1, serogroup 1	(3)
LELA3118	JR32 *dotA3118*::Kan^R (Δ*dotA*)	(3)
GS3011	JR32 *icmT3011*::Kan^R (Δ*icmT*)	(4)
CR01	JR32 *sidC-sdcA*::Kan^R (Δ*sidC-sdcA*)	(5)
Plasmids		
pET28a(+)	N-terminal His$_6$-fusion, P$_{T7}$, Kan^R	Novagen
pGEX4T-1	N-terminal GST-fusion, P$_{tac}$, Amp^R	Amersham
pMMB207-C-M45	pMMB207-C, Δ*mobC*, M45-(Gly)$_5$, Cam^R	(6)
pCaln-GFP	P$_{act15}$, calnexinA-RSSSKLK-GFP (S65T), G418	(7)
pCR01	pET28a(+), *His*$_6$-*sidC*$_{Lpn}$ (P$_{tac}$)	(6)
pCR02	pGEX4T-1, *GST-sidC*$_{Lpn}$ (P$_{tac}$)	(6)
pCR34	pMMB207-C, *M45-sidC*$_{Lpn}$ (P$_{tac}$)	(6)
pCR77	pMMB207-C-P$_{tac}$-RBS-*dsred*-RBS	(8)
pCR80	pMMB207-C-P$_{tac}$-RBS-*dsred*-RBS-*sidC*$_{Lpn}$	(8)
pGEX-PH$_{FAPP1}$	pGEX4T-1, *GST-PH*$_{FAPP1}$ (P$_{tac}$)	(9, 10)

pHP56	pGEX4T-1, *GST-sidC*$_{\text{Lpn\_609-776}}$ (P$_{tac}$)	(5)
pIH33	pLAW344-upstream *sidC*$_{\text{Llo}}$’-Kan^{R}-downstream *sidC*$_{\text{Llo}}$’	This study
pIH47	pMMB207-C-P$_{tac}$-RBS-*dsred*-RBS-*sdcA*$_{\text{Lpn}}$	This study
pIH60	pGEX4T-1, *GST-sidC*$_{\text{Lpn\_1-608-Llo\_609-969}}$	This study
pLAW344	*oriT* (RK2), *oriR* (ColE1), *sacB*, Cam^{R}, Amp^{R}	(11)
pMH01	pGEX4T-1, *GST-sidC*$_{\text{Llo\_1-608-Lpn\_609-917}}$	This study
pSD01	pET28a(+); *His*$_{6}$-*sidC*$_{\text{Llo}}$ (P$_{\text{T7}}$)	This study
pSD02	pET28a(+); *His*$_{6}$-*sidC*$_{\text{Llo}}$ (P$_{\text{T7}}$), *Bam*HI/*Sal*I deleted in *sidC*	This study
pSD03	pGEX4T-1, *GST-sidC*$_{\text{Llo\_609-782}}$ (P$_{tac}$)	This study
pSD04	pGEX4T-1, *GST-sidC*$_{\text{Llo\_1-340}}$ (P$_{tac}$)	This study
pSD05	pGEX4T-1, *GST-sidC*$_{\text{Llo\_341-608}}$ (P$_{tac}$)	This study
pSD06	pGEX4T-1, *GST-sidC*$_{\text{Llo\_783-969}}$ (P$_{tac}$)	This study
pSD07	pGEX4T-1, *GST-sidC*$_{\text{Llo}}$ (P$_{tac}$)	This study
pSD13	pMMB207-C, *M45-sidC*$_{\text{Llo}}$ (P$_{tac}$)	This study
pSD14	pMMB207-C-P$_{tac}$-RBS-*dsred*-RBS-*sidC*$_{\text{Llo}}$	This study
pSW001	pMMB207-C, Δ*lacI*^{q}, constitutive *dsred*	(12)
pUC4K	*oriR* (pBR322), Amp^{R}, MCS::Kan^{R}	Amersham

Abbreviations: ampicillin (Amp); chloramphenicol (Cam); kanamycin (Kan); geneticin (G418)

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TABLE S2. Oligonucleotides used in this study.

Oligo	**Sequence (5' - 3')** [a]	**Comments**
oCR1	AAAAACGCGGATCCATGGTGATAAACATGGTTGACG	5'of *sidC*, *BamH*I (Ref. 5)
oIH19	AAAAACGCTCTAGATCCTCTACTACCTTGTGAGT	5' upstr. *sidC*$_{\text{Llo}}$ (fo), *Xba*I
oIH20	AAAAACGCGGATCCGAAACATTAAGAAGTGTGCG	3' upstream *sidC*$_{\text{Llo}}$ (re)
oIH21	AAAAACGCGGATCCATCTGAATGAAGCAAAATTG	5' downstream *sidC*$_{\text{Llo}}$ (fo)
oIH22	AAAAACGCTCTAGAAATTTACTGACTTGCAATCA	3' downstream *sidC*$_{\text{Llo}}$ (re)
oIH23	ATCCAAACCATCGTCGTGTC	5' upstream oIH019 (fo)
oIH24	ATCCTGAGGAGTTGCAGAAAG	3' downstream oIH022 (re)
oIH39	AAAAACGCCTGCAGCTGACCAGGTAATTGC	3' of *sidC*$_{\text{Lpn1-608}}$ (re), *Pst*I
oIH40	AAAAACGCCTGCAGTTATTTCCTGGGAAAC	5' of *sidC*$_{\text{Llo609-969}}$ (fo), *Pst*I
oMH01	GGATCCACGCGGAACCAGATCCGATTTTGG	pGEX-4T-1 (re)
oMH02	CCGGAATTCCCGGGTCGACTCGAGCGGCCG	pGEX-4T-1 (fo)
oMH03	gttccgcgtggatccATGAGAGTCACTAAAATGCC	5' of *sidC*$_{\text{Llo1-608}}$ (fo)
oMH04	aggaatatttATTTTCTCTATTCACGTTTGC	3' of *sidC*$_{\text{Llo1-608}}$ (re)
oMH05	tagagaaaatAAATATTCCTCCAAGCCATTATTG	5' of *sidC*$_{\text{Lpn609-917}}$ (fo)
oMH06	acccgggaattccggCTATTTCTTTATAATTCCCGTGTAC	3' of *sidC*$_{\text{Lpn609-917}}$ (re)
oSD05	TTTTGGGATCCGAATATAGAGAACTAAAATG	5' flanking sequence *sidC*$_{\text{Llo}}$ (fo), *Bam*HI
oSD06	TTTTTGTCGACGAAATAAAGTTAAGTACGTGAATTAAAAGTACG	3' flanking sequence *sidC*$_{\text{Llo}}$ (re), *Pst*I
oSD07	TTTTCATATGATGAGAGTCACTAAAATGCCTAAAGAC	5' flanking sequence *sidC*$_{\text{Llo}}$ (fo), *Nde*I
oSD08	TTTTTGCTAGCTTAAGTACGTGAATTAAAAGTACGTCC	3' flanking sequence *sidC*$_{\text{Llo}}$ (re), *Nhe*I
oSD16	TTTTGGGATCCATGAGAGTCACTAAAATGCTTAAAGAC	5' of *sidC*$_{\text{Llo1-340}}$ (fo)
oSD17	TTTTTGTCGACTCATCCAGTGATTTTTTCTACGTC	3' of *sidC*$_{\text{Llo1-340}}$ (re)
oSD18	TTTTGGGATCCGCTGCTGTTATTTCCTGGG	5' of *sidC*$_{\text{Llo609-782}}$ (fo)
oSD19	TTTTTGTCGACTCATTCATTGAAAAAGTTAAGCGCTG	3' of *sidC*$_{\text{Llo609-782}}$ (re)
oSD22	GAAAATAATATCAAGGCATGGTCCACTGATCTTGAAGCAATCG	Quick Change *sidC*$_{\text{Llo}}$ (Δ*Sal*I) (fo)
oSD23	CGATTGCTTCAAGATCAGTGGACCATGCCTTGATATTATTTTC	Quick Change *sidC*$_{\text{Llo}}$ (Δ*Sal*I) (re)
oSD24	AAACGCGGATCCGATGAATCACAGCAAAAGGAAGC	5' of *sidC*$_{\text{Llo341-608}}$ (fo)

oSD25	AAACGCGTCGACTCAATTTTCTCTATTCACGTTTGCTGGAG	3' of *sidC*$_{\text{Llo341-608}}$ (re)
oSD26	AAACGCGGATCCTTGTCTTTACATGAGGTGCTTAAAGTAGC	5' of *sidC*$_{\text{Llo783-969}}$ (fo)
oSD27	AAACGCGTCGACTTAAGTACGTGAATTAAAAGTACGTCC	3' of *sidC*$_{\text{Llo783-969}}$ (re)
oSD28	GATGAGTTCTTTTTGATGGACCCCAATAGAAAAGG	Quick Change *sidC*$_{\text{Llo}}$ (Δ*Bam*HI) (fo)
oSD29	CCTTTTCTATTGGGGTCCATCAAAAAGAACTCATC	Quick Change *sidC*$_{\text{Llo}}$ (Δ*Bam*HI) (re)

[a] Restriction sites are underlined.