Supplemental material

Table S1 Bacterial strains used in the study

Strain	Description	Reference
	E. coli	
S17-1	*hsdR*17 *recA*1 RP4-2-*tet*::Mu-1*kan*::Tn7 Sm^R	(1)
	P. aeruginosa	
PAO1	Wild-type *P. aeruginosa*	(2)
	C. canimorsus	
C. canimorsus 5 (*Cc*5)	Isolated from human fatal septicemia after dog bite, 1995, Libramont, Belgium	(3)
*Cc*5Δ*PUL1*	Substitution of *PUL1* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL2*	Substitution of *PUL2* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL3*	Substitution of *PUL3* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL4*	Substitution of PUL4 by *ermF*; Em^R	(4)
*Cc*5Δ*PUL5*	Substitution of *PUL5* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL6*	Substitution of *PUL6* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL7*	Substitution of *PUL7* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL8*	Substitution of *PUL8* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL9*	Substitution of *PUL9* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL10*	Substitution of *PUL10* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL11*	Substitution of *PUL11* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL12*	Substitution of *PUL12* by *ermF*; Em^R	(4)
*Cc*5Δ*PUL13*	Substitution of *PUL13* by *ermF*; Em^R	(4)
*Cc*5Δ*Ccan_03610*	Substitution of *Ccan_03610* by *ermF* using pFL1; Em^R	This study
*Cc*5Δ*Ccan_03620*	Substitution of *Ccan_03620* by *ermF* using pFL2; Em^R	This study
*Cc*5Δ*Ccan_03630*	Substitution of *Ccan_03630* by *ermF* using pFL3; Em^R	This study
*Cc*5Δ*Ccan_03640*	Substitution of *Ccan_03640* by *ermF* using pFL4; Em^R	This study

Cc5ΔCcan_03650	Substitution of *Ccan_03650* by *ermF* using pFL5; Em^R	This study
Cc5ΔCcan_03660	Substitution of *Ccan_03660* by *ermF* using pFL6; Em^R	This study
Cc5ΔCcan_03670	Substitution of *Ccan_03670* by *ermF* using pFL7; Em^R	This study
Cc5ΔCcan_03680	Substitution of *Ccan_03680* by *ermF* using pFL8; Em^R	This study
Cc5ΔCcan_03690	Substitution of *Ccan_03690* by *ermF* using pFL9; Em^R	This study
Cc5ΔCcan_03700	Substitution of *Ccan_03700* by *ermF* using pFL10; Em^R	This study
Cc5ΔCcan_03710	Substitution of *Ccan_03710* by *ermF* using pFL11; Em^R	This study
Cc5ΔCcan_03720	Substitution of *Ccan_03720* by *ermF* using pFL12; Em^R	This study
Cc5ΔCcan_03730	Substitution of *Ccan_03730* by *ermF* using pFL13; Em^R	This study
Cc5ΔCcan_15860	Substitution of *Ccan_15860* (*furA*) by *ermF* using pFL61; Em^R	This study

Table S2 Primers used in the study

Lab.Ref.	Name	Sequence 5'-3' (restriction sites are underlined)	Restriction
		Deletions	
6953	fwd_03640_1.1	cgctgcaggctacctatatgatggagcc	*Pst*I
6954	rev_03640_1.2	aaaaatttcatccttcgtagaaaaacttcttacgattttttatttag	
7027	fwd_03640_2.1	gagtagataaaagcactgtttagggacaggacgtg	
7028	rev_03640_2.2	ggactagtatccgtctgtgccaataccc	*Spe*I
6957	fwd_03640_3.1	ctaaataaaaatcgtaagaagttttttctacgaaggatgaaattttttcagggacaac	
6958	rev_03640_3.2	ggacaggacacgtcctgtccctaaacagtgctttatctactccgatagcttc	
6959	fwd_03650_1.1	cgctgcagtttacgagcaggacatcc	*Pst*I
6960	rev_03650_1.2	aaaaatttcatccttcgtagaaatgataatctttg	
7050	fwd_03650_2.1	gagtagataaaagcactgttcacttggttacaacgttcc	
7051	rev_03650_2.2	ggactagtatccgagtgttttctacc	*Spe*I
6963	fwd_03650_3.1	caaagattatcatttctacgaaggatgaaattttttcagggacaac	
7052	rev_03650_3.2	ggaacgttgtaaccaagtgaacagtgctttatctactccgatagcttc	
6965	fwd_03660_1.1	cgctgcagccaaaacagtttacattgacgg	*Pst*I
6966	rev_03660_1.2	aaaaatttcatccttcgtagtctctactatttcctattttttac	
6967	fwd_03660_2.1	gagtagataaaagcactgttaataacaatatataaaaatagaatag	
6968	rev_03660_2.2	ggactagtacccaaatagcggaaagg	*Spe*I
6969	fwd_03660_3.1	gtaaaaaataggaaatagtagagactacgaaggatgaaattttttcagggacaac	
6970	rev_03660_3.2	ctattctattttttatatattgttattaacagtgctttatctactccgatagcttc	
6971	fwd_03670_1.1	cgctgcagaaatcagtgggaagtaaccgc	*Pst*I
6972	rev_03670_1.2	aaaaatttcatccttcgtagtttttatgttctttcttgtag	
6973	fwd_03670_2.1	gagtagataaaagcactgttttttttttagtatttgcccaacg	
6974	rev_03670_2.2	ggactagttttttccgttccgtaaggttctgccc	*Spe*I

6975	fwd_03670_3.1	ctacaagaaagaacataaaactacgaaggatgaaattttcagggacaac	
6976	rev_03670_3.2	cgttgggcaaatactaaaaaaaacagtgcttttatctactccgatagcttc	
6977	fwd_03680_1.1	cgctgcagattgggggagagcctcgtgc	*Pst*I
6978	rev_03680_1.2	aaaaatttcatccttcgtagatcatctgatattttattatttgatttgatgc	
6979	fwd_03680_2.1	gagtagataaaagcactgttttgtaaggaagggacgtgtcc	
6980	rev_03680_2.2	ggactagtccttctcatcgaaattattgacatcg	*Spe*I
6981	fwd_03680_3.1	gcatcaaatcaaataataaaaatatcagatgatctacgaaggatgaaattttcagggacaac	
6982	rev_03680_3.2	ggacacgtcccttccttacaaaaacagtgcttttatctactccgatagcttc	
7527	fwd_03690_1.1	ggctgcaggatttgtacgtaaccaatgtgcttttcacc	*Pst*I
7528	rev_03690_1.2	gttgcaaataccgatgagcgattattttttattttaagcggaaaggacacg	
7529	fwd_03690_2.1	cctgaaaaatttcatccttcgtagaatatgaaaaaatatcttattctgttggc	
7530	rev_03690_2.2	ccactagtgtattcacgagcgggttcaatagaattagtgg	*Spe*I
7531	fwd_03690_3.1	cgtgtcctttccgcttaaaataaaaaataatcgctcatcggtatttgcaac	
7532	rev_03690_3.2	gccaacagaataagatattttttcatattctacgaaggatgaaattttcagg	
7533	fwd_03700_1.1	ggctgcagcgcaagacttctgattgtacaagagaccg	*Pst*I
7534	rev_03700_1.2	gttgcaaataccgatgagcattttattgatttacgtatgatttaagtcgc	
7535	fwd_03700_2.1	cctgaaaaatttcatccttcgtagaaacaagctaaaaaataatatgac	
7536	rev_03700_2.2	ccactagtccatcttttgaaacggctgagatacttgc	*Spe*I
7537	fwd_03700_3.1	gcgacttaaatcatacgtaaatcaataaaatgctcatcggtatttgcaac	
7538	rev_03700_3.2	gtcatattattttttagcttgtttctacgaaggatgaaattttcagg	
6995	fwd_03710_1.1	cgctgcagcagaaaataatgttcagaaagc	*Pst*I
6996	rev_03710_1.2	aaaaatttcatccttcgtagattattttttagcttgtttctatttgtc	
6997	fwd_03710_2.1	gagtagataaaagcactgttacgtgttggaatgacagcgg	
6998	rev_03710_2.2	ggactagtttcctgcaatcgcacttgatac	*Spe*I
6999	fwd_03710_3.1	gacaaatagaaacaagctaaaaaataatctacgaaggatgaaattttcagggacaac	

7000	rev_03710_3.2	ccgctgtcattccaacacgtaacagtgctttatctactccgatagcttc	
7001	fwd_03720_1.1	cgctgcagtccattgataatcagcgagag	*Pst*I
7002	rev_03720_1.2	aaaaatttcatccttcgtagattttttctgtttgtaagaacaagaatcgcc	
7003	fwd_03720_2.1	gagtagataaaagcactgttagtaaaaaggattttcttttc	
7004	rev_03720_2.2	ggactagtctcctttgaagagaggaagcc	*Spe*I
7005	fwd_03720_3.1	ggcgattcttgttcttacaaacagaaaaaatctacgaaggatgaaattttcagggacaac	
7006	rev_03720_3.2	gaaaagaaatccttttactaacagtgctttatctactccgatagcttc	
7059	fwd_03610_1.1	cgctgcagaatactctatttacacgg	*Pst*I
7060	rev_03610_1.2	aaaaatttcatccttcgtagttttataaattttggtg	
7061	fwd_03610_2.1	gagtagataaaagcactgttttttttgaaactgtcatttgg	
7062	rev_03610_2.2	ggactagtaagttgcccaatttctgc	*Spe*I
7063	fwd_03610_3.1	caccaaaatttataaaactacgaaggatgaaattttcagggacaac	
7064	rev_03610_3.2	ccaaatgacagtttcaaaaaaaacagtgctttatctactccgatagcttc	
7065	fwd_03620_1.1	cgctgcagattagtatgttggcattgg	*Pst*I
7066	rev_03620_1.2	aaaaatttcatccttcgtagaatattttctttaaagtatgatc	
7067	fwd_03620_2.1	gagtagataaaagcactgttaatttgtttttttatcttacaatc	
7068	rev_03620_2.2	ggactagtttgagacagagtaaaagc	*Spe*I
7069	fwd_03620_3.1	gatcatactttaaagaaaatattctacgaaggatgaaattttcagggacaac	
7070	rev_03620_3.2	gattgtaagataaaaaacaaattaacagtgctttatctactccgatagcttc	
7085	fwd_03730_1.1	cgctgcagatagggtttatccctgctggggaagg	*Pst*I
7086	rev_03730_1.2	aaaaatttcatccttcgtagctctttttctatttatatctg	
7087	fwd_03730_2.1	gagtagataaaagcactgttaatctgtataaaaatgc	
7088	rev_03730_2.2	ggactagtcatcgcgaggatgaagcaaaatataatcc	*Spe*I
7089	fwd_03730_3.1	cagatataaatagaaaaagagctacgaaggatgaaattttcagggacaac	
7090	rev_03730_3.2	gcattttatacagattaacagtgctttatctactccgatagcttc	

7096	fwd_03630_1.1	cgctgcagacgctgataccagattgattgattttcaaacagg	*Pst*I
7097	rev_03630_1.2	aaaaatttcatccttcgtagatttcaatacttatcatttgtttttaatgc	
7098	fwd_03630_2.1	gagtagataaaagcactgttgcatcaatcagctacaaccaaaaatcc	
7099	rev_03630_2.2	ggactagttacttccgagtatttggttggc	*Spe*I
7100	fwd_03630_3.1	gcattaaaaacaaatgataagtattgaaatctacgaaggatgaaattttcagggacaac	
7101	rev_03630_3.2	ggattttggttgtagctgattgatgcaacagtgctttatctactccgatagcttc	
7102	FR227-1.1furAKOPstI	cgctgcagggaaatttggataaatacaataatg	*Pst*I
7103	FR228-1.2-furAKO	gagtagataaaagcactgttctgcttggtgttttcttttttag	
7104	FR229-2.1-furAKO	gaaaaatttcatccttcgtagccaagatggcagtagatttattac	
7105	FR230-2.2-furAKOSpeI	ggactagtattggcaaggttacgataacg	*Spe*I
7106	FR231-3.1-furAKO	ctaaaaaagaaaacaccaagcagaacagtgctttatctactc	
7107	FR232-3.2-furAKO	gtaataaatctactgccatcttggctacgaaggatgaaattttc	

	Trans-complementations and PCR screening		
7036	fwd_Ccan_03640	cgtaccatggcgtgttaccaaaagatagg	*Nco*I
7037	rev_Ccan_03640	tgactagttaaaacttcacattcactcc	*Spe*I
7038	fwd_Ccan_03650	cgtaccatggcgaatcaatcaatgataaagaaactactatatagcg	*Nco*I
7039	rev_Ccan_03650	tgactagttaaaacccaacatttacc	*Spe*I
7040	fwd_Ccan_03680	cgtaccatggcgcccaacgaaagagcatcaaatc	*Nco*I
7041	rev_Ccan_03680	tgactagttatcttggattgggtgctaaacc	*Spe*I
7042	fwd_Ccan_03690	cgtaccatggcgagaagaatatacataatattaacattgg	*Nco*I
7043	rev_Ccan_03690	tgactagttattgatttacgtatgatttaagtcgc	*Spe*I
7044	fwd_Ccan_03700	cgtaccatggcgaaaaaatatcttattctgttggc	*Nco*I
7045	rev_Ccan_03700	tgactagttatttgtcaactatttcagc	*Spe*I
7046	fwd_Ccan_03710	cgtaccatggcgacaatgaatagaaaatatttattttttgataatattactgggg	*Nco*I

7047	rev_Ccan_03710	tgactagttatggcaaaataatatactcgc	*Spe*I
7048	fwd_Ccan_03720	cgtaccatggcgtggaaatatacagttttaatagtgtccc	*Nco*I
7049	rev_Ccan_03720	tgactagttatctttttatatcattgattgaaattccg	*Spe*I
7077	fwd_Ccan_03660	cgtaccatggatagtcatatttggatagaaaagtgg	*Nco*I
7078	rev_Ccan_03660	tgactagttattgcttccgtgctacaaatcgg	*Spe*I
7079	fwd_Ccan_03670	cgtaccatggcgaagtcaaaaaaaatag	*Nco*I
7080	rev_Ccan_03670	tgactagttatctttcttcaaaataagc	*Spe*I
3451	fwd_16S	agagtttgatcctggctcag	
3454	rev_16S	gggttgcgctcgttg	

Sequencing			
3818	pMM25_fwd	gttttcccagtcacgac	
4730	pMM25_rev	ggcacgttccagttctttcag	
7125	ermF_seq1	atgctcaaattgtttgtttgtctcc	
7126	ermF_seq2	gagcaaacatataaccgaggaacaaagtgc	

qPCR			
7335	03640-F-qPCR	caatgcggctcgaatgactg	
7336	03640-R-qPCR	gggaatgggcgtagaaacca	
7337	03650-F-qPCR	tcggtgaggtggttgttacg	
7338	03650-R-qPCR	tacgcgtccttcgagcatac	
7339	03680-F-qPCR	caggcaaacaaagcgttgga	
7340	03680-R-qPCR	gttccgtaaggttctgccca	
7341	08720-F-qPCR	ggacagtgtttacttgttatcaagtc	
7342	08720-R-qPCR	gctataatgtgacgagctaaatcac	
7343	16S -F-qPCR	tgagtggctaagcgaaagtga	

7344	16S -R-qPCR	cttggtaaggttcctcgcgt	

pPM5 construction			
5470	PM177_ Fj_Pompa_fw	cgatgtcgactttttttttaacatttgattttgtatttaaaaaatttggtgttacttttgc	*Sal*I
5471	PM178_Fj_Pompa_rv	cgatccatggttaattttttttaattacaatttagttaattacaagcaaaagtaacacc	*Nco*I

Table S3 Plasmids used in the study

Plasmid	Description	Reference
	Vectors	
pMM13	*ori*ColE1, Em^R.	(5)
pMM25	*ori*ColE1, Km^R, Cfx^R.	(5)
pMM47.A	*ori*ColE1, *ori* pCC7, Ap^R, Cfx^R.	(5)
pPM5	*ori*ColE1, *ori* pCC7, Ap^R, Cfx^R; promoter of *ompA* (*Fjoh_0697*) from *Flavobacterium johnsoniae* was amplified by PCR using primers 5470 and 5471, digested with *Sal*I and *Nco*I, and inserted into the corresponding sites of pMM47.A, replacing the original *ermF* promoter.	This study

	Mutator Plasmids	
pFL1	*ermF* framed by the 5' and 3' regions of *Ccan_03610* cloned into pMM25	This study
pFL2	*ermF* framed by the 5' and 3' regions of *Ccan_03620* cloned into pMM25	This study
pFL3	*ermF* framed by the 5' and 3' regions of *Ccan_03630* cloned into pMM25	This study
pFL4	*ermF* framed by the 5' and 3' regions of *Ccan_03640* cloned into pMM25	This study
pFL5	*ermF* framed by the 5' and 3' regions of *Ccan_03650* cloned into pMM25	This study
pFL6	*ermF* framed by the 5' and 3' regions of *Ccan_03660* cloned into pMM25	This study
pFL7	*ermF* framed by the 5' and 3' regions of *Ccan_03670* cloned into pMM25	This study

pFL8	*ermF* framed by the 5' and 3' regions of *Ccan_03680* cloned into pMM25	This study
pFL9	*ermF* framed by the 5' and 3' regions of *Ccan_03690* cloned into pMM25	This study
pFL10	*ermF* framed by the 5' and 3' regions of *Ccan_03700* cloned into pMM25	This study
pFL11	*ermF* framed by the 5' and 3' regions of *Ccan_03710* cloned into pMM25	This study
pFL12	*ermF* framed by the 5' and 3' regions of *Ccan_03720* cloned into pMM25	This study
pFL13	*ermF* framed by the 5' and 3' regions of *Ccan_03730* cloned into pMM25	This study
pFL61	*ermF* framed by the 5' and 3' regions of *Ccan_15860* cloned into pMM25	This study

Trans-complementation Plasmids		
pFL14	*Ccan_03640* amplified with 7036 & 7037 and cloned into pPM5	This study
pFL15	*Ccan_03650* amplified with 7038 & 7039 and cloned into pPM5	This study
pFL16	*Ccan_03660* amplified with 7077 & 7078 and cloned into pPM5	This study
pFL17	*Ccan_03670* amplified with 7079 & 7080 and cloned into pPM5	This study
pFL18	*Ccan_03680* amplified with 7040 & 7041 and cloned into pPM5	This study
pFL19	*Ccan_03690* amplified with 7042 & 7043 and cloned into pPM5	This study
pFL20	*Ccan_03700* amplified with 7044 & 7045 and cloned into pPM5	This study
pFL21	*Ccan_03710* amplified with 7046 & 7047 and cloned into pPM5	This study
pFL22	*Ccan_03720* amplified with 7048 & 7049 and cloned into pPM5	This study

Table S4 Protein and iron concentration of products used in the study

	[Iron] (µM)	[Protein] (g/l)
Serotransferrin	41.2 ± 3.0	5.4 ± 0.2
Apotransferrin	0.5 ± 0.2	4.4 ± 0.1
Lactoferrin	37.4 ± 7.2	3.5 ± 0.1
Bovine transferrin	38.1 ± 3.5	4.3 ± 0.2
Hemoglobin	257.4 ± 16.3	5.9 ± 0.6
Human serum, heat inactivated (Millipore)	18.1 ± 1.0	49.0 ± 1.1
Human serum, heat inactivated (University Hospital of Basel)	19.5 ± 1.7	57.2 ± 5.2
Protein depleted human serum, heat inactivated	0.9 ± 0.6	N/A

Fig.S1
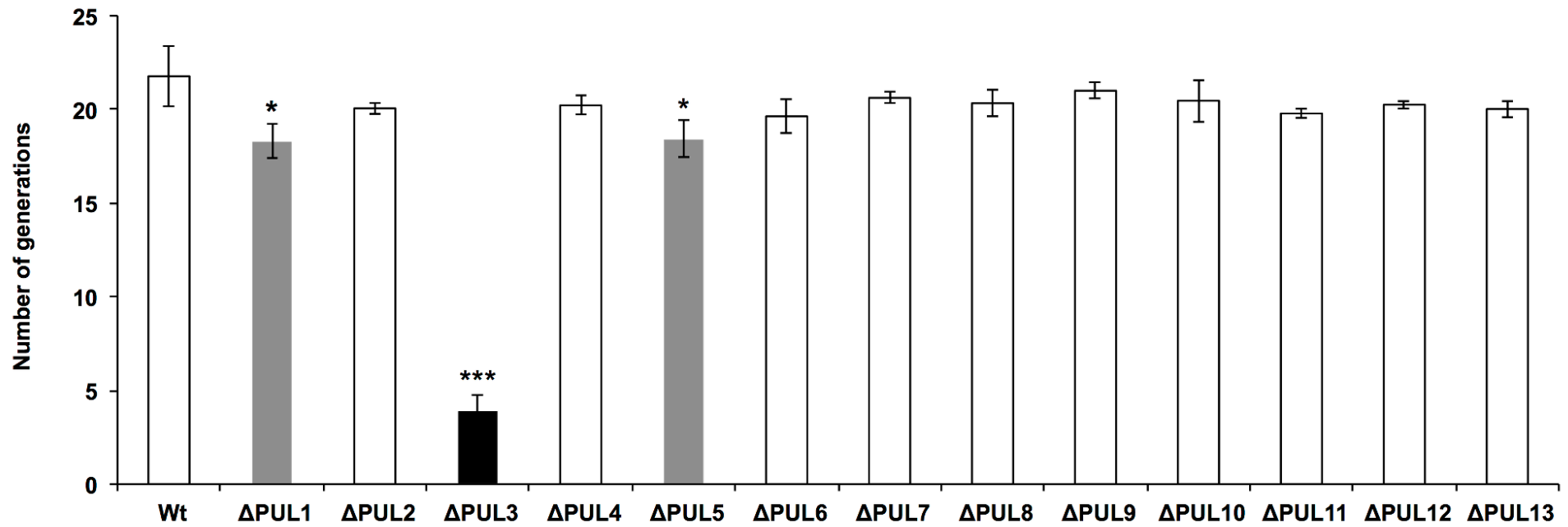
Figure S1.

Growth in HIHS of *C. canimorsus 5* mutants deleted from individual PULs

Number of generations achieved by each of the individual *PUL* deletion mutant after 23 hours in HIHS. The black bar and to a lesser extent the dark grey bars indicate significantly reduced growth scores with respect to wt. Error bars indicate standard deviations (average of 3 experiments).

(*) and (***) apply to comparisons to wt values and stand for *t*-test based error probabilities of <0.05 and <0.001 respectively.
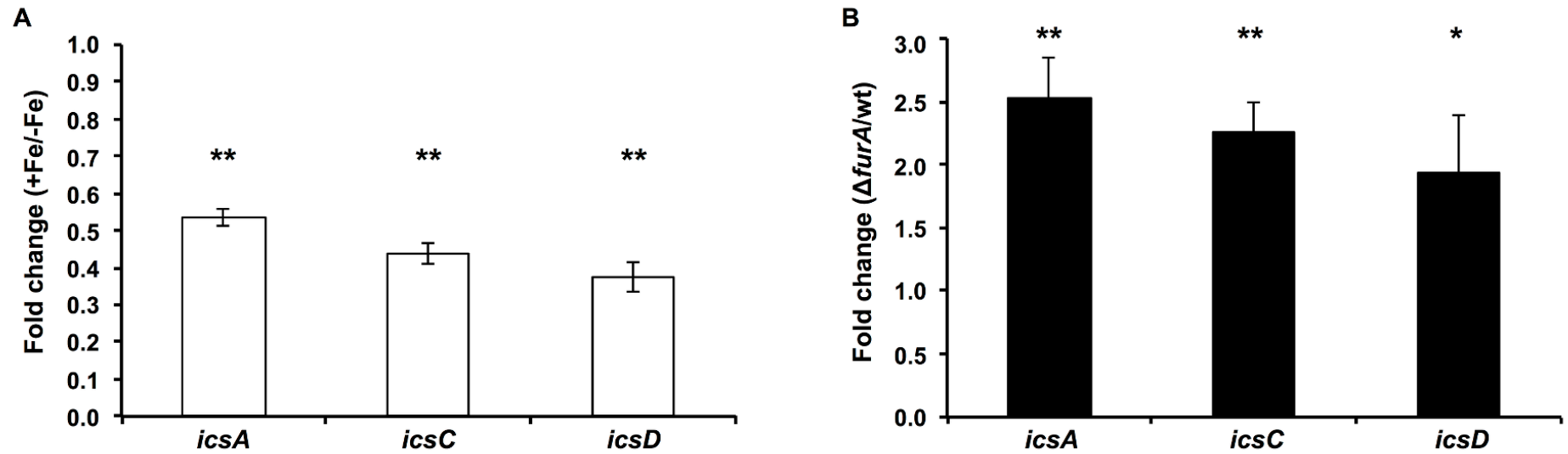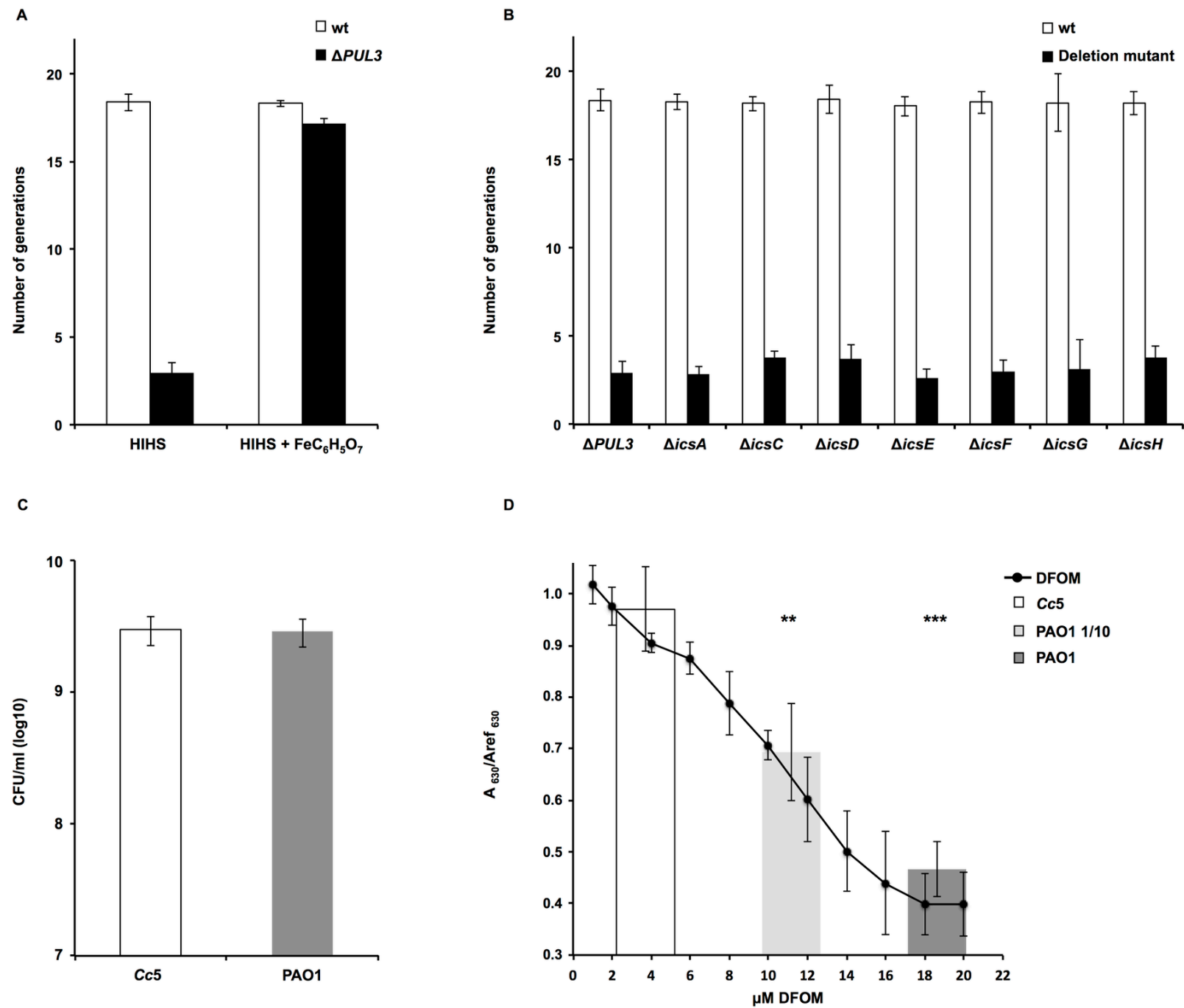
Figure S2.

Regulation of transcription of *PUL3* by free iron and the FurA transcriptional regulator

Fold change of mRNA levels of the two *susC* homologues *Ccan_03640* and *Ccan_03650* and the *susD* homologue *Ccan_03680*. (A) Relative mRNA levels from wt bacteria grown in HIHS plus iron (III) citrate (+Fe) *vs.* HIHS with no iron supplementation (-Fe). (B) Relative mRNA levels of *ΔfurA vs*. wt *Cc*5 grown in HIHS. Error bars represent the standard deviation (average of 3 experiments). (*) and (**) apply to comparisons to wt values and stand for *t*-test based error probabilities of <0.05 and <0.01 respectively.

Fig.S3

A

Number of generations

☐ wt
■ ΔPUL3

HIHS   HIHS + FeC$_6$H$_5$O$_7$

B

Number of generations

☐ wt
■ Deletion mutant

ΔPUL3 ΔicsA ΔicsC ΔicsD ΔicsE ΔicsF ΔicsG ΔicsH

C

CFU/ml (log10)

Cc5   PAO1

D

A$_{630}$/Aref$_{630}$

—●— DFOM
☐ Cc5
☐ PAO1 1/10
■ PAO1

**   ***

µM DFOM

Figure S3.

Iron capture from transferrin does not involve soluble factors

(A) Number of generations achieved by wt (white bars) and *ΔPUL3* (black bars) *C. canimorsus* bacteria after 23 hours of co-culture in HIHS alone or supplemented with 0.25 mM iron (III) citrate ($FeC_6H_5O_7$). (B) Number of generations achieved by the wt (white bars) and each of the individual *ics* deletion mutants (black bars) after 23 hours of co-culture in HIHS. (C) Total growth in HIHS of *P. aeruginosa* PAO1 wt (dark grey bar) and *Cc*5 wt (white bar). (D) Siderophore detection in *Cc*5 wt (white bar) and *P. aeruginosa* PAO1 wt (light and dark grey bars) HIHS culture supernatants using the chrome azurol S assay. Decrease of the ratio A/A_{ref} at 630 nm indicates presence of siderophore. Dots: dilution series of the iron chelator desferrioxamine mesylate (DFOM) used as standard curve. PAO1 1/10: PAO1 supernatant diluted 1 to 10 in ddH$_2$O. Error bars in all panels represent standard deviation (average of 3 experiments). (**) and (***) apply to comparisons to *Cc*5 wt values and stand for *t*-test based error probabilities of <0.01 and <0.001 respectively.
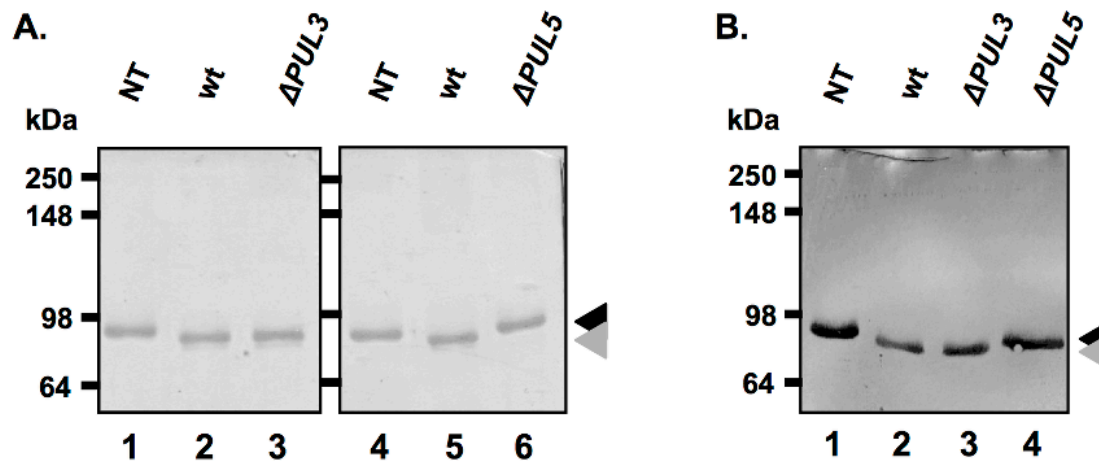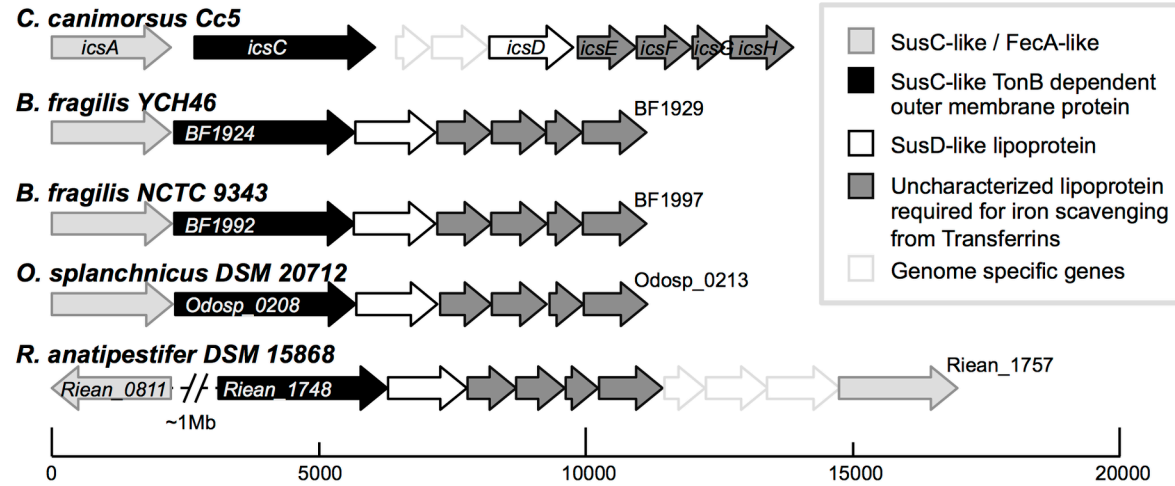
Figure S4.

Cleavage of human serotransferrin *N*-glycans by the Gpd complex

(A) Coomassie staining of SDS-PAGE loaded with STF incubated in absence (NT, lane 1 & 4) or presence of wt (lane 2 & 5), *PUL3* deleted (lane 3) or *PUL5* deleted (lane 6) *C. canimorsus*. (B) *Sambucus Nigra* Lectin (SNA) staining of human STF incubated in absence (NT, lane 1) or presence of wt (lane 2), *PUL3* deleted (lane 3) or *PUL5* deleted (lane 4) *C. canimorsus*. Numbers on the left indicate protein mass of the references in kDa. Grey and black arrows indicate a shift in electrophoretic mobility of STF.

Fig.S5

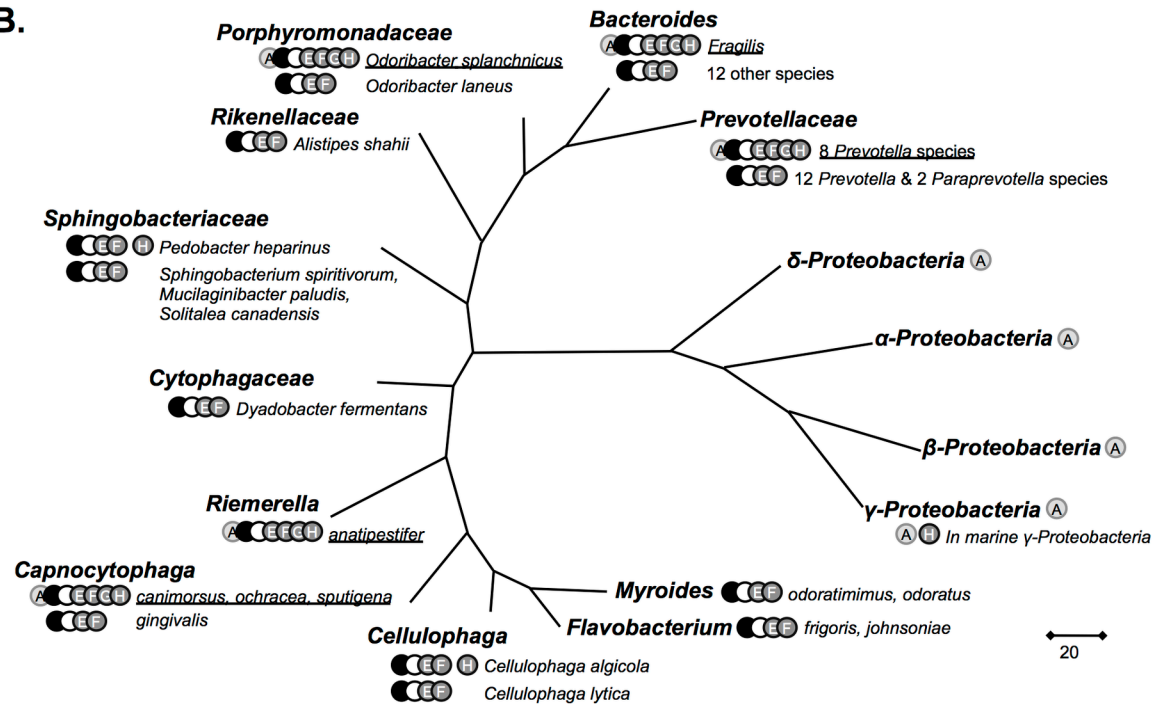**Figure S5.**

The ICS is mostly found among pathogenic members from the *Bacteroidetes* phylum and has broad species specificity

(A) Orthologous *PULs* of *Cc5 PUL3* identified in the Complete Genomes database. The *PULs* display has been limited to the genes implicated in iron scavenging with a putative TonB-dependent outer membrane protein ortholog to either *icsA* or *icsC*. For the sake of readability, only the largest SusC like homologs and the last represented genes are tagged here. In the case of *R. anatipestifer* DSM 15868, an additional FecA-like protein that shares higher similarity with other orthologs than with its paralog is found at approximately 1 Mb from the SusC like protein. (B) Non-exhaustive occurrences of *PUL3* genes among other bacteria spotted on a representative 16S rRNA phylogenetic tree. The evolutionary history has been inferred using the Maximum Parsimony method and the consensual 16S rRNA sequences from the different taxa where genes from *PUL3* were found. Spots indicate major combinations of *PUL3* encoded genes found within each taxon. Letters in the round spots refer to the proteins encoded by *PUL3*, namely IcsA (A), IcsC (C), IcsD (D), IcsE (E), IcsF (F), IcsG (G) and IcsH (H). Underlined taxon names indicate the occurrence of strains exhibiting all seven *ics* genes in their genome.

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