

Table S1. Primers used in this study.

Primer	Sequence (5' - 3')
Gene Disruption Primers	
<i>fdhU</i> -FW	GCTTTAGCACTGATTTTTGGTTTTGTTTTGGC
<i>fdhU</i> -RV	CCTTGGATAGCAGGTATTTTACTCAGTGC
<i>fdhT</i> -FW	TTGAATTCCTTTAAACAAAAATATTTAATCAATTTTTGGG
<i>fdhT</i> -RV	CCTTTAAGTTGATTTTTAAAAAGTGTTTTTTGTAAAATAC
<i>fdhA</i> -FW	CATTTGGTTATGGCGCTATGACAAACC
<i>fdhA</i> -RV	CATTTTCCATCCTTACTGATTCTACAAAGCC
<i>fdhU</i> -iPCR-FW	GATATCGGTACCCTATAAGTAATTTTCACTGTTTATCCTTTAAGTTG
<i>fdhU</i> -iPCR-RV	GATATCGGTACCGTGGACCCACACTAAGATTTTTAATCCAAAAGCC
Complement Primers	
<i>fdhU</i> -C-FW	GATATCTCTAGACAACCTAAAGGATAAACAGTGAAAATTACTTATAG
<i>fdhU</i> -C-RV	GATATCCAATTGGAGTTTTGAGAATAAAAAGCCTTTTTTAAGGC
<i>fdhT</i> -C-FW	GGCACTAGTGATTACATTTTTAGGATCTTCTTTGAATTCTTTAAAC
<i>fdhT</i> -C-RV	CCGCAATTGCACTGTTTATCCTTTAAGTTGATTTTTAAAAAGTG
Operon Primers	
Primer-A	GGGAGCATTTTTGTTTGGTTTTGG
Primer-B	TATACCTTCTTTAAAAGCTTTTGGTAAAAAG
Primer-C	GAAAATTACTTATAGTTTAAATTTACAAGGTGAAGC
Primer-D	CGGTTTTTGCATCTTGAGGTATGG
RT-q-PCR Primers	
<i>fdhU</i> -q-FW	AACTTTCCTGCTGTAGCTGTGG
<i>fdhU</i> -q-RV	CCTTCAAAGGCACGATAAGTCCAACC
<i>fdhT</i> -q-FW	AGGGCTTAATGGTTGGAGTCCTGA
<i>fdhT</i> -q-RV	AGTACTCGCCAGCAACTTCGTCTT
<i>rpoA</i> -q-FW	CGAGCTTGCTTTGATGAGTG
<i>rpoA</i> -q-RV	AGTCCCACAGGAAAACCTA

Table S2. Plasmids used in this study.

Plasmid	Description	Reference
pGem-T	<i>E. coli</i> replicating plasmid with Ampicillin resistance cassette used for construction of <i>C. jejuni</i> gene disruption constructs.	Promega
pUC18-K2	Parent plasmid containing the <i>aphA-3</i> kanamycin resistance cassette.	(4)
pRY109	Parent plasmid containing the <i>CAT</i> chloramphenicol resistance cassette	(5)
pRY112	<i>C. jejuni</i> replicating plasmid with <i>CAT</i> chloramphenicol resistance cassette	(5)
<i>PatpF'</i> ::GFP pRY112	<i>C. jejuni</i> replicating plasmid with GFP expressed from the <i>atpF'</i> regulatory region	(1)
pRRC	<i>C. jejuni</i> integrative plasmid with a <i>CAT</i> chloramphenicol resistance cassette	(2)

Table S3. *C. jejuni* strains used in this study.

Strain	Description	Reference
Wild Type <i>C. jejuni</i> strain 81-176	Wild type <i>C. jejuni</i>	(3)
$\Delta fdhU$	Gene <i>fdhU</i> disrupted with the kanamycin resistance cassette	This study
$\Delta fdhT$	Gene <i>fdhT</i> disrupted with the kanamycin resistance cassette	This study
$\Delta fdhU^c$	Strain $\Delta fdhU$ complemented with pRRC driving expression of <i>fdhU</i> from the Pchlor regulatory region.	This study
$\Delta fdhT^c$	Strain $\Delta fdhT$ complemented with pRRC driving expression of <i>fdhT</i> from the Pchlor regulatory region.	This study
$\Delta fdhA$	Gene <i>fdhA</i> disrupted with the kanamycin resistance cassette	This study
$\Delta fdhA$	Gene <i>fdhA</i> disrupted with the chloramphenicol resistance cassette	This study
$\Delta fdhU\Delta fdhA$	Gene <i>fdhU</i> disrupted with the kanamycin resistance cassette and <i>fdhA</i> disrupted with the chloramphenicol resistance cassette	This study
$\Delta fdhU$ <i>PatpF'::GFP</i> pRY112	Strain $\Delta fdhU$ containing the <i>PatpF'::GFP</i> pRY112 plasmid	This study
$\Delta fdhT$ <i>PatpF'::GFP</i> pRY112	Strain $\Delta fdhT$ containing the <i>PatpF'::GFP</i> pRY112 plasmid	This study
$\Delta fdhA$ <i>PatpF'::GFP</i> pRY112	Strain $\Delta fdhA$ containing the <i>PatpF'::GFP</i> pRY112 plasmid	This study

Table S4. FdhT and FdhU are conserved in a variety of bacterial species. Shown are select homologs derived from BLAST searches of FdhT and FdhU against other bacterial genomes.

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	FdhT					FdhU				
	Identity	Similarity	Coverage	E Value	Accession Number	Identity	Similarity	Coverage	E Value	Accession Number
<i>Campylobacter coli</i>	88%	94%	99%	0.00	ZP_07401456.1	92%	99%	100%	3.00E-50	ZP_07401457.1
<i>Campylobacter fetus</i>	65%	78%	98%	0.00	YP_891776.1	73%	92%	98%	4.00E-41	YP_891777.1
<i>Helicobacter hepaticus</i>	48%	67%	99%	5.00E-135	NP_860829.1	68%	86%	96%	2.00E-34	NP_860830.1
<i>Arcobacter butzleri</i>	48%	65%	99%	1.00E-136	ZP_07890639.1	66%	83%	93%	5.00E-34	ZP_07890640.1
<i>Helicobacter mustelae</i>	47%	65%	99%	1.00E-118	YP_003516553.1	57%	75%	96%	3.00E-28	YP_003516552.1
<i>Enterobacter aerogenes</i>	46%	63%	99%	1.00E-126	YP_004593790.1	67%	83%	93%	3.00E-35	YP_004593789.1
<i>Klebsiella pneumoniae</i>	45%	62%	99%	5.00E-123	YP_001335167.1	64%	83%	93%	5.00E-33	YP_001335166.1
<i>Salmonella Typhimurium</i> ^a	44%	62%	98%	5.00E-123	NP_460918.2	66%	84%	93%	1.00E-34	NP_460919.1
<i>Shigella flexneri</i>	44%	62%	99%	2.00E-113	NP_837542.1	66%	84%	93%	6.00E-34	NP_837543.1
<i>Citrobacter rodentium</i>	44%	62%	98%	1.00E-122	YP_003365568.1	64%	84%	93%	2.00E-33	YP_003365569.1
<i>Pseudomonas aeruginosa</i>	44%	57%	93%	3.00E-92	NP_252323.1	51%	72%	98%	3.00E-26	NP_252322.1
<i>Escherichia coli</i>	43%	62%	98%	8.00E-113	NP_416439.1	66%	84%	93%	8.00E-35	NP_416440.1
<i>Lactobacillus oris</i>	43%	62%	96%	4.00E-107	ZP_07730384.1	48%	80%	92%	2.00E-27	ZP_07730371.1
<i>Yersinia pestis</i>	43%	60%	98%	4.00E-118	NP_667871.1	64%	84%	93%	3.00E-33	NP_667872.1
<i>Thermincola potens</i>	41%	56%	99%	2.00E-96	YP_003641387.1	45%	68%	100%	6.00E-22	YP_003641386.1

^a*Salmonella enterica* serovar Typhimurium

1. **Apel, D., Ellermeier, J., Pryjma, M., DiRita, V. J., Gaynor, E. C.** Submitted. Characterization of *Campylobacter jejuni* racRS mutants reveals a role in the heat shock response, motility, and maintenance of cell length population homogeneity. *J Bacteriol*.
2. **Karlyshev, A. V., and B. W. Wren.** 2005. Development and application of an insertional system for gene delivery and expression in *Campylobacter jejuni*. *Appl Environ Microbiol* **71**:4004-13.
3. **Korlath, J. A., M. T. Osterholm, L. A. Judy, J. C. Forfang, and R. A. Robinson.** 1985. A point-source outbreak of campylobacteriosis associated with consumption of raw milk. *J Infect Dis* **152**:592-6.
4. **Menard, R., P. J. Sansonetti, and C. Parsot.** 1993. Nonpolar mutagenesis of the ipa genes defines IpaB, IpaC, and IpaD as effectors of *Shigella flexneri* entry into epithelial cells. *J Bacteriol* **175**:5899-906.
5. **Yao, R., R. A. Alm, T. J. Trust, and P. Guerry.** 1993. Construction of new *Campylobacter* cloning vectors and a new mutational cat cassette. *Gene* **130**:127-30.