Table S1. *perR* mutations identified in the spontaneous OX^R mutants from *C. jejuni* 11168 P_{katA}-*cat* and CMT P_{katA}-*cat* isolates

11168 P_{katA}-*cat*		CMT P_{katA}-*cat*	
Mutation*	AA change	Mutation*	AA change
+A (120-121)	Frameshift	C380A	127Ala→Asp
-T (209)	Frameshift	G115T	39Glu→TAA
-AT (251-252)	Frameshift	G337T	113Glu→TAA
-A (338)	Frameshift	G286T	96Glu→TAA
-A (338)	Frameshift	G337T	113Glu→TAG
-A (36)	Frameshift	G328T	110Glu→TAG
-A (36)	Frameshift	G286T	96Glu→TAA
-G (33)	Frameshift	C137A	46Ser→TAA
-G (33)	Frameshift	C137A	46Ser→TAA
-A (39)	Frameshift	G296T	99Ser→Ile
G275A	92Cys→Tyr	G286T	96Glu→TAA
+T (123-124)	Frameshift	G244T	82Glu→TAA
+T (240-241)	Frameshift	C396A	132Cys→TGA
+T (240-241)	Frameshift	G266T	89Cys →Phe
+A (344-345)	Frameshift	G337T	113Glu→TAA
		G244T	82Glu→TAA

*The numbers are in relative to the first nucleotide sequence of the *perR* gene or the first amino acid in the PerR protein. "+" or "-" in front of a nucleotide indicates either a base insertion or a deletion.

Table S2 PCR primers used in this study

Primers	Sequences	PCR products or purposes
cat-F	TGGAGCGGACAACGAGTAAA	*cat* gene
cat-R	TCAGTGCGACAAACTGGGATT	
mutY-5F	TCGGGTTTTAGCGTATTGCT	*mutY*-5’ fragment
mutY-5R	TTTACTCGTTGTCCGCTCCAAGCCCCAAACTTATCCACG	
mutY-3F	AATCCCAGTTTGTCGCACTGAATTTGCGATACAGAAAAGCCAA	*mutY*-3’ fragment
mutY-3R	GCTGTTTTTGGAGGATCTGC	
mutY-cF	GTTGGATCACCTCCTTTACTTCCTCCGCTACAAAAAT	*mutY* gene for chromosomal complementation
mutY-cR	AGACTTATTACTTTGTACTATGCTGTTTTTGGAGGATCT	
perR-5F	CAAGTGATCCATGATTGTGC	*perR*-5’ fragment
perR-5R	TTTACTCGTTGTCCGCTCCACACATAGTCTTTGCGGAGTA	
perR-3F	AATCCCAGTTTGTCGCACTGAATGTTGTTTGCACCAAATGT	*perR*-3’ fragment
perR-3R	TCGCATAAACTTTGCTTATCT	
perR-cF	AGACTTATTACTTTGTACTTGAAAATGTTAAAATTGGC	*perR* gene for chromosomal complementation
perR-cR	GTTGGATCACCTCCTTTTCTCTAAAAGAGTGCAATCAG	
pRRK-lF	AGTACAAAGTAATAAGTCTCACAACTATTACTTCA	For linearization of the pRRK plasmid
pRRK-lR	AAAGGAGGTGATCCAACCGC	
pRRK-seqF	GAATCAGCGACTGGGGTG	For sequencing of inserts in the pRRK plasmid
pRRK-seqR	AAGCGCGCTGCCTAT	
perR-rF	AGGTTATGGACAAGGTGTGG	A 949 bp fragment, see experimental procedures
perR-rR	TTTACTCGTTGTCCGCTCCAAGAGTGCAATCAGATAGTAAAAAG	
0323-rF	AATCCCAGTTTGTCGCACTGAGAAGGCGATTGCAAAGATAGGT	A 802 bp fragment, see experimental procedures
0323-rR	TGAACTCACGCCAAAGCTAA	
perR-HisF	CACCATCACCATCACGGATCCGAATTACTACAAATGCTTAAAAAAC	*perR* gene for cloning into pQE-30 plasmid
perR-HisR	CCAAGCTCAGCTAATTAAGCTTTTAAAATATATGGGTTATTTTAACC	
perR-rtF	TCAATCTCTTTAGCGACGGTTT	qRT-PCR amplicon of *perR* gene
perR-rtR	CACATTTGGTGCAAACAACA	
katA-rtF	GAACGCGATGTGAGAGGTTT	qRT-PCR amplicon of *katA* gene
katA-rtR	CGGATGAAGAATGTCGGAGT	
ahpC-rtF	TTCGTTCTTGCTTGATGCTG	qRT-PCR amplicon of *ahpC* gene
ahpC-rtR	TTCATCGCCCTTATTCCATC	
*cat*ORF-F	AGACTTATTACTTTGTACTAAATTCTCCTTTGTGATTTTTAAAATATATTTTG	*cat* gene sequence without promoter
*cat*ORF-R	GAATTGCATTGTTTTCTCCTAAATAATAAATTTTATTAATTAG	
PkatA-F	GAGAAAACAATGCAATTCACAAAGATTG	Promoter sequence of *katA* gene
PkatA-R	GTTGGATCACCTCCTTTTTATTTATTCAGCAAGTCTTGTAATTC	
ahpC-seqF	ACGCATTTGTTTGCATAGAC	A 1069 bp ahpC gene sequencing product
ahpC-seqR	TCTTCGCCTGCCATATTTTA	
katA-seqF	TCACAATACACACAACTTACAC	A 1987 bp katA gene sequencing product
katA-seqR	TTCTTGCAAAATTAAAAGCCA	
katA-seqM	GGAATTTATAAGCATCGCGG	
perR-seqF	ATGGAAAAACAAGTGAGGTG	A 757 bp perR gene sequencing product
perR-seqR	CACTATGATTTGAAGTTATTTGAGT	
sodB-seqF	AAGCACCTAGTAATGCTGAG	A 996 bp sodB gene sequencing product
sodB-seqR	CCATTCTAGCACAAAAAGGATT	
fur-seqF	TTTTTGTGTAGCAAGAATCG	A 852 bp fur gene sequencing product
fur-seqR	CAACAACAGCATTGACACTT	

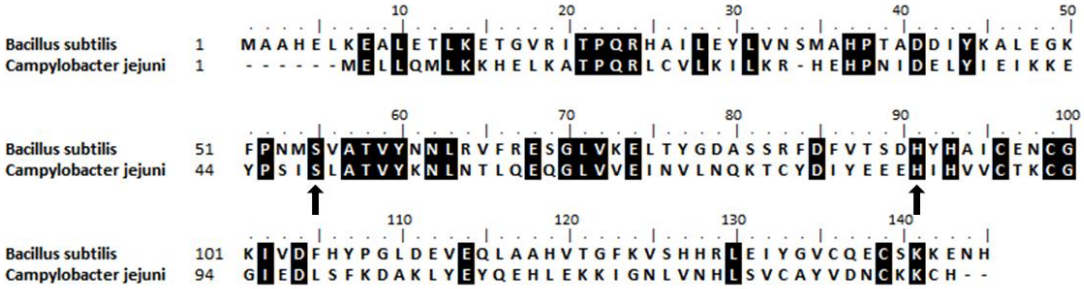

Fig. S1. Alignment of PerR amino acid sequences between *Bacillus subtilis* and *C. jejuni*. The bacterial species are indicated on the left. The solid arrows represent the 48Ser and 84His that are mutated sites of two *C. jejuni* spontaneous OX^R mutants

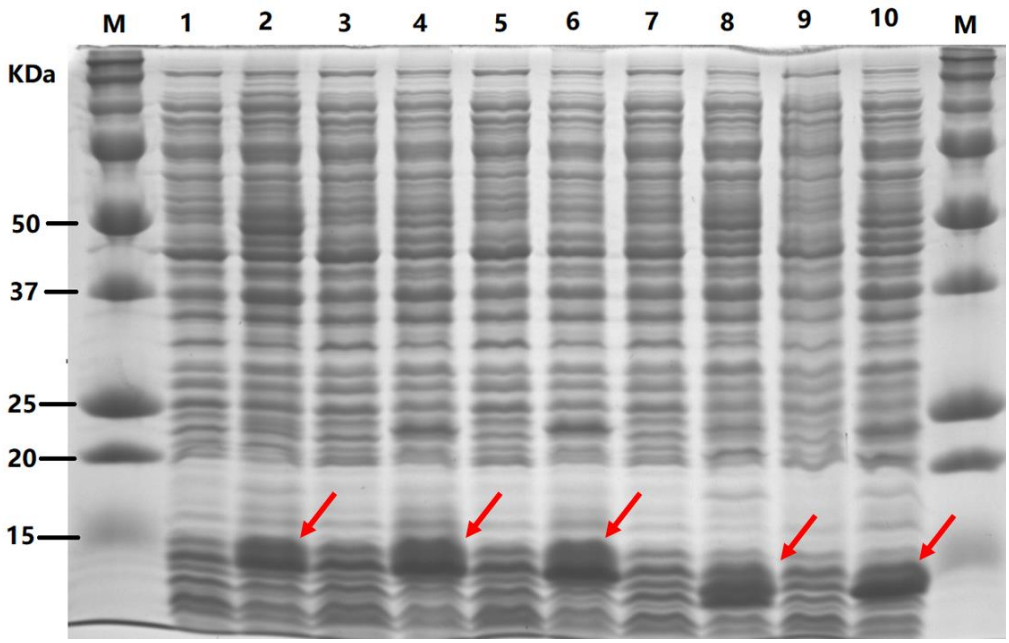

Fig. S2. SDS-PAGE analysis of rPerR produced in *E. coli*. Lane M, prestained molecular mass markers (Bio-Rad); Lanes 1, 3, 5, 7, and 9, whole-cell lysates of *E. coli* constructs expressing PerR of 11168, CMT $perR_{C250A}$, CMT $perR_{C143A}$, CMT $perR_{G319T,}$ and 11168 $perR_{A338Del}$, respectively, before induction; Lanes 2, 4, 6, 8, and 10, whole-cell lysates of *E. coli* constructs expressing PerR of 11168, CMT $perR_{C250A}$, CMT $perR_{C143A}$, CMT $perR_{G319T,}$ and 11168 $perR_{A338Del,}$ respectively, after induction with 1 mM isopropyl-β-D-thiogalactopyranoside (IPTG). Red arrows indicate the locations of rPerR proteins expressed in different *E. coli* isolates