Supplemental Material:

	C. jejuni	*C. jejuni*	*C. coli*	*C. coli*	Standard[a]
antibiotic	S	R	S	R	
gentamicin	<=2	>=4	<=2	>=4	NARMS
telithromycin	<=4	>=8	<=4	>=8	NARMS
clindamycin	<=0.5	>=1	<=1	>=2	NARMS
azithromycin	<=0.25	>=0.5	<=0.5	>=1	NARMS
erythromycin	<=4	>=8	<=8	>=16	CLSI
chloramphenicol	<=16	>=32	<=16	>=32	NARMS
ciprofloxacin	<=0.5	>=1	<=0.5	>=1	CLSI
nalidixic acid	<=16	>=32	<=16	>=32	NARMS
doxycycline	<=0.5	>=1	<=1	>=2	NARMS
tetracycline	<=1	>=2	<=2	>=4	CLSI

Table S2: *Campylobacter* sp. breakpoints used in this study.
[a]Standard refers to whether the breakpoint was established by CLSI or, if there is no CLSI breakpoint, by NARMS. Units are μg/ml.

antibiotic	S	I	R	Standard[a]
gentamicin	<= 4	8	>=16	CLSI
streptomycin	<=32	N/A	>=64	NARMS
amoxicillin-clavulanic acid	<=8/4	16/8	>=32/16	CLSI
cefoxitin	<=8	16	>=32	CLSI
ceftiofur	<=2	4	>=8	CLSI
ceftriaxone	<=1	2	>=4	CLSI
sulfamethoxazole/sulfisoxazole	<=256	N/A	>=512	CLSI
co-trimoxazole	<=2/38	N/A	>=4/76	CLSI
azithromycin	<=16	N/A	>=32	NARMS
ampicillin	<=8	16	>=32	CLSI
chloramphenicol	<=8	16	>=32	CLSI[b]
ciprofloxacin	<=0.06	0.12-0.5	>=1	CLSI[c]
nalidixic acid	<=16	N/A	>=32	CLSI
tetracycline	<= 4	8	>=16	CLSI
amikacin	<=16	32	>=64	CLSI

Table S3: *E. coli* and *S. enterica* breakpoints.
[a]Standard refers to whether the breakpoint was established by CLSI or, if there is no CLSI breakpoint, by NARMS. Units are μg/ml.
[b]For E. coli isolates, the NARMS convention of using Salmonella breakpoints was followed.
[c]For S. enterica, isolates were scored as resistant to ciprofloxacin if they were intermediately susceptible ("I").

Gene as determined by AMRFinder	Predicted antibiotic resistance
aac(3)	gentamicin
aac(3)-I	gentamicin
aac(3)-Id	gentamicin
aac(3)-II	gentamicin
aac(3)-IId	gentamicin
aac(3)-IV	gentamicin
aac(3)-VIa	gentamicin
aac(6')-Ib	amikacin
aac(6')-Ib4	gentamicin
aac(6')-Ie	amikacin, gentamicin
aac(6')-IIc	gentamicin
aadA	streptomycin
aadA1	streptomycin
aadA12	streptomycin
aadA13	streptomycin
aadA15	streptomycin
aadA2	streptomycin
aadA21	streptomycin
aadA22	streptomycin
aadA25	streptomycin
aadA29	streptomycin
aadA4	streptomycin
aadA5	streptomycin
aadA6	streptomycin
aadA7	streptomycin
aadA8	streptomycin
aadE	streptomycin

abc-f	azithromycin
ampC	amoxicillin-clavulanic acid, ampicillin
ant(2'')-Ia	gentamicin, kanamycin
ant(3'')	streptomycin
ant(6)	streptomycin
ant(6)-Ia	streptomycin
aph(2'')-Ig	amikacin, gentamicin
aph(2'')-IIIa	amikacin, gentamicin
aph(3'')	streptomycin
aph(3'')-Ib	streptomycin
aph(3')-I	kanamycin
aph(3')-Ia	kanamycin
aph(3')-Id	kanamycin
aph(3')-II	kanamycin
aph(3')-IIa	kanamycin
aph(3')-IIIa	amikacin, kanamycin
aph(3')-VIIa	kanamycin
aph(6)-I	streptomycin
aph(6)-Ic	streptomycin
aph(6)-Id	streptomycin
armA	amikacin, gentamicin
bla_{CARB-2}	ampicillin
bla_{CMY}	amoxicillin-clavulanic acid, ampicillin, cefoxitin, ceftiofur, ceftriaxone
bla_{CMY-2}	amoxicillin-clavulanic acid, ampicillin, cefoxitin, ceftiofur, ceftriaxone

bla$_{CMY-5}$	amoxicillin-clavulanic acid, ampicillin, cefoxitin, ceftiofur, ceftriaxone
bla$_{CMY-61}$	amoxicillin-clavulanic acid, ampicillin, cefoxitin, ceftiofur, ceftriaxone
bla$_{CMY-7}$	amoxicillin-clavulanic acid, ampicillin, cefoxitin, ceftiofur, ceftriaxone
bla$_{CTX-M}$	ampicillin, ceftriaxone
bla$_{CTX-M-1}$	ampicillin, ceftriaxone
bla$_{CTX-M-24}$	ampicillin, ceftriaxone
bla$_{CTX-M-65}$	ampicillin, ceftriaxone
bla$_{HER}$	ampicillin
bla$_{HER-1}$	ampicillin
bla$_{HER-3}$	ampicillin
bla$_{LAT-1}$	amoxicillin-clavulanic acid, ampicillin, cefoxitin, ceftiofur, ceftriaxone
bla$_{OXA}$	ampicillin
bla$_{OXA-1}$	ampicillin
bla$_{OXA-184}$	ampicillin, amoxicillin-clavulanic acid, cefoxitin, ceftriaxone, meropenem

bla$_{OXA-193}$	ampicillin, amoxicillin-clavulanic acid, cefoxitin, ceftriaxone, meropenem
bla$_{OXA-2}$	ampicillin
bla$_{OXA-449}$	ampicillin
bla$_{OXA-450}$	ampicillin
bla$_{OXA-460}$	ampicillin
bla$_{OXA-461}$	ampicillin
bla$_{OXA-489}$	ampicillin
bla$_{OXA-493}$	ampicillin
bla$_{OXA-61}$	ampicillin
bla$_{SHV-12}$	ampicillin, ceftriaxone
bla$_{SHV-2A}$	ampicillin, ceftriaxone
bla$_{TEM}$	ampicillin
bla$_{TEM-1}$	ampicillin
bla$_{TEM-116}$	ampicillin
bla$_{TEM-135}$	ampicillin
catA1	chloramphenicol
catA2	chloramphenicol
catB3	chloramphenicol
cmlA	chloramphenicol

cmlA1	chloramphenicol
cmlA5	chloramphenicol
cmlA6	chloramphenicol
dfr7	trimethoprim-sulfamethoxazole*
dfrA1	trimethoprim-sulfamethoxazole*
dfrA12	trimethoprim-sulfamethoxazole*
dfrA14	trimethoprim-sulfamethoxazole*
dfrA15	trimethoprim-sulfamethoxazole*
dfrA17	trimethoprim-sulfamethoxazole*
dfrA19	trimethoprim-sulfamethoxazole*
dfrA5	trimethoprim-sulfamethoxazole*
dfrB	trimethoprim-sulfamethoxazole*
dfrI	trimethoprim-sulfamethoxazole*
ere(A)	azithromycin, erythromycin
erm(42)	azithromycin, clindamycin, erythromycin
floR	chloramphenicol, florfenicol
lnu(G)	clindamycin
mef(B)	azithromycin, erythromycin
mph(A)	azithromycin, erythromycin
mph(E)	azithromycin, erythromycin
msr(E)	azithromycin, erythromycin
oqxA	ciprofloxacin, nalidixic acid
oqxB	ciprofloxacin, nalidixic acid
qnrA1	ciprofloxacin, nalidixic acid
qnrB	ciprofloxacin, nalidixic acid
qnrB19	ciprofloxacin, nalidixic acid
qnrB2	ciprofloxacin, nalidixic acid
qnrB77	ciprofloxacin, nalidixic acid
qnrS1	ciprofloxacin, nalidixic acid

qnrS2	ciprofloxacin, nalidixic acid
sul1	sulfamethoxazole, sulfisoxazole, trimethoprim-sulfamethoxazole*
sul1delta	sulfamethoxazolesulfisoxazole, trimethoprim-sulfamethoxazole*
sul2	sulfamethoxazole, sulfisoxazole, trimethoprim-sulfamethoxazole*
sul3	sulfamethoxazole, sulfisoxazole, trimethoprim-sulfamethoxazole*
tet	tetracycline
tet(32)	tetracycline
tet(A)	tetracycline
tet(B)	tetracycline
tet(C)	tetracycline
tet(D)	tetracycline
tet(G)	tetracycline
tet(M-W-O-S)	tetracycline
tet(M)	tetracycline
tet(O)	tetracycline
tetA	tetracycline

Table S4: Predicted susceptibility based on acquired resistance.
*trimethoprim-sulfamethoxazole requires both *dfr*-family and *sul* family genes.

Species	drug	mutation[a]	n	# resistant (%)	# sensitive (%)
C. coli	ciprofloxacin	GyrA:T86I	87	87 (100%)	0
C. coli	ciprofloxacin	none observed	207	0	207 (100%)
C. jejuni	ciprofloxacin	GyrA:T86I	85	84 (99%)	1 (1%)
C. jejuni	ciprofloxacin	GyrA:T86K	1	1 (100%)	0
C. jejuni	ciprofloxacin	GyrA:T86V	1	1 (100%)	0
C. jejuni	ciprofloxacin	none observed	389	3 (1%)	386 (99%)
C. coli	nalidixic acid	GyrA:T86I	87	87 (100%)	0
C. coli	nalidixic acid	none observed	207	3 (2%)	204 (98%)
C. jejuni	nalidixic acid	GyrA:T86I	85	83 (98%)	2 (2%)
C. jejuni	nalidixic acid	GyrA:T86K	1	1 (100%)	0
C. jejuni	nalidixic acid	GyrA:T86V	1	1 (100%)	0
C. jejuni	nalidixic acid	none observed	389	3 (1%)	386 (99%)

Table S5: Known fluoroquinolone resistance mutations are highly correlated with fluoroquinolone resistance in *Campylobacter* spp. [a]Mutations refer to the position in GyrA (AJW58405.1 for *C. coli*; YP_002344422.1 for *C. jejuni*). "None observed" describes those isolates lacking any previously described fluoroquinolone resistance mutations.

Species	drug	mutation[a]	n	# resistant (%)	# sensitive (%)
C. coli	azithromycin	23S:A2075G	29	29 (100%)	0
C. coli	azithromycin	no mutation	265	0	265 (100%)
C. coli	clindamycin	23S:A2075G	29	29 (100%)	0
C. coli	clindamycin	no mutation	265	17 (6%)	248 (94%)
C. coli	erythromycin	23S:A2075G	29	29 (100%)	0
C. coli	erythromycin	no mutation	265	0	265 (100%)
C. coli	telithromycin	23S:A2075G	29	21/29 (72%)	8/29 (28%)
C. coli	telithromycin	no mutation	265	0	265 (100%)

Table S6: Known macrolide resistance mutations are highly correlated with fluoroquinolone resistance in *C. coli.*
[a]Mutations refer to the position in *C. coli* 23S (CP011015.1, pos. 39330-42399, VC76_00160). "No mutations" describes those isolates lacking any previously described macrolide resistance mutations.