**Table S1.** Summary of transcriptome responses.

| Groups | Total[a] | Up-regulated | Down-regulated |
|---|---|---|---|
| Control vs G1 | 791 | 334 | 457 |
| Control vs G2 | 227 | 95 | 132 |
| Control vs G3 | 293 | 54 | 239 |
| G1 vs G2 | 370 | 284 | 86 |
| G1 vs G3 | 723 | 386 | 337 |
| G2 vs G3 | 301 | 92 | 209 |

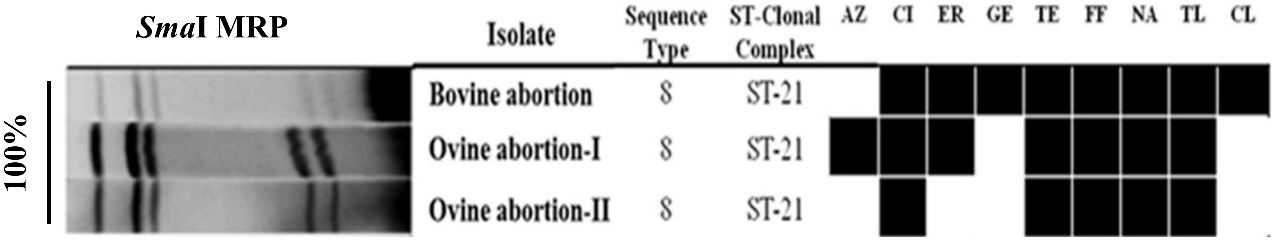
[a] Total number of differentially expressed probes. Differential expression of probes were determined using a fold change cutoff ± ≥ or ≤ 2

## Supplemental Figure Legends

**Fig. S1.** *Sma*I Macro Restriction Profiles, Sequence Types and antimicrobial resistance profiles of ovine and bovine *C.jejuni* abortion-associated isolates. Similarity analysis was performed using the Dice coefficient, and clustering was performed by the unweighted pair-group method with arithmetic averages UPGMA (optimization, 1% and position tolerance, 1.5%) (Sanad et al., 2011; Ribot et al., 2001). Numbers on bootstraps represent Cophenetic correlations. Black boxes indicate resistance to different antimicrobials tested as described previously (Sanad et al., 2011; Sanad et al., 2013). Antimicrobials; azithromycin (AZ) (Breakpoint for a resistant *Campylobacter* isolate: ≥8 μg $ml^{-1}$); ciprofloxacin (CI) (≥4 μg $ml^{-1}$); erythromycin (ER) (≥32 μg $ml^{-1}$); gentamicin (GE) (≥8 μg $ml^{-1}$); tetracycline (TE) (≥16 μg $ml^{-1}$); florfenicol (FF) (≥8 μg $ml^{-1}$); nalidixic acid (NA) (≥64 μg $ml^{-1}$); telithromycin (TL) (≥8 μg $ml^{-1}$); and clindamycin (CL) (≥8 μg $ml^{-1}$). Minimal inhibitory concentrations (MIC) were determined according to the Clinical and Laboratory Standards Institute (CLSI 2006). Multilocus sequence typing (MLST) was conducted as described previously (Sanad et al., 2011; Dingle et al., 2001).

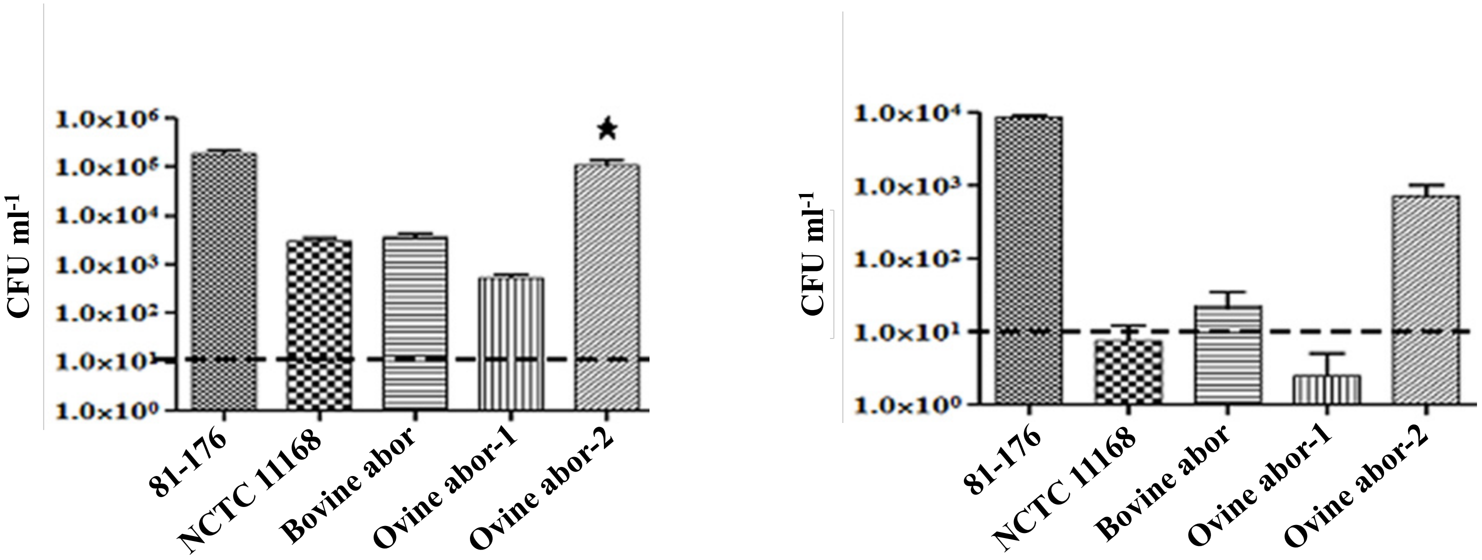
**Fig. S2:** Invasion and intracellular survival of ovine and bovine *C. jejuni* isolates in INT407 cells. Invasion and survival assays were performed as described previously (Sanad et al., 2011; Konkel et al., 1992; Prasad et al., 1996). **A.** CFU $ml^{-1}$ representing the number of the internalized bacteria which could be retrieved after treatment of cells with gentamicin. **B.** Intracellular survival of *C. jejuni* isolates in INT 407cells. CFU $ml^{-1}$ representing the numbers of internalized bacteria retrieved after 24 h of incubation. The INT407 were infected with 1:100 MOI of *C. jejuni* strains. *C. jejuni* 81–176 and NCTC11168 were used as controls. The detection limit of the assay is represented by the dashed line. Each bar represents the mean ± SE of three independent experiments performed in duplicate for each sample ($P<0.01$).

Fig. S1



| Isolate | Sequence Type | ST-Clonal Complex | AZ | CI | ER | GE | TE | FF | NA | TL | CL |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bovine abortion | 8 | ST-21 |  | ■ | ■ | ■ | ■ | ■ | ■ | ■ | ■ |
| Ovine abortion-I | 8 | ST-21 | ■ | ■ | ■ |  | ■ | ■ | ■ | ■ |  |
| Ovine abortion-II | 8 | ST-21 |  | ■ |  |  | ■ | ■ | ■ | ■ |  |

Fig. S2:



CFU ml$^{-1}$
1.0×10⁶
1.0×10⁵
1.0×10⁴
1.0×10³
1.0×10²
1.0×10¹
1.0×10⁰
★
81-176
NCTC 11168
Bovine abor
Ovine abor-1
Ovine abor-2
CFU ml$^{-1}$
1.0×10⁴
1.0×10³
1.0×10²
1.0×10¹
1.0×10⁰
81-176
NCTC 11168
Bovine abor
Ovine abor-1
Ovine abor-2

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