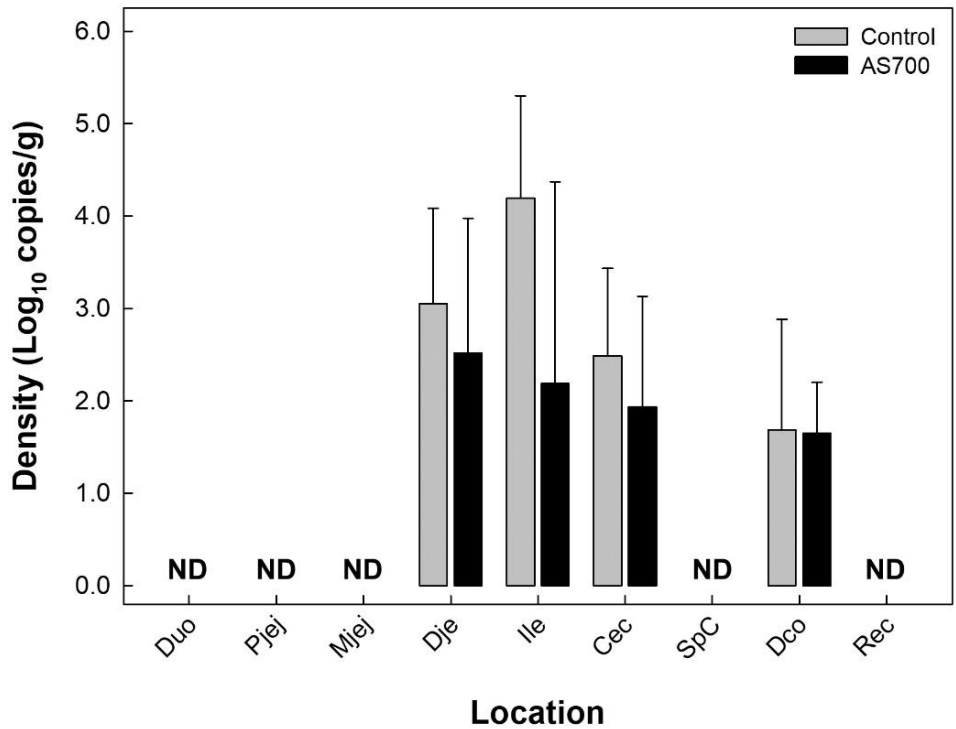


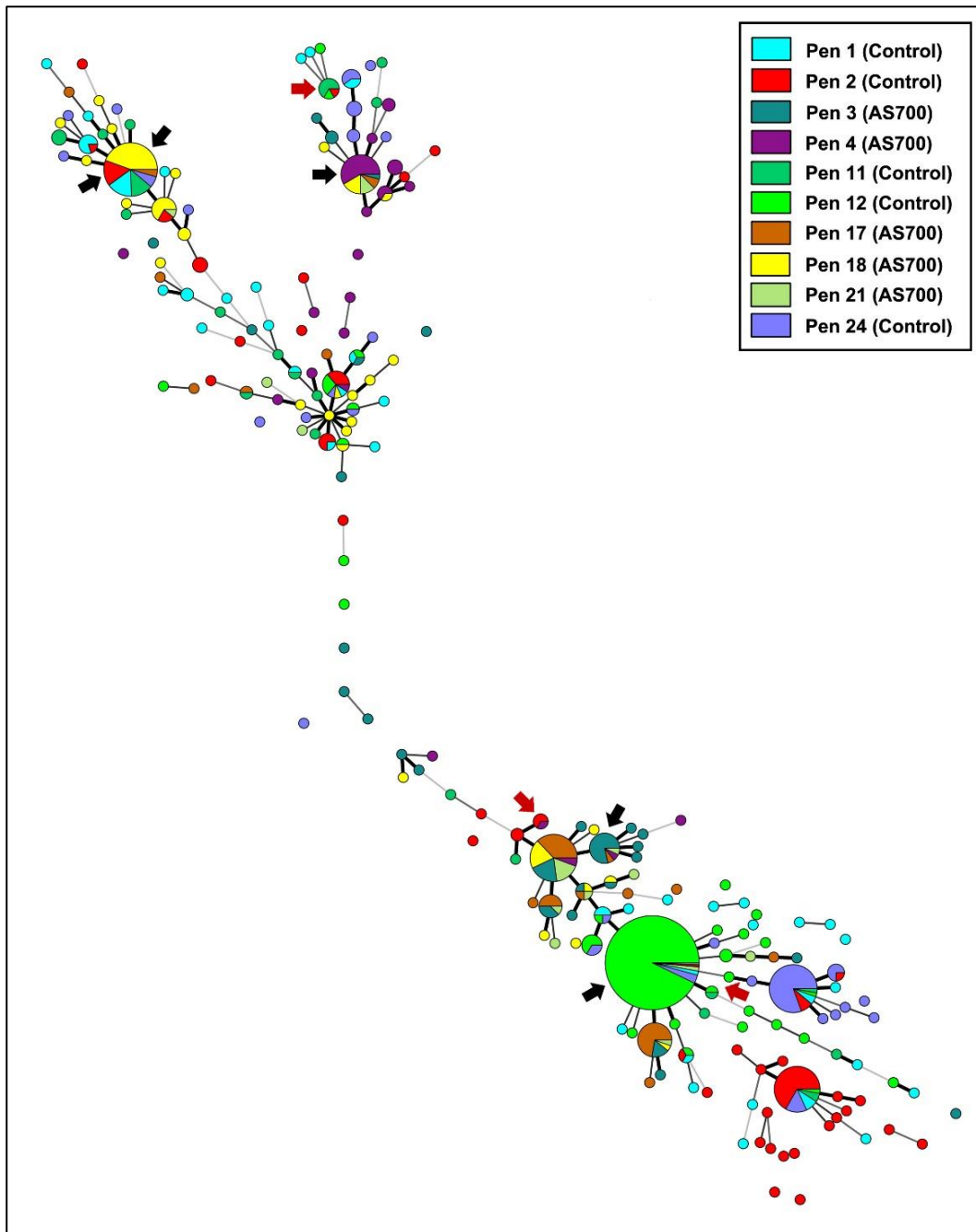
SUPPLEMENTAL MATERIAL



**FIG S1** Densities of *Campylobacter jejuni* cells within intestinal digesta in the duodenum (Duo), proximal jejunum (Pje), mid jejunum (Mje), distal jejunum (Dje), ileum (Ile), cecum (Cec), spiral colon (SpC), descending colon (DCo), and rectum (Rec) of cattle administered chlortetracycline and sulfamethazine (AS700) or no antibiotics during their time in a confined feeding operation. Vertical lines with histogram bars represent standard errors of the mean (n=5). ND is not determined.

Cluster_95	Cj0483	Cj0181	Cj0570	Cj0728	Cj0298	Cj1427	Cj0733	Cj1431	Cj0860	Cj0057	Cj1585	Cj0008	Cj0264	Cj1727	Cj0297	Cj0566	Cj1334	Cj0177	Cj1329	Cj1550	Cj0625	Cj0569	Cj0486	Cj0033	Cj0421	Cj1136	Cj1141	Cj0967	Cj0763	Cj0755	Cj1679	Cj1721	Cj1439	Cj1552	Cj1134	Cj0035	Cj1324	Cj0307	Cj1151	Cj1294		
1	1	1	1	1	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
5	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	1	0	0	1	1	0	0	0	0	0	0	
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0
27	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	1	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0
30	0	0	0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0
44	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
46	0	1	1	1	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	1	1	0	1	0	0	0	0	1	0	0	0	1	1	1	0	1	1	0	
48	0	0	0	0	1	0	0	1	0	1	1	0	1	1	0	0	0	1	1	1	1	1	1	1	0	1	0	0	0	1	0	0	0	1	1	0	1	1	0	1	1	0
49	0	1	1	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0
76	0	0	1	1	1	0	0	0	1	1	0	0	1	1	0	0	0	0	0	1	1	0	0	0	1	0	0	1	1	0	0	0	0	0	1	0	1	0	1	1	0	
88	1	1	1	1	1	1	0	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	0	1	1	1	1	0	0	1	1	1	1	1	1	1	1
98	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
103	1	1	1	1	1	0	0	0	0	1	1	0	1	1	0	0	1	1	1	1	1	1	1	1	0	1	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	0
114	1	1	1	1	1	0	1	0	1	1	0	0	0	0	1	1	0	1	0	0	1	1	1	0	1	0	0	1	1	1	0	0	0	0	0	0	0	1	1	1	0	1
118	1	1	1	1	1	0	0	0	1	1	0	0	1	1	0	1	0	1	0	0	1	1	1	0	1	0	0	1	1	1	0	0	0	0	0	0	0	1	1	1	0	1
120	1	1	1	1	1	0	0	0	1	1	0	0	0	0	0	1	0	1	0	0	1	1	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	1	1	0	0
121	1	1	1	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1	0	1	1	1	0	1	0	0	1	1	1	0	0	0	0	0	0	0	1	1	1	1	0

**FIG S2** Comparative genomic fingerprint subtype cluster profiles (95% level of resolution) of representative *Campylobacter jejuni* isolates recovered from an individual animal (i.e. Steer 470) that was not administered AS700 and housed in Pen 1 (i.e. Control treatment).



**FIG S3** *Campylobacter jejuni* Comparative Genomic Fingerprinting (CGF) subtypes recovered from beef cattle throughout the production continuum by pen that were administered chlortetracycline and sulfamethazine (i.e. AS700 treatment) or no antibiotics (i.e. control treatment). The minimum spanning tree was generated in Bionumerics (version 6.6, Applied Maths), and isolate data from the three animals per pen were combined. Furthermore, data were combined across sample type. The size of the circle is proportional to the number of isolates within each CGF subtype (100% level of resolution), the thickness of lines connecting subtypes represent mismatched loci (i.e. one to three loci), and subtypes with no line represent  $\geq$  four mismatched loci between respective subtypes. Black arrows show examples of cases where subtypes recovered from hides were linked to the digesta/feces from the same animal, and red arrows show examples of cases where subtypes recovered from carcasses were linked to the animal. *Campylobacter jejuni* subtypes isolated from cattle housed in adjacent pens (i.e. pens 1-4, pens 11-12, pens 17-18) did not disproportionately cluster together indicating that the transmission of subtypes amongst animals housed in adjacent pens was minimal.