Supplemental Material

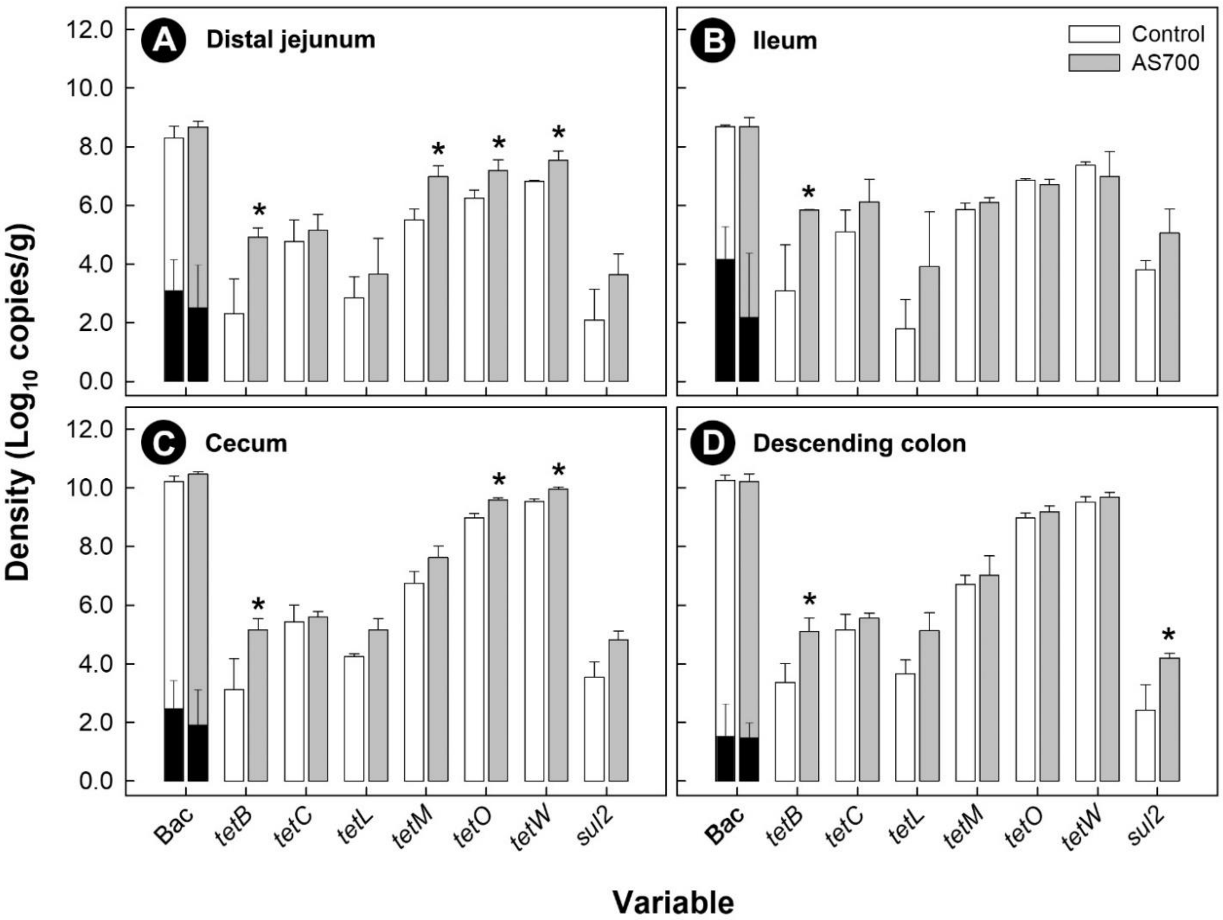

Figure S1. Densities of total bacteria (Bac) and resistance determinants (*tetB*, *tetC*, *tetL*, *tetM*, *tetO*, *tetW*, and *sul2*) in digesta from the distal jejunum (**A**), ileum (**B**), cecum (**C**), and descending colon (**D**) of beef cattle administered chlortetracycline and sulfamethazine (AS700) or no antibiotics in feed after euthanization. Black histogram bars are *Campylobacter jejuni* densities. Vertical lines with histogram bars represent standard errors of the mean (n=5). AS700 treatment histogram bars indicated by an asterisk (*) differ (P<0.050) from the control treatment at the corresponding variable.

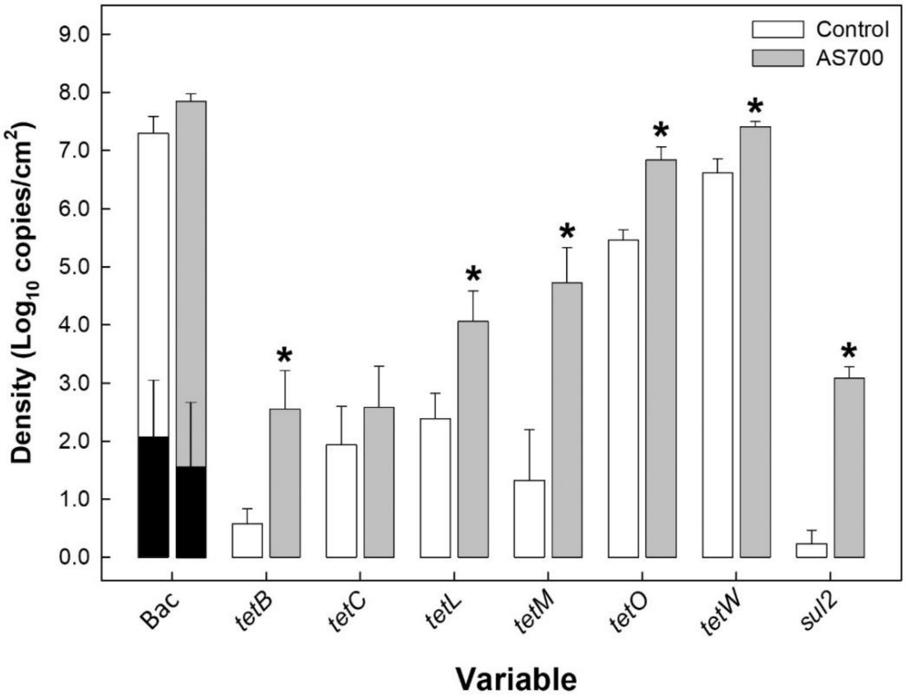

Figure S2. Densities of total bacteria (Bac) and resistance determinants (*tetB*, *tetC*, *tetL*, *tetM*, *tetO*, *tetW*, and *sul2*) associated intestinal mucosa in the rectums of beef cattle administered chlortetracycline and sulfamethazine (AS700) or no antibiotics in feed, and housed in a beef cattle confined feeding operation for ca. 7.5 months. Black histogram bars are *Campylobacter jejuni* densities. Vertical lines with histogram bars represent standard errors of the mean (n=5). AS700 treatment histogram bars indicated with an asterisk (*) differ (P<0.050) from the control treatment at the corresponding variable.

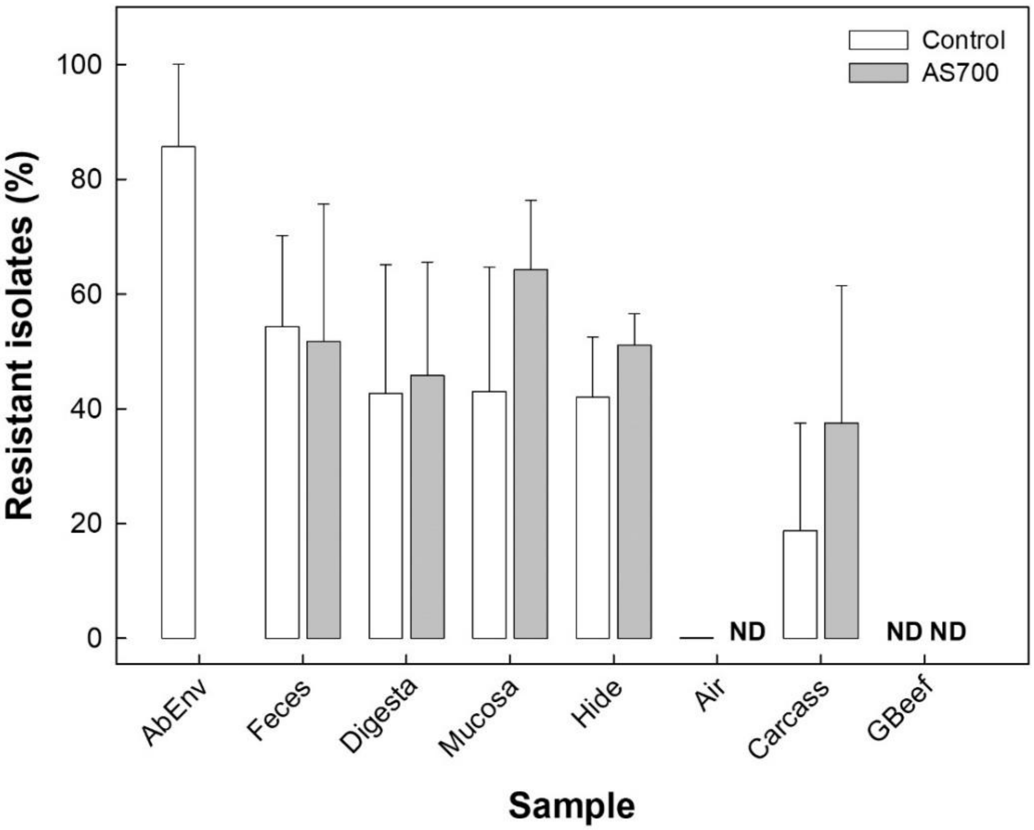

Figure S3. Prevalence of *Campylobacter jejuni* isolates resistant to tetracycline recovered from the abattoir environment (AbEnv), feces, intestine (digesta and mucosa-associated), hides, air, and carcasses from/of cattle administered chlortetracycline and sulfamethazine (AS700) or no antibiotics in the beef cattle confined feeding operation. The bacterium was not detected (ND) in the abattoir air during the removal of hides from cattle that were administered AS700 in the CFO, nor from ground beef (GBeef) generated from carcasses for either treatment. Vertical lines with histogram bars represent standard errors of the mean (n=5).

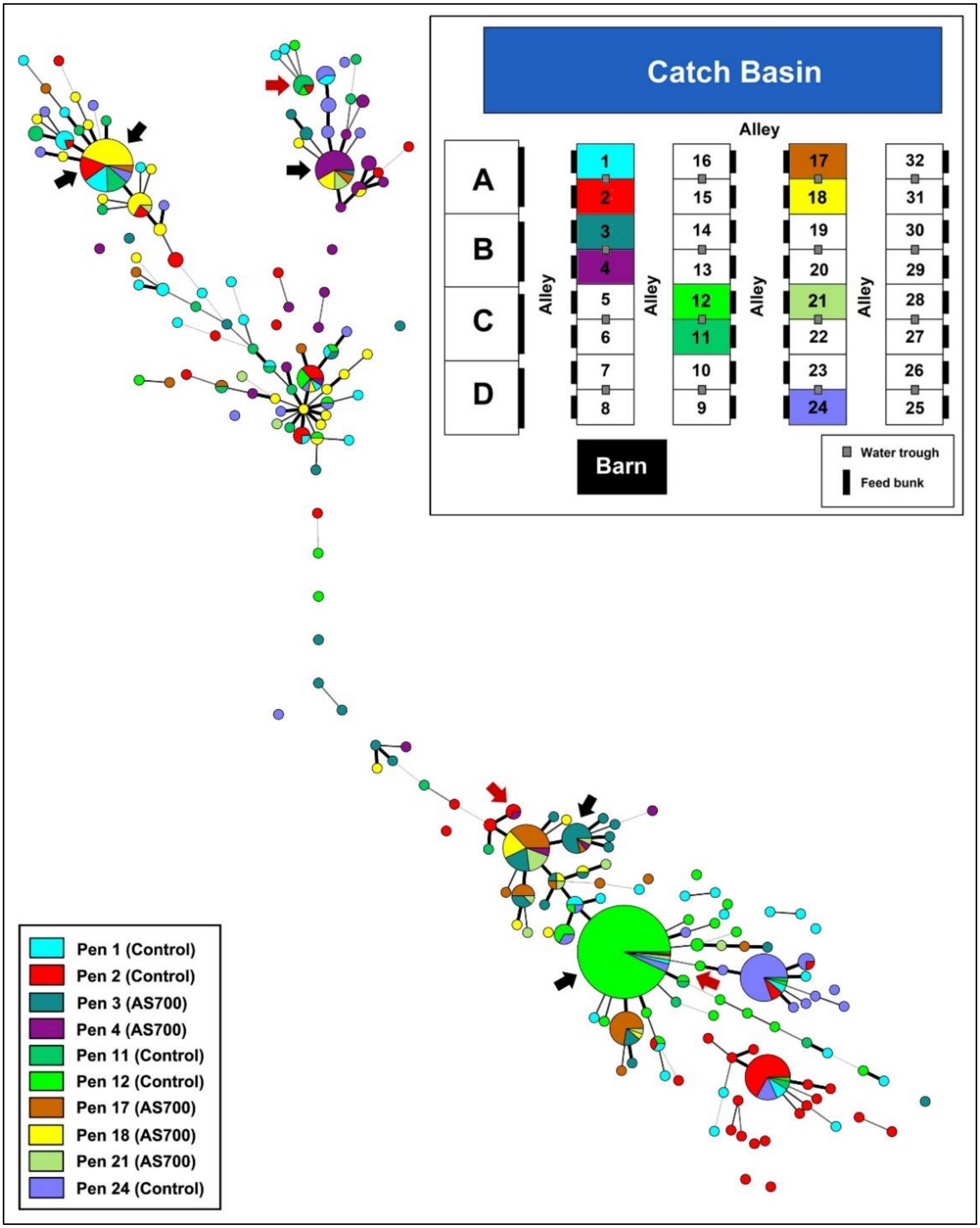

Figure S4. *Campylobacter jejuni* Comparative Genomic Fingerprinting (CGF) subtypes recovered from beef cattle throughout the production continuum by pen that were administered chlortetracycline and sulfamethazine (i.e. AS700 treatment) or no antibiotics (i.e. control treatment). The minimum spanning 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 ≥ four mismatched loci between respective subtypes. Black arrows represent cases where subtypes recovered from hides were linked to the digesta/feces from the same animal, and red arrows show cases where subtypes recovered from carcasses were linked to the animal. It is noteworthy that *C. jejuni* subtypes originating from adjacent pens (see Confined Feeding Operation map insert) did not disproportionately cluster together indicating that the transmission of subtypes amongst animals housed in adjacent pens was minimal (e.g. isolates denoted as red from Pen 2 *versus* those denoted as light blue from Pen 1 and those denoted as teal from Pen 3).

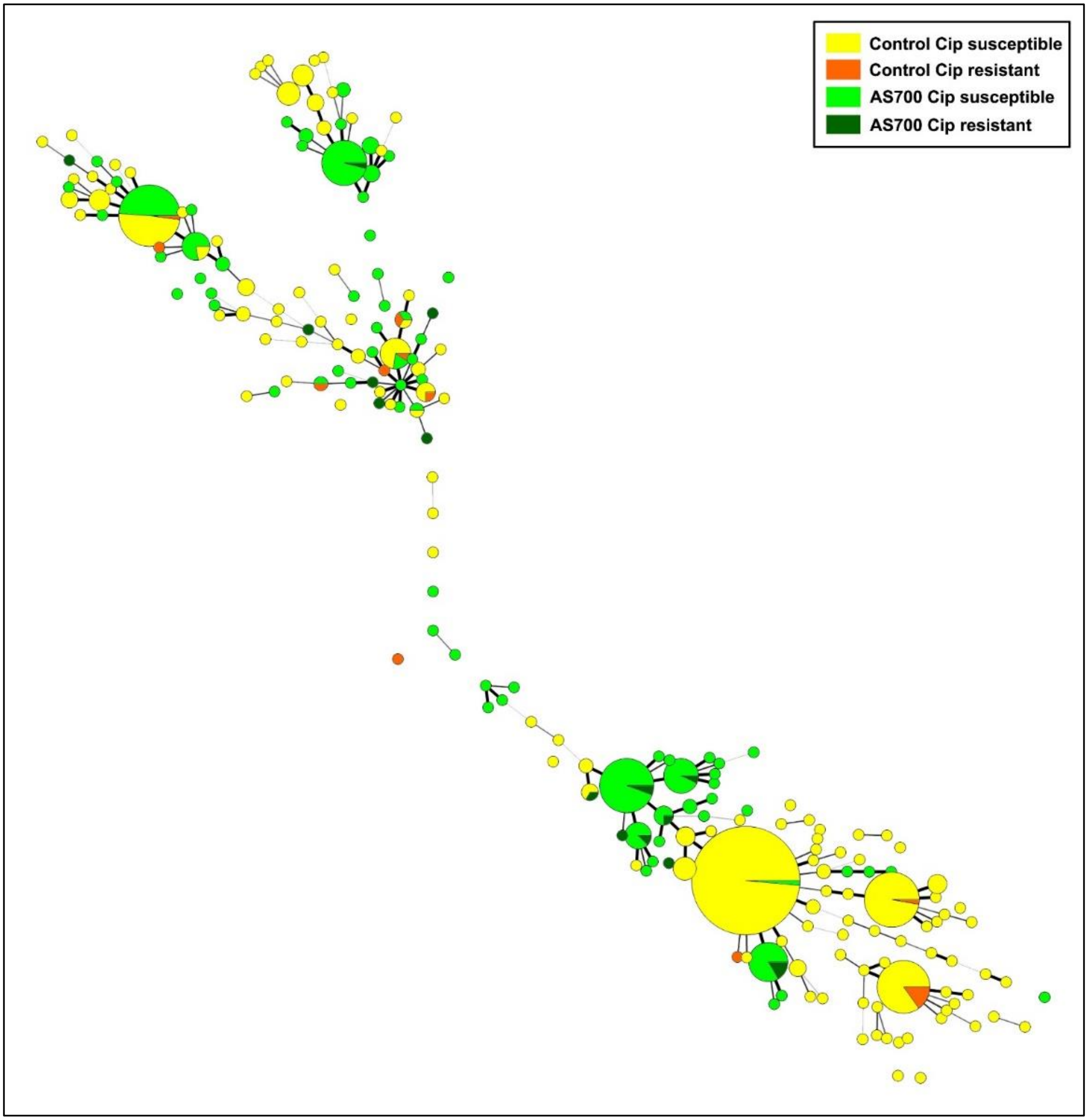

Figure S5. *Campylobacter jejuni* Comparative Genomic Fingerprinting (CGF) subtypes recovered from beef cattle throughout the production continuum that were administered chlortetracycline and sulfamethazine (i.e. AS700 treatment) or no antibiotics (i.e. control treatment), and were resistant or susceptible to ciprofloxacin. The minimum spanning tree was generated in Bionumerics (version 6.6, Applied Maths), and data were combined across pens and 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 ≥ four mismatched loci between respective subtypes.