

Supplemental Table 1. Serotype data from culture analysis of isolates collected in the Ohta *et al* 2017 study

	Cattle ID ^a	Serovars ^{b,c}		
		Day 0	Day 20	Day 26 ^e
All cattle in each pen treated with CTC, one animal per pen treated with CCFA	2266	Mbandaka	-	-
	2272	Give	-	-
	2379	Anatum	-	Give
	2389	Give	-	-
	2403	Montevideo	-	Mbandaka
	2415	Mbandaka ^d	Reading	Reading
	2268	-	Reading ^d	-
	2331	Mbandaka	Reading ^d	Reading
	2337	Montevideo	-	Give
	2345	Give	-	-
	2378	Give	-	Montevideo
	2399	Montevideo	-	-
	2244 ^f	Mbandaka	Reading	Reading
	2276	Give	-	-
	2285	Mbandaka	-	-
	2296	Kentucky	-	-
	2324	Kentucky	Reading	Reading
	2326 ^f	Kentucky	-	Give
	2357	Mbandaka	Reading	Reading
	2409	Mbandaka	-	Reading
	2239	Mbandaka	-	Kentucky
	2247	Mbandaka	Reading ^d	Montevideo
	2261	Give	-	-
	2264	Mbandaka	-	-
	2265	Mbandaka ^d	Reading	Mbandaka
	2307	Give ^d	-	-
	2341	Kentucky ^d	-	-
	2358	Mbandaka	-	Kentucky
	2366 ^f	Mbandaka	Reading ^d	Reading
	2392 ^f	Mbandaka	-	Reading
2410	Kentucky	-	Reading	
All cattle treated with CTC and with CCFA	2283	Give	-	-
	2287	Give	-	Give
	2323	Give	-	-
	2332	Give	-	-
	2336	Give ^d	-	-
	2347	Give	Give	Give
	2384	Give ^d	-	Mbandaka
	2391	Give	-	-
	2394	Give	-	-
	2421	Mbandaka	-	-
	2254	Mbandaka	-	-
	2274	Mbandaka	-	Give
	2279	-	Give	Give
	2304	Mbandaka	-	-
	2312	Montevideo	-	-
	2313 ^f	Mbandaka	-	Mbandaka
	2371	Give	-	-
	2372	Give	Reading	Mbandaka
	2377	Mbandaka	-	-
	2413	Give	-	-
	2302	Give	Reading	-
	2321	Montevideo	-	-
	2327	Montevideo	-	Kentucky
	2339	Give	-	Reading
	2353	Give	-	-
	2238	Give	-	Reading
	2255 ^f	Mbandaka	-	-
	2303	Mbandaka ^d	-	-
	2328	Montevideo	-	Kentucky
	2354	Mbandaka	-	Reading
2359	Montevideo	-	-	
2374	Mbandaka ^d	-	Mbandaka	
2383	Give ^d	Reading ^d	-	
2398	Mbandaka	Reading	-	
2400	Mbandaka ^d	Reading	Mbandaka	
2411	Give	-	Reading	

^a Separate pens are delineated by a bold line

^b *In silico* serotyping from whole genome sequences was performed on a single colony from each fecal sample

^c -: Samples were *Salmonella* negative

^d Samples that were analyzed in Ohta *et al.* (2017), but which were not analyzed in this study due to either showing up as *Salmonella*-negative in the new enrichments performed in this study, poor sequencing after being repeated twice, or contaminating *E. coli* sequence reads which resulted in less than 1000 *Salmonella* CRISPR reads.

^e Data not shown for additional cattle that were positive at Day 26 but negative at Day 0 and Day 20

^f Samples where CRISPR-SeroSeq identified ser. Reading at day 0

Reference

Ohta N, Norman KN, Norby B, Lawhon SD, Vinasco J, den Bakker H, Loneragan GH, Scott HM. 2017. Population dynamics of enteric *Salmonella* in response to antimicrobial use in beef feedlot cattle. *Sci Rep* 7:14310.