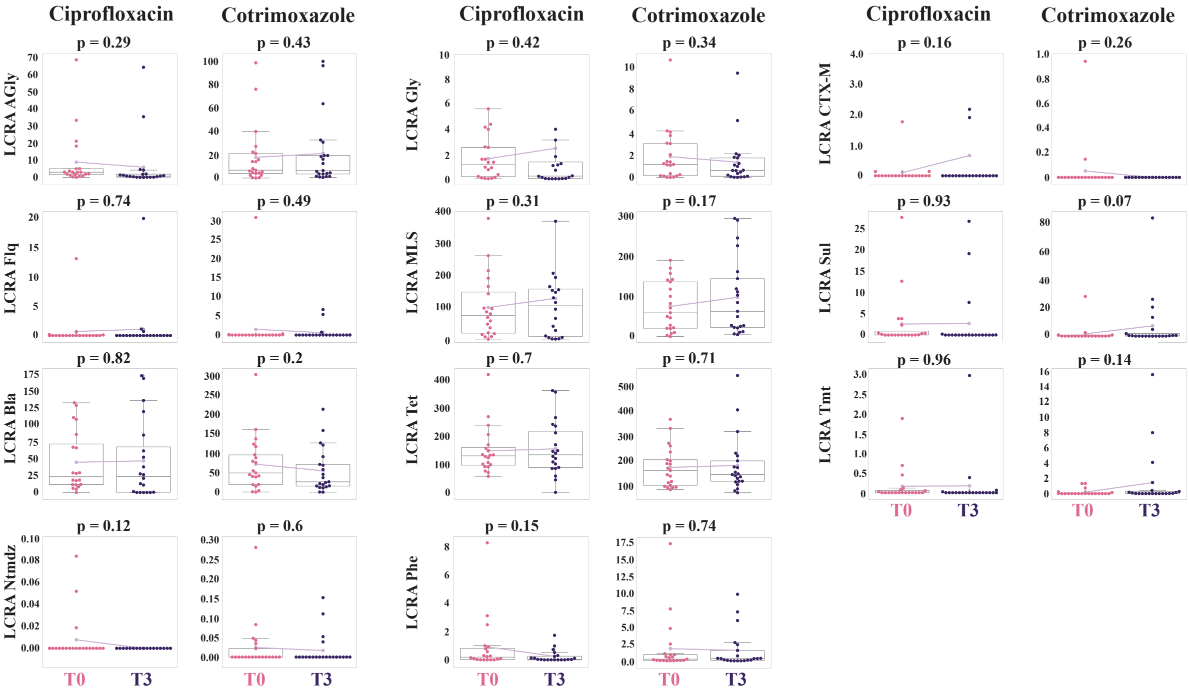
Ciprofloxacin
Cotrimoxazole
Ciprofloxacin
Cotrimoxazole
Ciprofloxacin
Cotrimoxazole
p = 0.29
p = 0.43
p = 0.42
p = 0.34
p = 0.16
p = 0.26
LCRA AGly
LCRA Gly
LCRA CTX-M
p = 0.74
p = 0.49
p = 0.31
p = 0.17
p = 0.93
p = 0.07
LCRA Flq
LCRA MLS
LCRA Sul
p = 0.82
p = 0.2
p = 0.7
p = 0.71
p = 0.96
p = 0.14
LCRA Bla
LCRA Tet
LCRA Tmt
p = 0.12
p = 0.6
p = 0.15
p = 0.74
LCRA Ntmdz
LCRA Phe
T0
T3

Figure S4. Comparison of length corrected relative abundances from antimicrobial resistance gene classes before treatment and at the end of observation.

Trajectories of antimicrobial resistance genes quantification by LCRA before treatment (T0) and at the end of the observation period (T3) are shown for both antibiotic treatments. Pink data points are measurements at T0, purple data points at T3. Boxplots indicate the distribution of data. The connecting magenta line shows the means at each time point and their development under treatment (paired t-test). Trends for LCRA changes are prominent but do not reach statistical significance. The following ARG classes are depicted: aminoglycosides (AGly), beta-lactamases (Bla), fluoroquinolones (Flq), glycopeptides (Gly), macrolide-lincosamide-streptogramin (MLS), nitroimidazoles (Ntmdz), phenicols (Phe), sulfonamides (Sul), tetracyclines (tet), and trimethoprim (Tmt). CTX-M are cefotaximase enzymes that mediate an ESBL phenotype.