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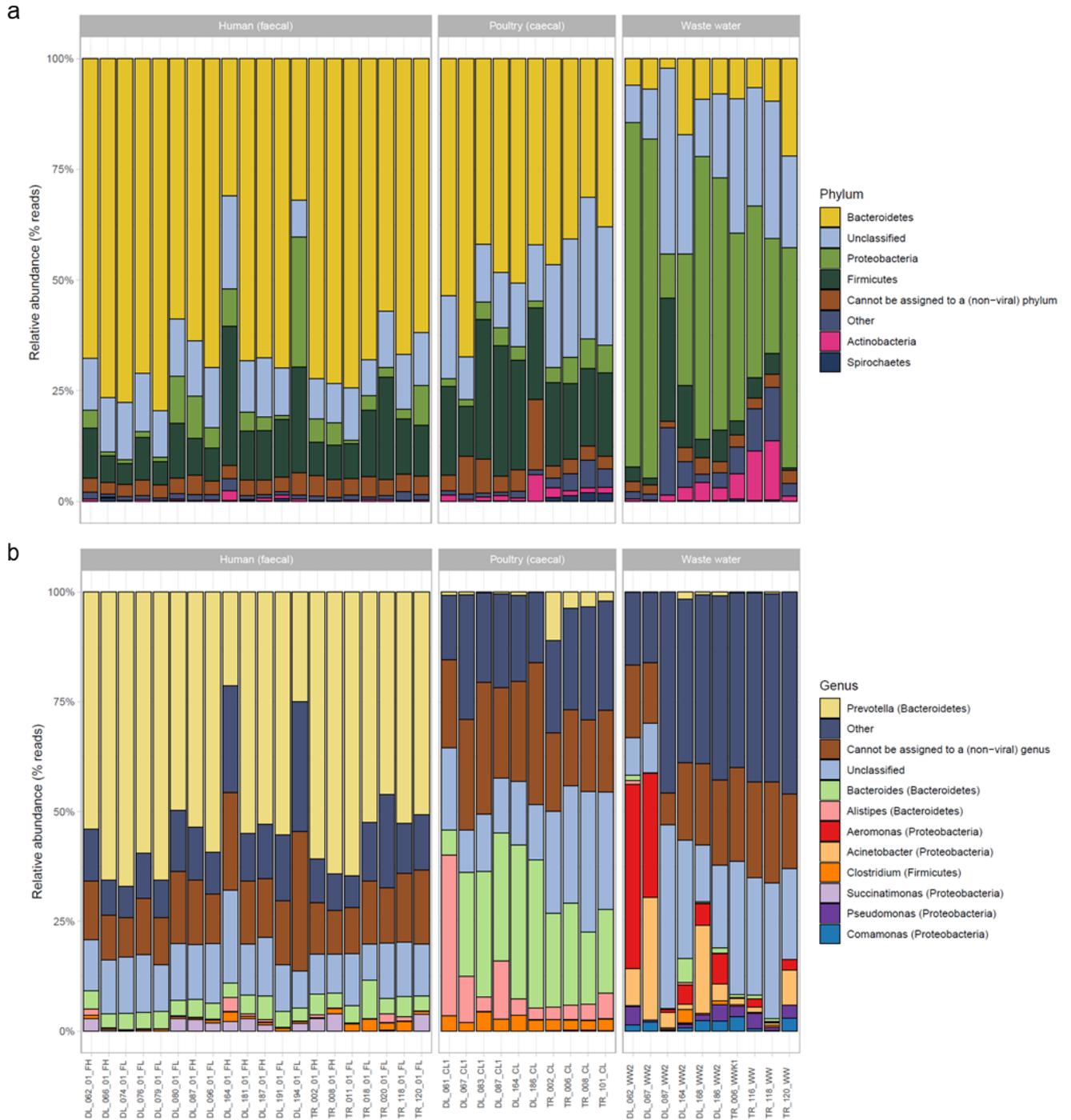
Williams, A. D., Rousham, E., Neal, A. L., Amin, M. B., Hobman, J. L., Stekel, D. and Islam, M. A. 2023. Impact of Contrasting Poultry Exposures on Human, Poultry, and Wastewater Antibiotic Resistomes in Bangladesh. *Microbiology Spectrum*.
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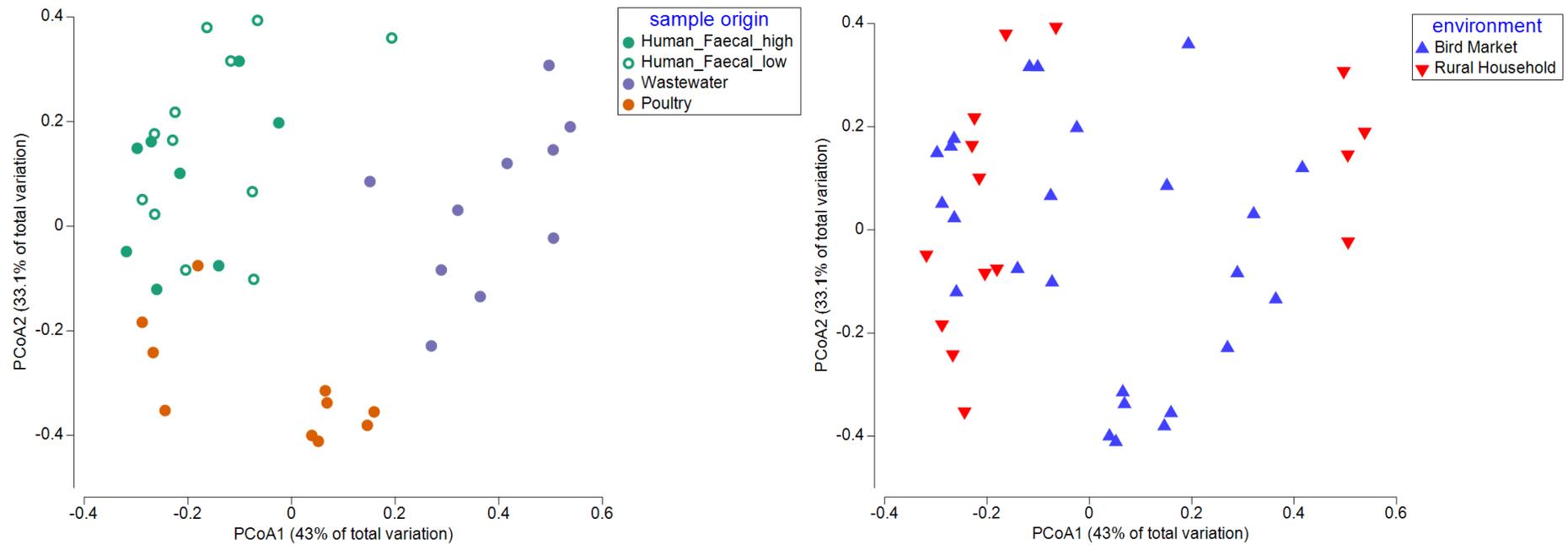
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Supplementary Figure 1. Stacked bar charts showing the most abundant phyla and genera (relative abundances shown). a) Phylum level breakdown of read compositions grouped by sample origin. The ‘other’ category includes reads belonging to bacterial phyla, archaea, eukaryote, and viral domains which sum to <1% in 38 of the total 40 samples. b) Genus level breakdown of read compositions grouped by sample origin. The ‘other’ category includes reads belonging to bacteria genera, archaea, eukaryote and viral domains which sum to <2% in 36 of the total 40 samples. Sample ID is displayed on the axis; (DL = urban wet market, TR= rural household, FL = low exposure human faecal, FH = high exposure human faecal, CL = poultry cloacal and WW = wastewater).

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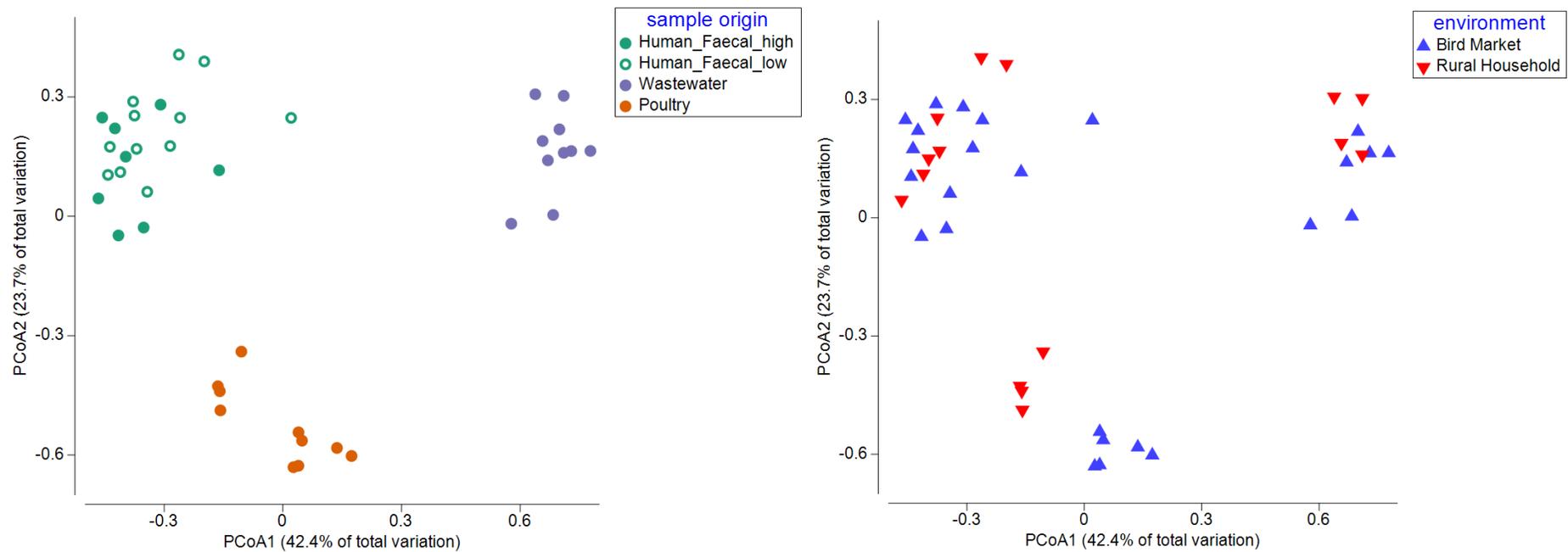
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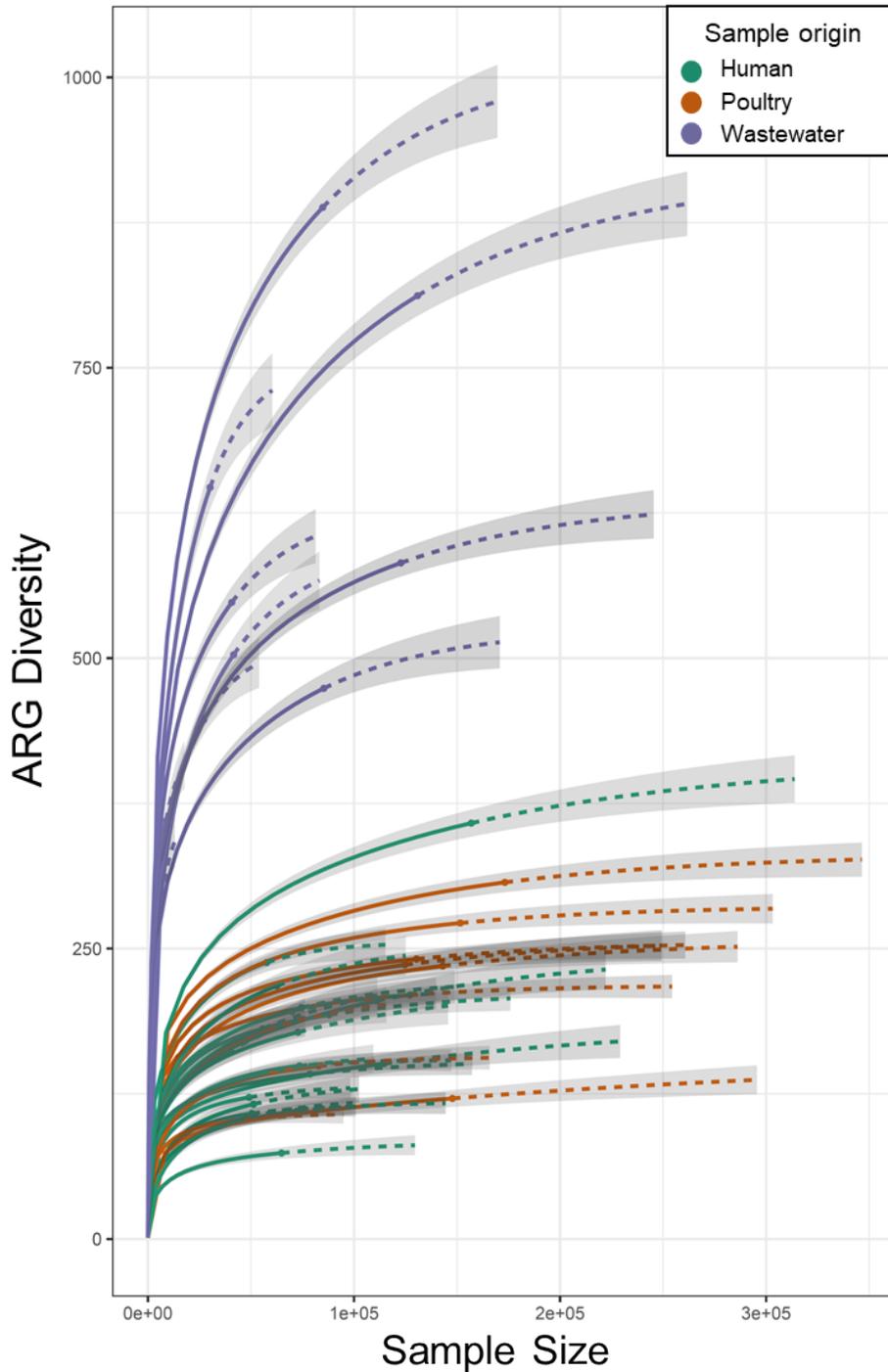
16 **Supplementary Figure 2. Ordinations showing the separation of antibiotic resistome compositions by sample origin and setting at**
17 **the level antibiotic category.** a) Unconstrained antibiotic resistance gene category PCoA based upon Hellinger distances of cell normalised
18 ARG abundance coloured to show origin of samples (human faecal, poultry caecal and wastewater); b) coloured to show the same samples by
19 urban wet market or rural sampling location.

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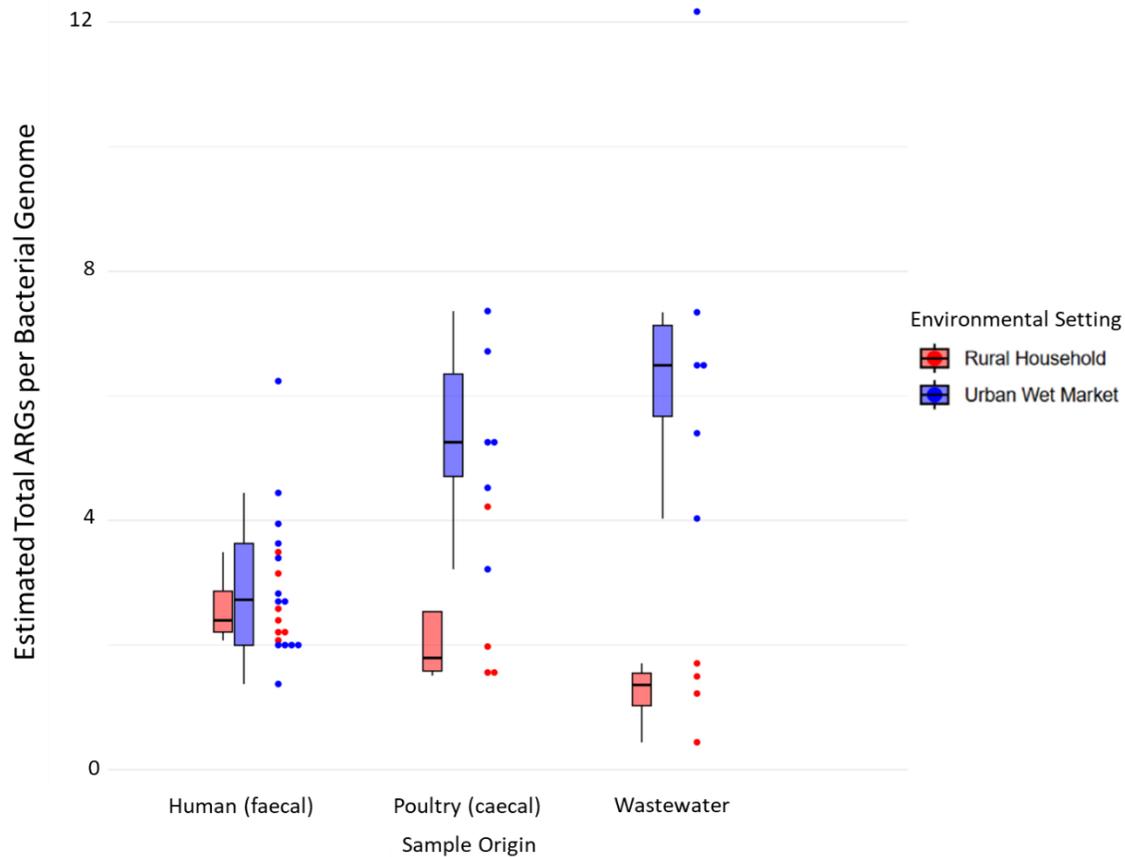
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22 **Supplementary Figure 3. Ordinations showing the separation of antibiotic resistome compositions by sample origin and setting at**
 23 **the level antibiotic resistance gene subtype.** a) Unconstrained antibiotic resistance gene category PCoA based upon Hellinger distances of
 24 cell normalised ARG abundance coloured to show origin of samples (human faecal, poultry caecal and wastewater); b) coloured to show the
 25 same samples by urban wet market or rural sampling location.

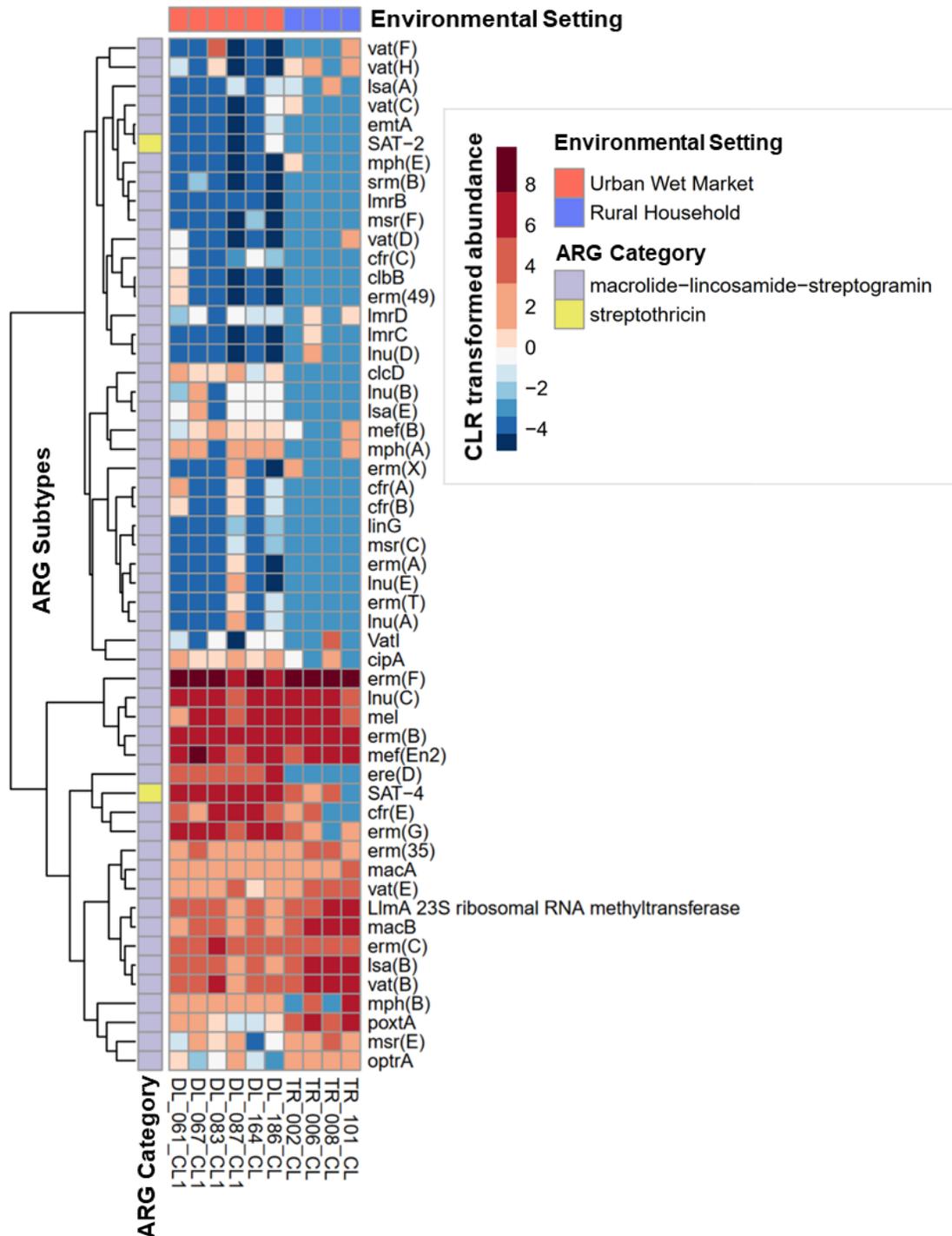


Supplementary Figure 4. Showing the interpolated and extrapolated ARG subtype diversity of wastewater is consistently greater than human and poultry samples.

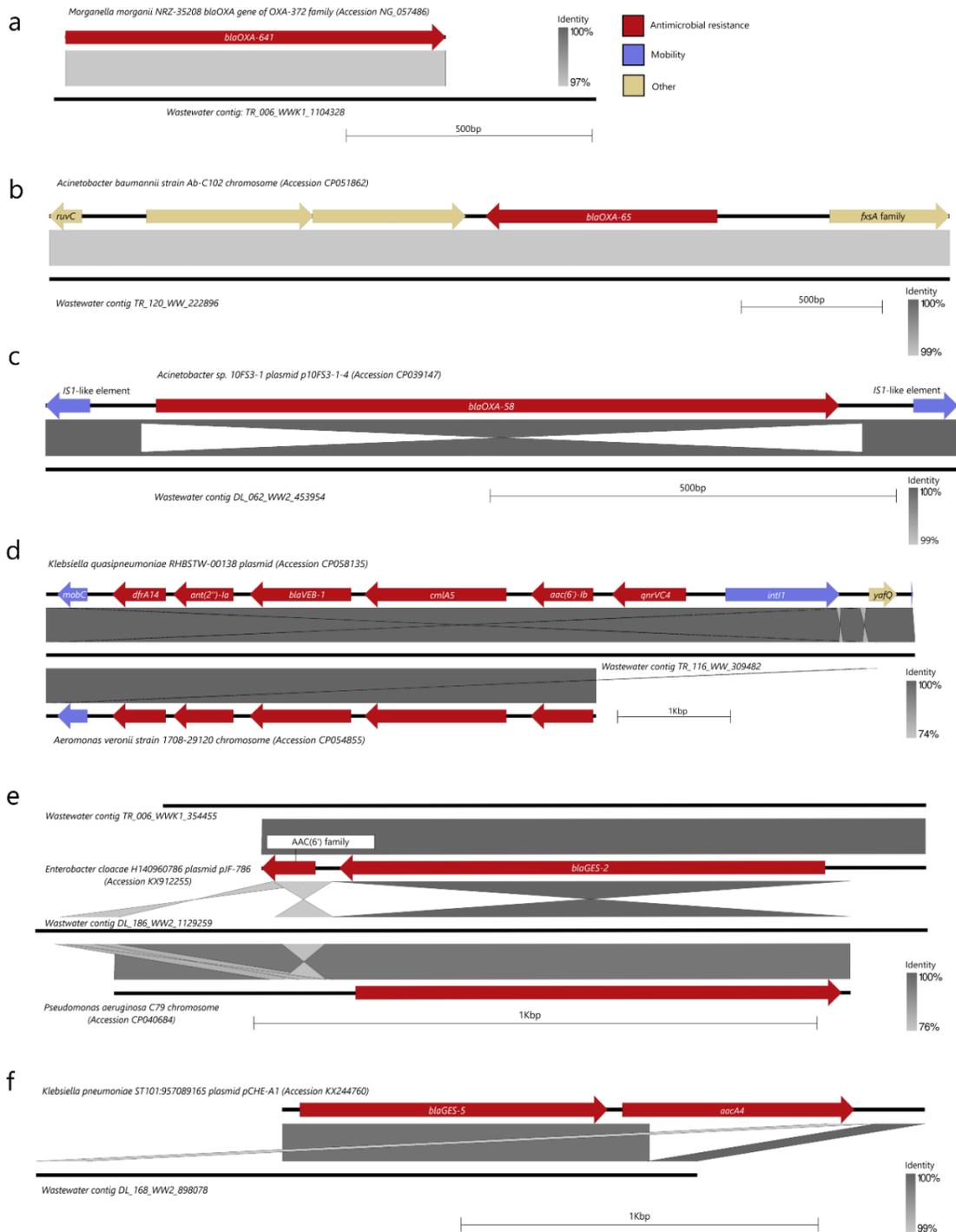
Estimated q_0 diversity calculated using Hill numbers implemented by the *iNEXT* package for R. Solid lines indicate interpolations, dashed lines indicate extrapolations. Bootstrapped ($n = 399$) 95% confidence intervals shown in grey.



Supplementary Figure 5. Showing the observed trend that wastewater samples collected from urban wet markets consistently have higher estimated total antibiotic resistance gene (ARG) abundance compared to those collected from rural households. Data displayed as boxplots and stacked dot plots and summarised sample origin (human faecal, poultry caeca and wastewater) as well as environmental setting (urban wet market and rural household).

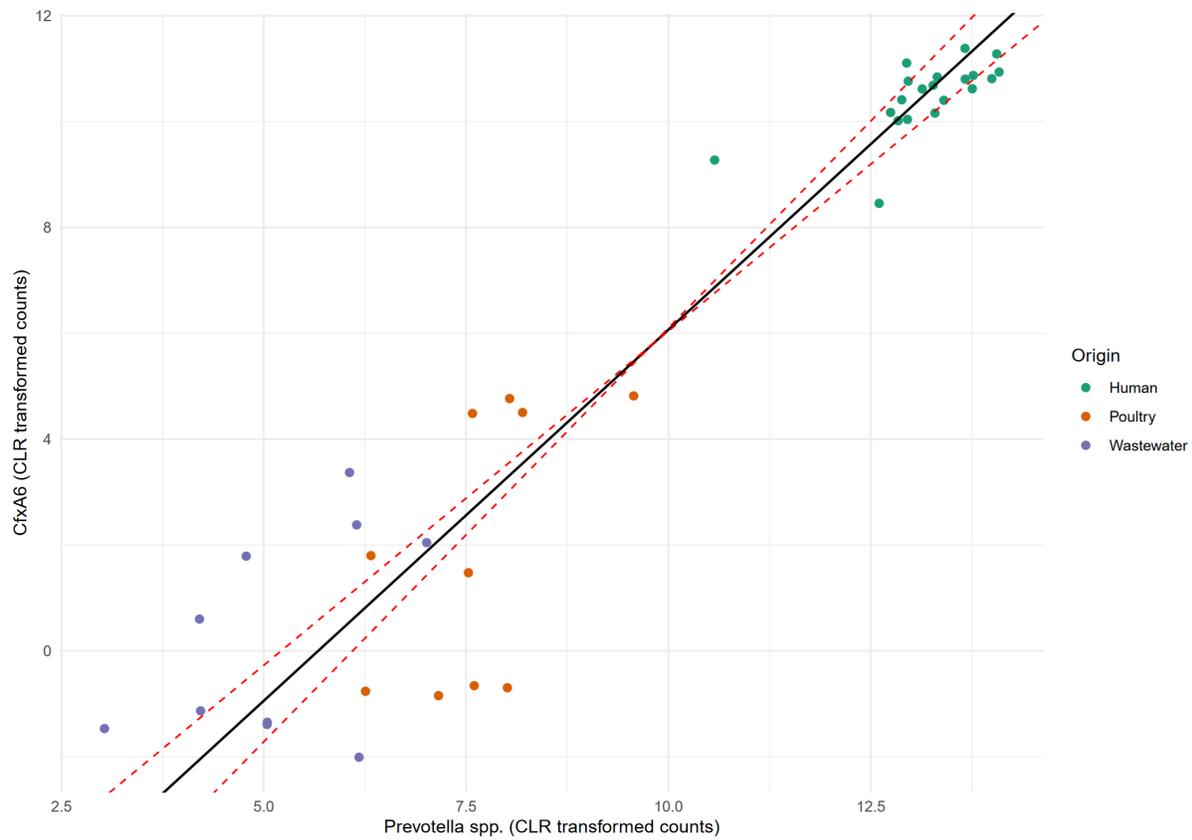


Supplementary Figure 6. Heatmap comparing the abundance of macrolide-streptogramin-lincosamide antibiotic resistance gene (ARG) subtypes in rural household and urban wet market poultry cloacal samples. Centre log ratio (CLR) of estimated ARGs per bacterial genome is shown by a descending red-blue scale. ARG subtypes (rows) are clustered using complete-linkage.



Supplementary Figure 7. ESBL and carbapenem resistance gene contig maps.

Red: antibiotic resistance genes (ARGs); blue: mobilisation genes, beige: other. Nucleotide identities shown for individual maps. ARG categories are as follows: a) *blaOXA-641*-like (beta-lactam), b) *blaOXA-65* (beta-lactam), c) *blaOXA-58* (beta-lactam), d) *drfA14* (trimethoprim), *ant(2'')-Ia* (aminoglycoside), *blaVEB-1* (beta-lactam), *cmlA5* (chloramphenicol), *aac(6')-1b* (aminoglycoside) and *qnrVC4* (quinolone), e) AAC(6') family-like (aminoglycoside), *blaGES-2* (beta-lactam), f) *blaGES-5* (beta-lactam), *aacA4* (aminoglycoside) (only partial sequence contained in wastewater contig).



Supplementary Figure 8. Showing the relationship between the abundance of *Prevotella* spp. and *cfxA6* antibiotic resistance genes. Major axis regression plot showing association between centre log ratio (CLR) transformed counts of *Prevotella* spp. and predicted *cfxA6* gene counts across all samples ($n = 40$). $R = 0.95$; $t = 18.954$, $p = 5.799111e^{-21}$. H statistic used for computing confidence intervals of major axis: 0.0025.