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Supplementary Materials for

The pet café is a neglected site for transmission of antimicrobial-resistant *Escherichia coli* in urban life

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29 **Supplemental Tables**

30 **Table S1. Metadata of 163 strains sequenced in this study**

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32 **Table S2. Antimicrobial susceptibility testing of 60 *Escherichia coli* and 9 *Klebsiella***
33 ***pneumoniae* strains (MICs, mg/L)**

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35 **Table S3. ARG genotype of 60 *Escherichia coli* strains**

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37 **Table S4. Virulence factor genotype of 60 *Escherichia coli* strains**

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39 **Table S5. Pairwise comparison of single nucleotide polymorphisms of 60 *Escherichia coli***
40 **isolates**

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42 **Table S6. Information regarding of 190 ST328 *Escherichia coli* strains obtained from the**
43 **NCBI database**

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45 **Table S7. Pairwise comparison of single nucleotide polymorphisms of 209 ST328**
46 ***Escherichia coli* strains**

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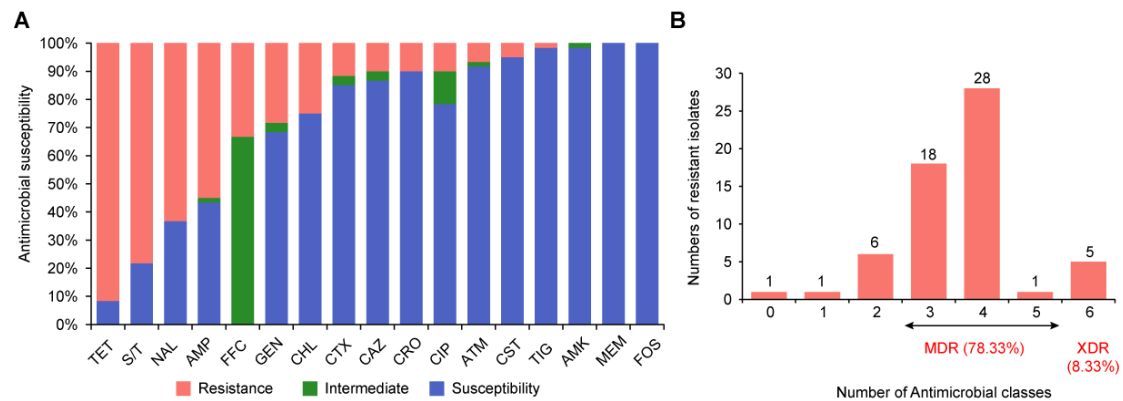
48 **Table S8. Statistics and MOB genotypes of the 117 reconstructed plasmids**

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50 **Table S9. Details of five isolates with complete genome sequences finished by Illumina and**
51 **ONT sequencing**

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53 **Supplemental Figures**



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55 **Figure S1. Antimicrobial resistance characteristics of 60 *Escherichia coli* strains**
56 **isolated from this study**

57 **(A)** The percentage of *E. coli* isolates resistant to each of the antibiotics tested;

58 **(B)** Numbers of *E. coli* isolates resistant to different antibiotic classes tested.

59 TET: tetracycline, S/T: sulfamethoxazole/trimethoprim, NAL: nalidixic acid, AMP:

60 ampicillin, FFC: florfenicol, GEN: gentamicin, CHL: chloramphenicol, CTX:

61 cefotaxime, CAZ: ceftazidime, CRO: ceftriaxone, CIP: ciprofloxacin, ATM: aztreonam,

62 CST: colistin, TIG: tigecycline, AMK: amikacin, MEM: meropenem, FOS: Fosfomycin.

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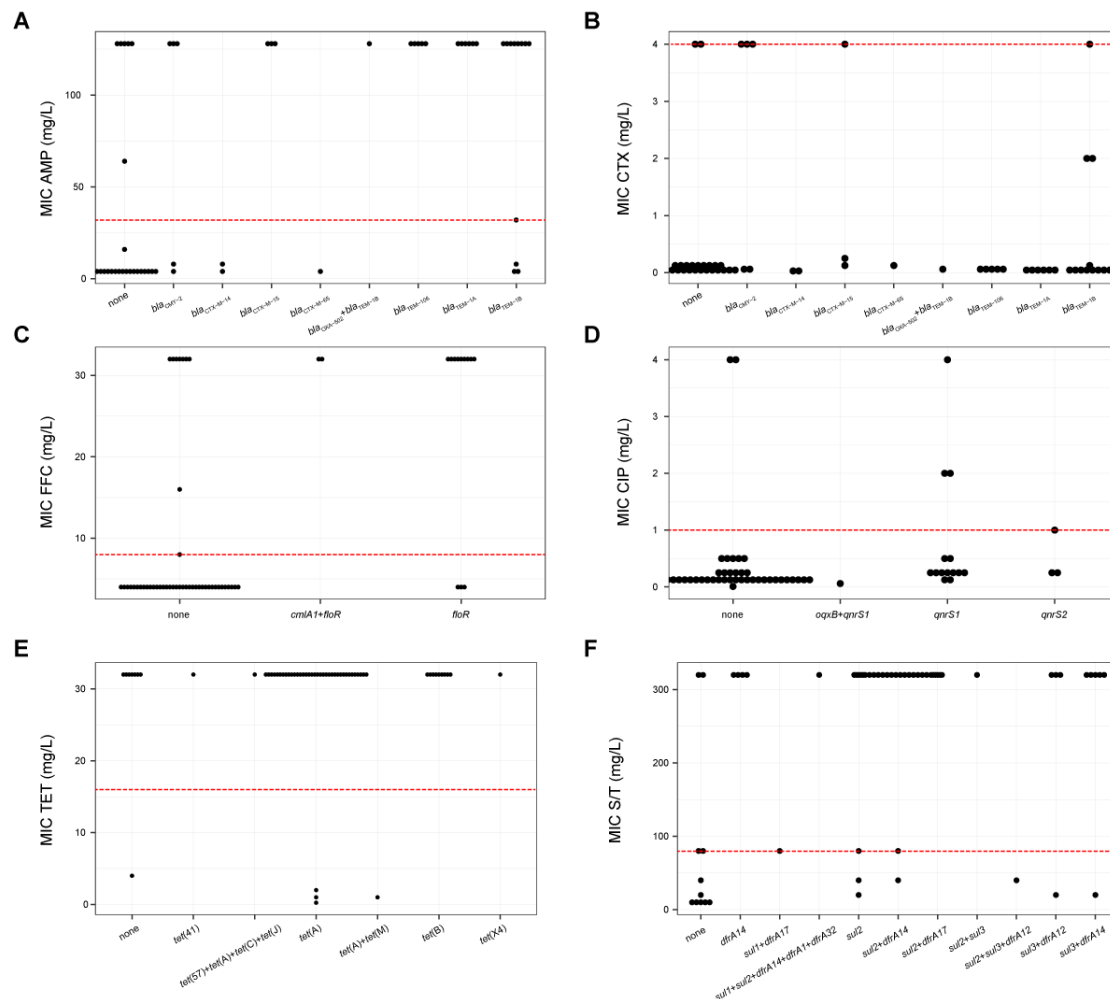


Figure S2. Association of AMR genotype and phenotype for first- and second-line antimicrobials

Genotype-phenotype association for ampicillin (A), ceftriaxone (B), florfenicol (C), ciprofloxacin (D), tetracycline (E), sulfamethoxazole/trimethoprim (F). Dots indicate the minimum inhibitory concentration (MIC) (y-axis) for each of 60 isolates harbouring a certain combination of genomic resistance markers (shown on the x- axis). The dashed line in red indicates the CLSI M100-S28 and VET01-S2 breakpoint for clinical resistance.

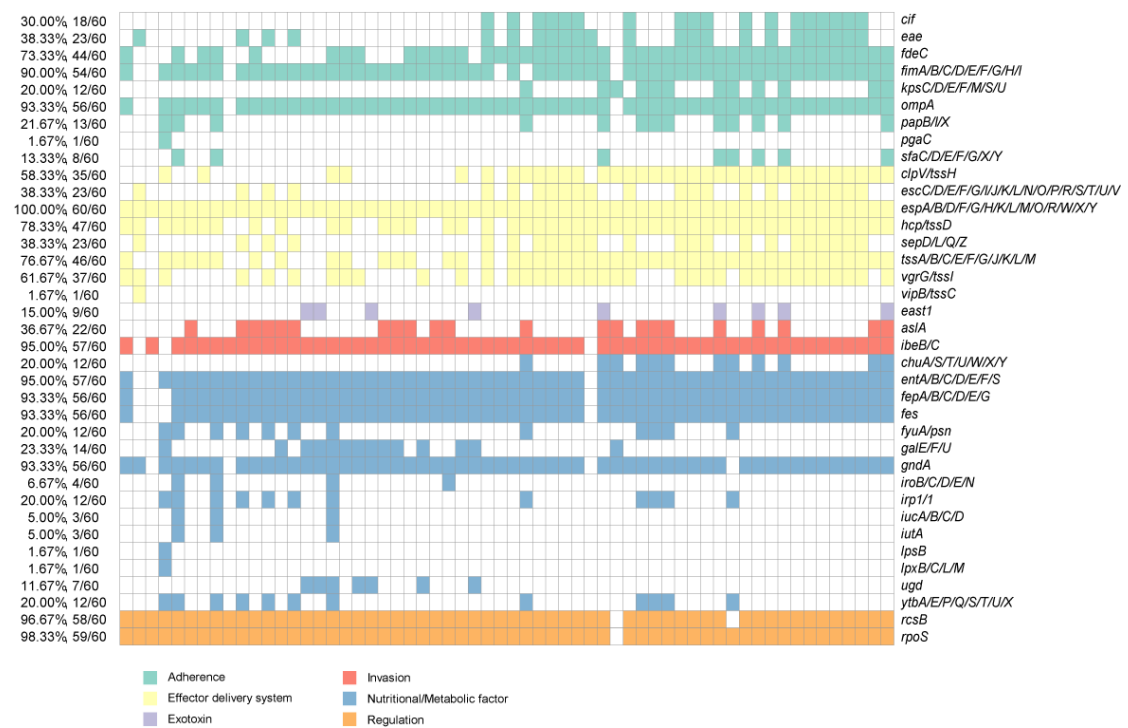


Figure S3. Virulence factors and genes in 60 *Escherichia coli* from pet cafés

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Figure S4. Minimum spanning trees of *Escherichia coli* by MLST type and gene allele profile from pet cafés