

Supplementary Materials

Core and variable antimicrobial resistance genes in the gut microbiomes of Chinese and European pigs

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Supplementary Figure S1 Characteristics of ARG profiles and microbiome

A: Abundance and alpha diversity of ARGs between groups. B: Abundance and alpha diversity of MGEs between groups. C and D: Proportion of dominant ARG types (C) and phyla (D) in Chinese and European pigs. Mann-Whitney tests: *P<0.05, **P<0.01, ***P<0.001, ***P<0.001.



Supplementary Figure S2 Overview of core resistome in Chinese and European pigs

A: Proportion of number and abundance of core ARGs between groups. B: Sankey diagram of co-occurrence of core ARGs and microbiomes (phylum level), with corresponding group illustrated in different colors. C and D: Prevalence of core ARGs in pigs and humans from China (E) and Europe (D), respectively. Note: core ARGs were identified in pigs from China and Europe, respectively.



Supplementary Figure S3 Core microbiome of Chinese and European pigs

A: Distribution of genus prevalence in all samples of Chinese and European pigs. Gray lines show defined cutoffs. B: Proportion of number and abundance of core microbiome between groups. C: Quantitative profile of core microbiome (coverage, ×/cell, log2 transferred).



Supplementary Figure S4 Proportion of number and abundance of ARG markers

between groups



Supplementary Figure S5 Biomarkers between Chinese and European pigs

A: Top 43 bacterial families identified by RF classification of relative abundance of microbiota in Chinese and European pigs, ranked in descending order of importance to the accuracy of the model. Inset represents ten-fold cross-validation error for number of input families differentiating Chinese and European pigs. Higher mean decrease accuracy implies more important predictors. Significance levels: *P<0.05 and **P<0.01. B: PCA and Adonis analysis were based on 43 biomarkers in Chinese and European pigs. C: Proportion of number and abundance of biomarkers between groups.



Supplementary Figure S6 Overview of indicators of ARG contamination in Chinese and European pigs

A: Proportion of number and abundance of indicators between groups. B: Sankey diagram of co-occurrence of indicators and microbiomes, with corresponding group illustrated in different colors.



Supplementary Figure S7 Spearman correlation analysis between abundances of indicators and all ARGs in tested samples from (A) Chinese and (B) European pigs

Note: Chinese pigs included Guangdong and Jiangxi provinces.



Supplementary Figure S8 Quality assessment and taxonomic classification of ARGs in recovered MAGs

A: Estimated completeness and contamination of recovered MAGs; only 9261 genomes with completeness \geq 50% and contamination \leq 10% are shown. High-quality genomes (completeness \geq 90%, contamination \leq 5%) are shown in red, medium-quality genomes (completeness \geq 80%, 5%<contamination \leq 10%) are shown in purple (genomes were retained for downstream analysis), and partial genomes (completeness \geq 50%, contamination<10%) are shown in gray. B and C: Number and proportion of MAGs containing ARGs in Chinese (B) and European (C) pigs.

Supplementary Table S1 Different antibiotic exposure regimes in different countries

Supplementary Table S2 Information on human samples

Supplementary Table S3 Full list of ARG types and subtypes in Chinese and European pigs

Supplementary Table S4 Feature importance of random-forest model of ARG subtypes

Supplementary Table S5 Accuracy of initial and simplified random-forest models of ARG subtypes

Supplementary Table S6 Accuracy of random-forest model at each taxonomic level

Supplementary Table S7 Feature importance of random-forest model at family level

Supplementary Table S8 Accuracy of initial and simplified random-forest models at family level

Supplementary Table S9 Importance of ARG markers in Chinese pigs

Supplementary Table S10 Importance of ARG markers in European pigs

Supplementary Table S11 Number of MAGs in Chinese and European pigs after each analysis step

Supplementary Table S12 Information on retained MAGs

Supplementary Table S13 Information on novel species

Supplementary Table S14 Information on MAGs carrying ARGs

Supplementary Tables S1–S14 are listed as separate excel files due to their large size.