

Supplementary Material Legends

Fig. S1 Analyses of gut microbial NR gene numbers and diversity of gut microbial NR genes in pigs. **A** The number of gut microbial NR genes quantified in 112 pigs from seven breeds. **B** Shannon indexes of gut microbial NR genes quantified in 112 pigs from seven breeds. **C** PCoA of gut microbial NR genes quantified in 112 pigs from seven breeds. Data are presented as mean \pm SEM ($n = 8$) and were evaluated by the Kruskal-Wallis test. $**p < 0.01$.

Fig. S2 Comparative analyses of gut microbial KEGG pathways in pigs. Comparative analyses of the relative abundances of microbial genes involved in KEGG pathways, including biosynthesis of unsaturated fatty acids (**A**), secondary bile acid biosynthesis (**B**), tryptophan metabolism (**C**), phenylalanine metabolism (**D**), propanoate metabolism (**E**), butanoate metabolism (**F**), purine metabolism (**G**), pyrimidine metabolism (**H**), methane metabolism (**I**), and nitrogen metabolism (**J**), benzoate degradation (**K**), and dioxin degradation (**L**), respectively. Data are presented as the mean \pm SEM ($n = 8$). Significantly differentially abundant KEGG pathways were identified using the Kruskal-Wallis test. $**p < 0.01$, $*p < 0.05$; ns, not significant.

Fig. S3 Correlation analysis of gut microbial species and antimicrobial resistance genes. Heatmap for the Spearman's correlation analysis of microbial species (relative abundance $>0.5\%$) and antimicrobial resistance genes. $**p < 0.01$, $*p < 0.05$.

Fig. S4 Correlation analysis of gut microbial species and antimicrobial resistance types. Heatmap for the Spearman's correlation analysis of microbial species (relative abundance $>0.5\%$) and antimicrobial resistance types. $**p < 0.01$, $*p < 0.05$.

Fig. S5 Rarefaction curves and heatmap analysis of gut bacterial community as revealed using 16S rRNA gene sequencing. **A** Rarefaction curves for Chao index. **B** Heatmap analysis of bacterial genera.

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31 **Fig. S6 Gut microbial taxonomic compositions in seven pig breeds. A-D** Gut
32 microbial taxonomic compositions, including kingdom (A), class (B), order (C), and
33 family (D), as revealed using metagenomics. **E-G** Gut bacterial taxonomic
34 compositions, including class level (E), order level (F), and family level (G), as
35 revealed using 16S rRNA gene sequencing.

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37 **Fig. S7 Heatmap analysis of relative abundances of three core-predominant**
38 **microbial species. A** Heatmap analysis of relative abundances of *P. succinatutens*, *P.*
39 *copri*, and *O. valericigenes* in the feces of the mice (FMT group) revealed by
40 metagenomics. **B** Heatmap analysis of relative abundances of *O. valericigenes* in the
41 feces of the mice (SPF group) revealed using 16S rRNA gene sequencing.

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43 **Fig. S8 Effects of core-predominant microbes on composition of fecal metabolites**
44 **in germ-free mice. A-C** OPLS-DA for fecal metabolites in mice from groups (Ctrl and
45 PS) (A), groups (Ctrl and PC) (B), groups (Ctrl and OV) (C) (Ctrl, control; PS, *P.*
46 *succinatutens*; PC, *P. copri*; OV, *O. valericigenes*). **D-F** Volcano plot analysis of fecal
47 metabolites in mice from groups (Ctrl and PS) (D), groups (Ctrl and PC) (E), and groups
48 (Ctrl and OV) (F). **G** Venn diagram analysis of the fecal metabolites that are upregulated
49 by the treatments with the three core gut microbes, respectively. **H** Venn diagram
50 analysis of the fecal metabolites that are downregulated by the treatments with the three
51 core gut microbes, respectively. **I-K** The KEGG enrichment analyses of the fecal
52 metabolites altered by the treatments with *P. succinatutens* (I), *P. copri* (J), and *O.*
53 *valericigenes* (K), respectively. **L** UpSet plot comparing the KEGG pathways enriched
54 with the fecal differentially metabolites induced by the treatments with *P. succinatutens*,
55 *P. copri*, and *O. valericigenes*, respectively. The differentially abundant metabolites
56 were assessed based on $VIP \geq 1$ from the OPLS-DA, absolute Log_2 (fold change) ≥ 1 ,
57 and p value < 0.05 .

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59 **Fig. S9 Analyses of complete genome sequences of core-predominant microbes. A**

60 Circular representation of genome of *P. succinatutens* (PS, *P. succinatutens*). **B** KEGG
61 pathway classification of *P. succinatutens* at level 2. **C** Venn diagram analysis of the
62 KEGG pathways (level 3) annotated in *P. succinatutens* and the KEGG pathways (level
63 3) enriched by the fecal metabolites in GF mice that were orally administrated with *P.*
64 *succinatutens*. **D** Circular representation of genome of *P. copri* (PC, *P. copri*). **E** KEGG
65 pathway classification of *P. copri* at level 2. **F** Venn diagram analysis of the KEGG
66 pathways (level 3) annotated in *P. copri* and the KEGG pathways (level 3) enriched by
67 the fecal metabolites in GF mice that were orally administrated with *P. copri*. **G** Circular
68 representation of genome of *O. valericigenes* (OV, *O. valericigenes*). **H** KEGG
69 pathway classification of *O. valericigenes* at level 2. **I** Venn diagram analysis of the
70 KEGG pathways (level 3) annotated in *O. valericigenes* and the KEGG pathways (level
71 3) enriched by the fecal metabolites in GF mice that were orally administrated with *O.*
72 *valericigenes*.

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