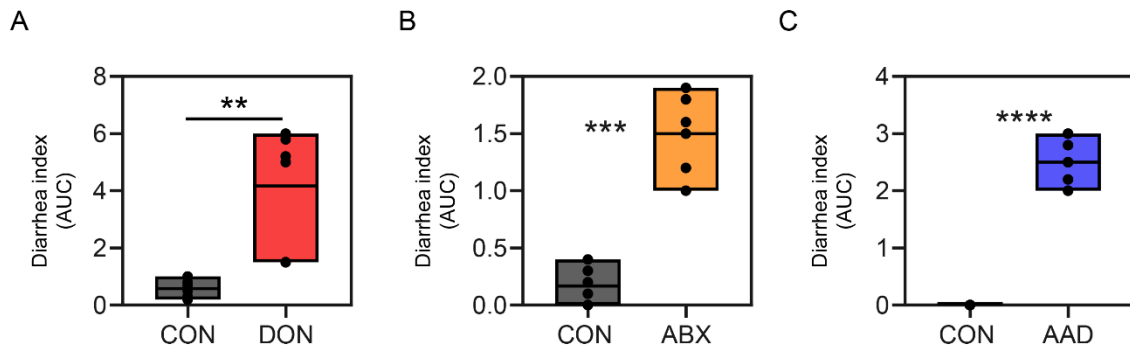
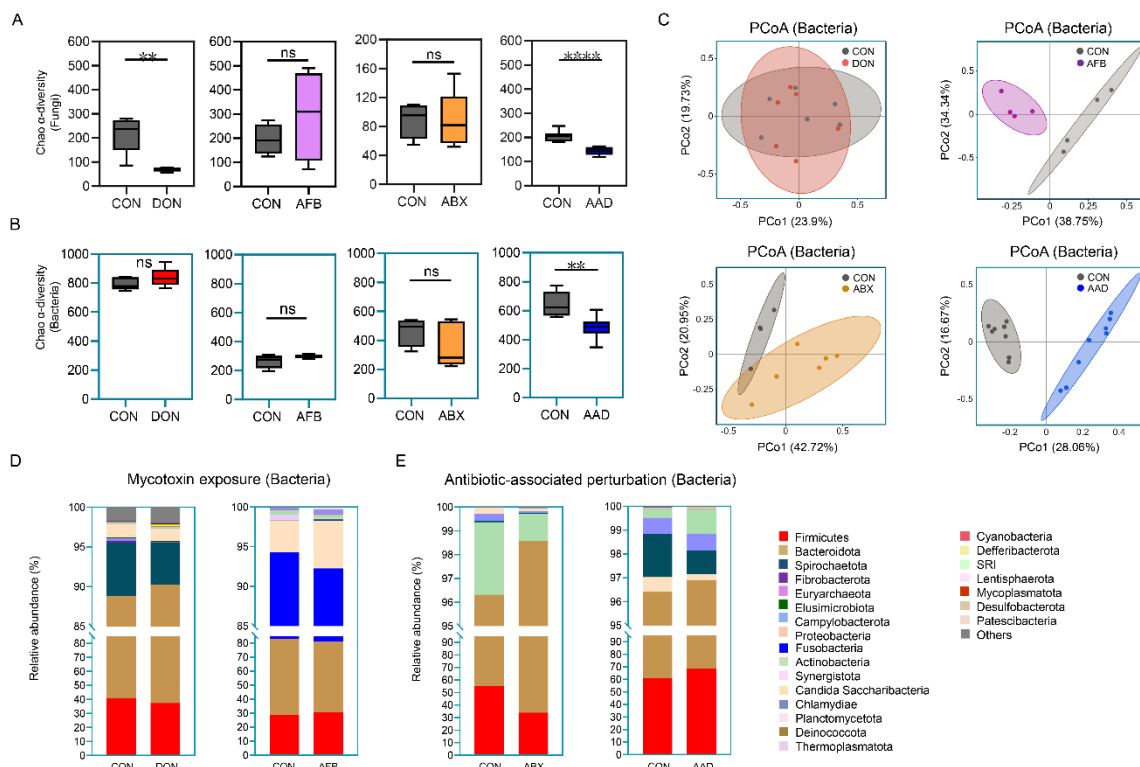
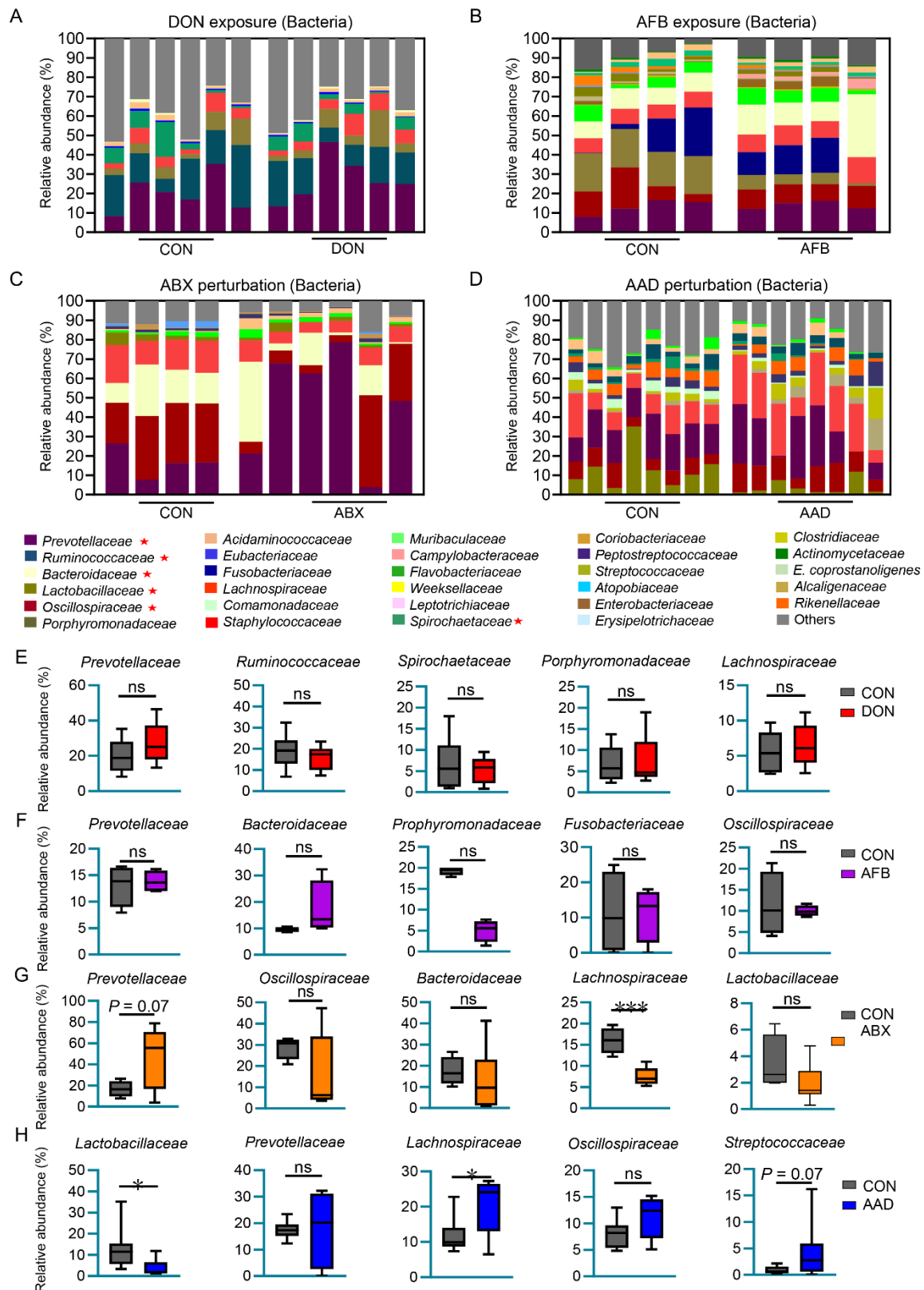




Supplementary Fig. 1. DON and antibiotic-associated perturbation elevate diarrhea index in piglets. **A** Area under the curve (AUC) of diarrhea index in the DON experimental group. **B** Area under the curve (AUC) of diarrhea index in the low-antibiotic mix (ABX) experimental group. **C** Area under the curve (AUC) of diarrhea index in the antibiotic-associated diarrhea experimental group. Box plots show median values with interquartile ranges (IQR); whiskers extend to 1.5× IQR. Sample size: n = 5-6 per group. Statistical significance was assessed using an unpaired two-tailed Student's t-test (** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).



Supplementary Fig. 2. Differential effects of mycotoxin exposure and antibiotics on alpha diversity, bacterial community structure, and phylum-level composition. **A, B** Chao1 alpha diversity index for fungal (A) and bacterial (B) communities across the DON, AFB, ABX, and



Supplementary Fig. 4. Mycotoxin exposure and antibiotic-associated perturbation drive distinct bacterial community restructuring. **A-D** Relative abundance of bacterial taxa at the family level for each independent group: **A** deoxynivalenol (DON; n = 6 per group); **B** aflatoxin (AFB; n = 6 per group); **C** low-dose antibiotic mix (ABX; n = 6 per group); **D** antibiotic-associated diarrhea (AAD; n = 8 per group). **E-H** Relative abundance of the five most abundant

bacterial families for each experimental group: **E** DON (*Prevotellaceae*, *Ruminococcaceae*, *Spirochaetaceae*, *Porphyromonadaceae*, and *Lachnospiraceae*); **F** AFB *Prevotellaceae*, *Bacteroidaceae*, *Prophyromonadaceae*, *Fusobacteriaceae*, and *Oscillospiraceae*); **G** ABX (*Prevotellaceae*, *Oscillospiraceae*, *Bacteroidaceae*, *Lachnospiraceae*, and *Lactobacillaceae*); **H** AAD (*Lactobacillaceae*, *Prevotellaceae*, *Lachnospiraceae*, *Oscillospiraceae*, and *Streptococcaceae*). Box plots show median values with interquartile ranges (IQR); whiskers extend to 1.5× IQR. Sample size: n = 4-8 per group. Statistical significance was assessed using unpaired Student's t-test.

A Statistical comparison with equivalent random networks

Network Indexes	Fun DON		Fun AAD		Bac DON		Bac AAD		Fun-Bac DON		Fun-Bac AAD	
	Empirical Network	Random network	Empirical Network	Random network	Empirical Network	Random network	Empirical Network	Random network	Empirical Network	Random network	Empirical Network	Random network
Average clustering coefficient (AvgCC)	0.417	0.053±0.002	0.565	0.106±0.002	0.177	0.009±0.0002	0.1	0.018±0.006	0.287	0.089±0	0.592	0.301±0
Average path length	4.39	3.091±0.004	2.352	2.331±0.002	4.163	3.610±0.0006	5.242	5.575±0.02	2.001	1.913±0	1.716	1.699±0
Geodesic efficiency (E)	0.23	0.324±0.001	0.425	0.429±0.0003	0.24	0.277±0	0.19	0.179±0.001	0.499	0.523±0	0.583	0.589±0
Graph Density(D)	0.052	0.052±0	0.107	0.107±0	0.01	0.01±0	0.013	0.013±0	0.089	0.089±0	0.301	0.301±0
Connectedness (Con)	0.86	0.990±0.001	0.63	0.999±0.0003	0.99	0.999±0	0.63	0.875±0.002	1	1±0	1	1±0
Modularity (fast-greedy)	0.649	0.42±0.002	0.323	0.301±0.001	0.545	0.339±0.0004	0.761	0.659±0.002	0.283	0.096±0.0002	0.172	0.054±0.0001

B Topological properties of the fungal and bacterial interaction network

Type	No. Of Nodes	No. Of Edges	Avg. Degree	Network Diameter	Positive Interaction(%)	Negative Interaction(%)
Fungi DON	86	191	4.442	11	46.6	53.4
Fungi AAD	68	243	7.147	8	99.59	0.41
Bacteria DON	701	2412	6.882	12	33.58	66.42
Bacteria AAD	189	226	2.392	12	30.97	69.03
Fungal-Bacterial DON	779	26891	69.04	3	51.86	48.14
Fungal-Bacterial AAD	535	42992	160.718	3	50.09	49.91

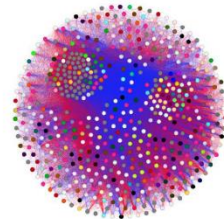
C

Total correlation of the Fungal-Bacterial network of DON

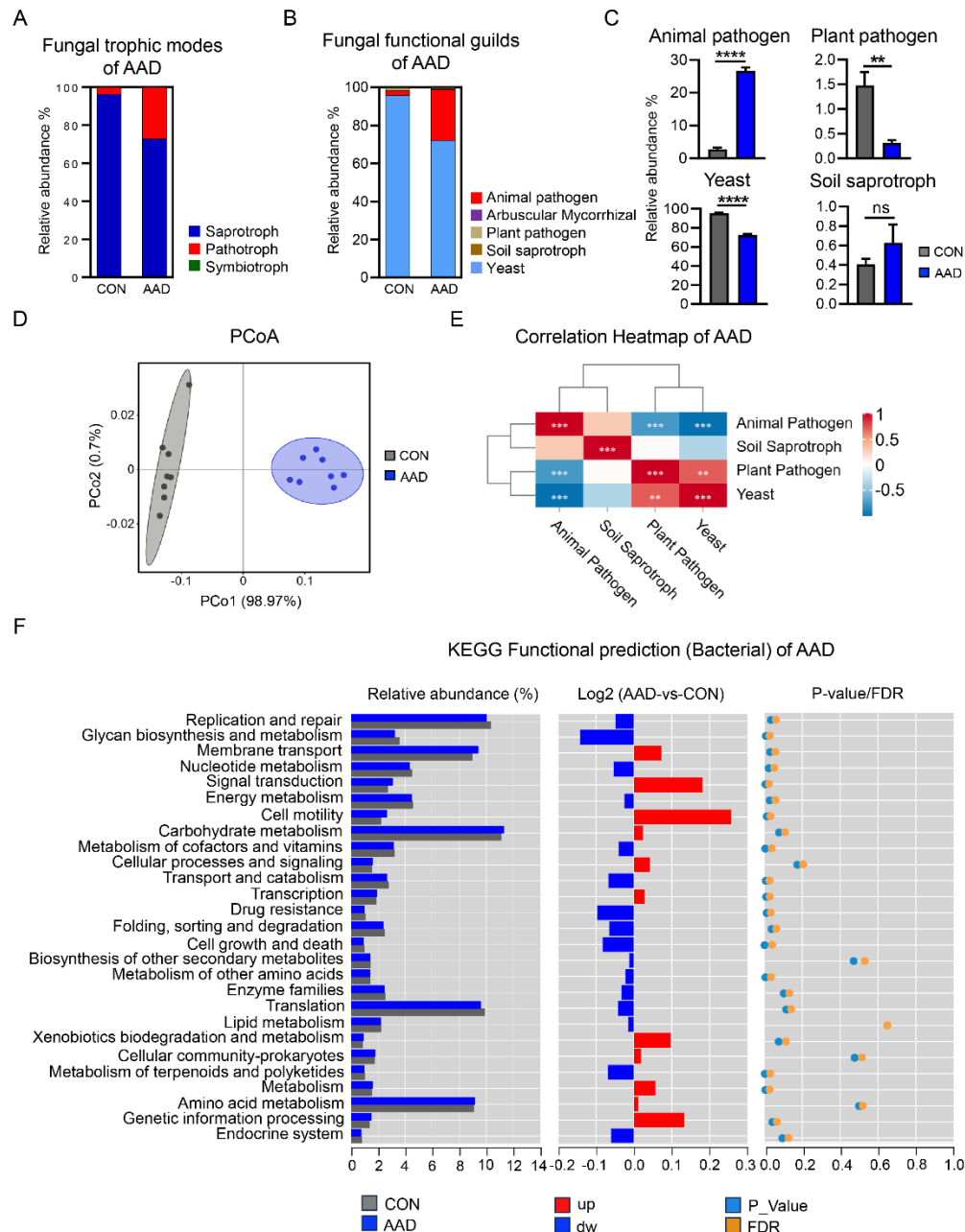


D

Total correlation of the Fungal-Bacterial network of AAD

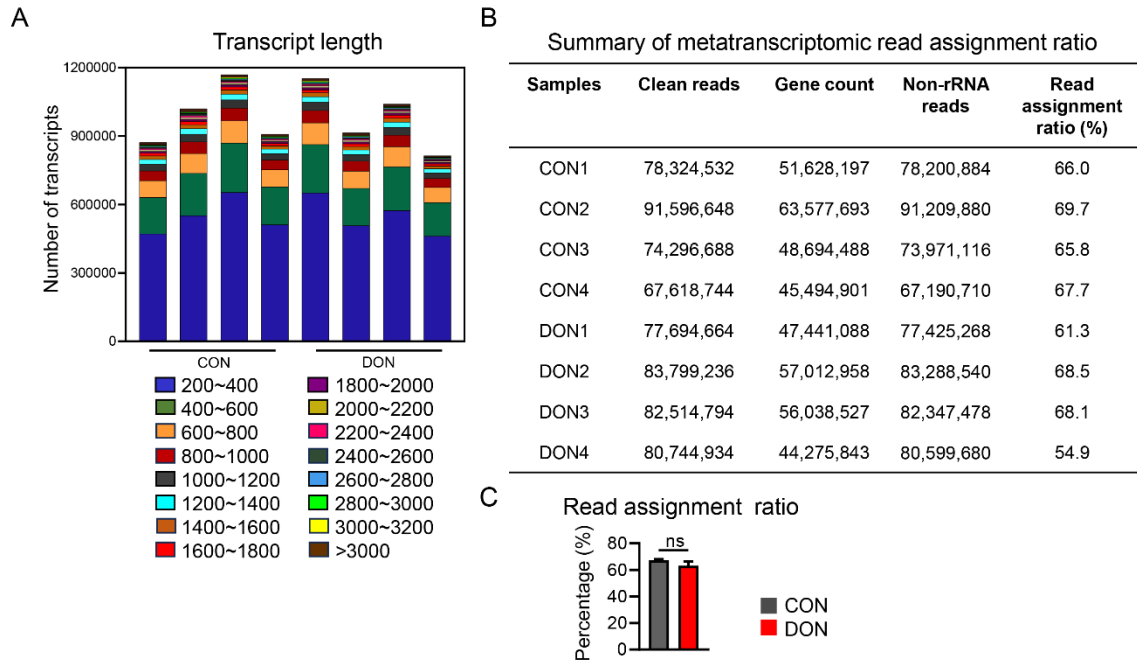


Supplementary Fig. 5. Network topology and random model validation for the DON and AAD experiments. **A** Table showing the statistical comparison with equivalent random networks after 100 iterations. **B** Table showing the topological properties of the fungal and bacterial interaction networks. **C** Total correlations of the fungal-bacterial network in the DON experiment. **D** Total correlations of the fungal-bacterial network in the AAD experiment.

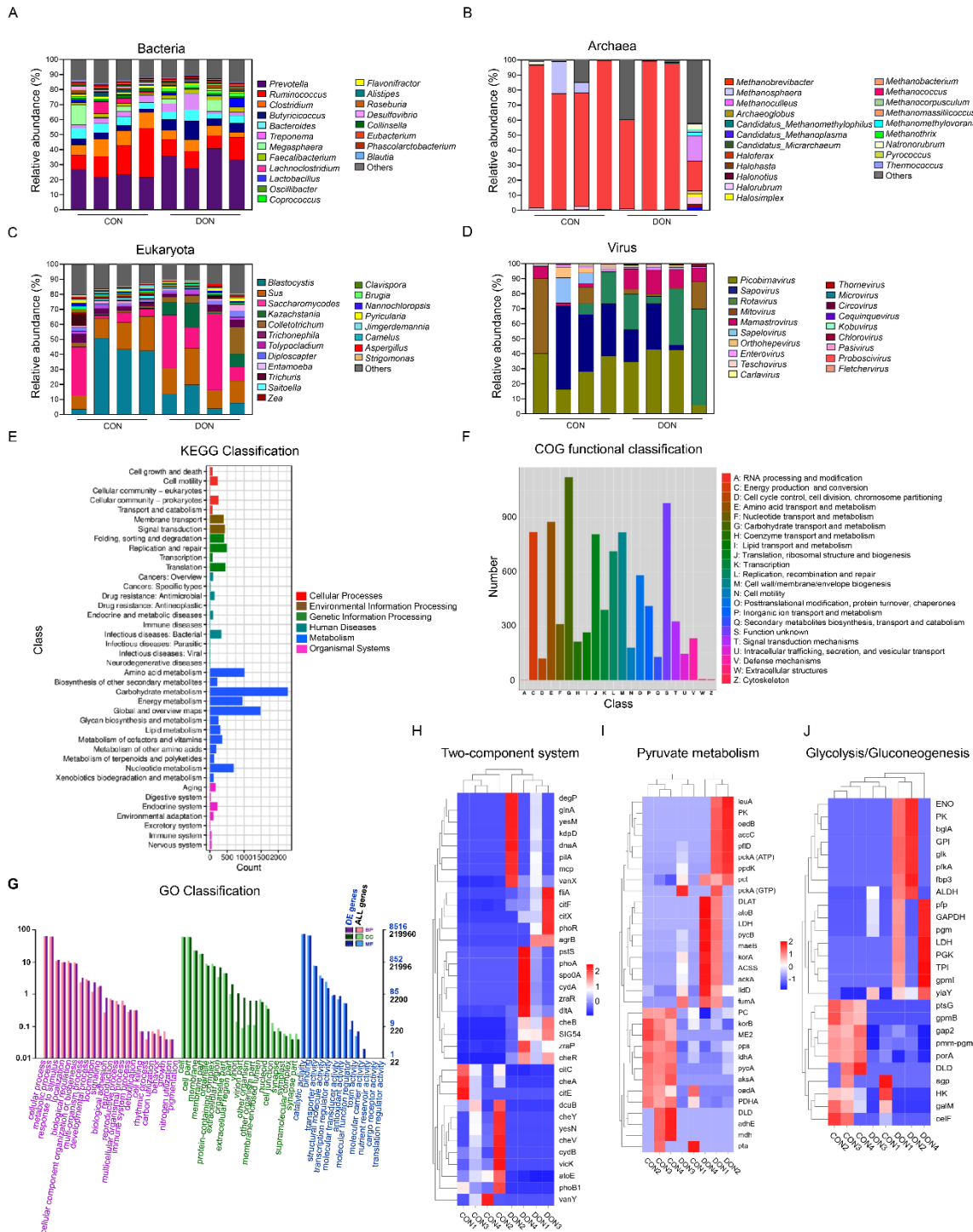


Supplementary Fig. 6. AAD perturbation drives functional restructuring of gut fungi and bacteria. **A–E** Fungal functional prediction using a custom-curated database of 300 well-characterized fungal taxa integrating FUNGuild and FunTraits annotations. **A** Relative abundance of fungal trophic modes (pathotroph, saprotroph, and symbiotroph) in control (CON) and AAD-treated piglets. **B** Distribution of predicted fungal functional guilds. **C** Treatment-specific comparison of selected guilds (animal pathogens, plant pathogens, yeasts, soil saprotrophs) in CON and AAD. **D** Principal coordinates analysis (PCoA) based on functional guild composition showing dissimilarities between CON and AAD. **E** Spearman correlation heatmap illustrating within-group associations among dominant fungal guilds. **F** KEGG functional predictions for bacterial communities in the AAD group. Data are presented as mean $\pm$ SEM. Sample size: $n = 8$ per group. Statistical significance was assessed using unpaired

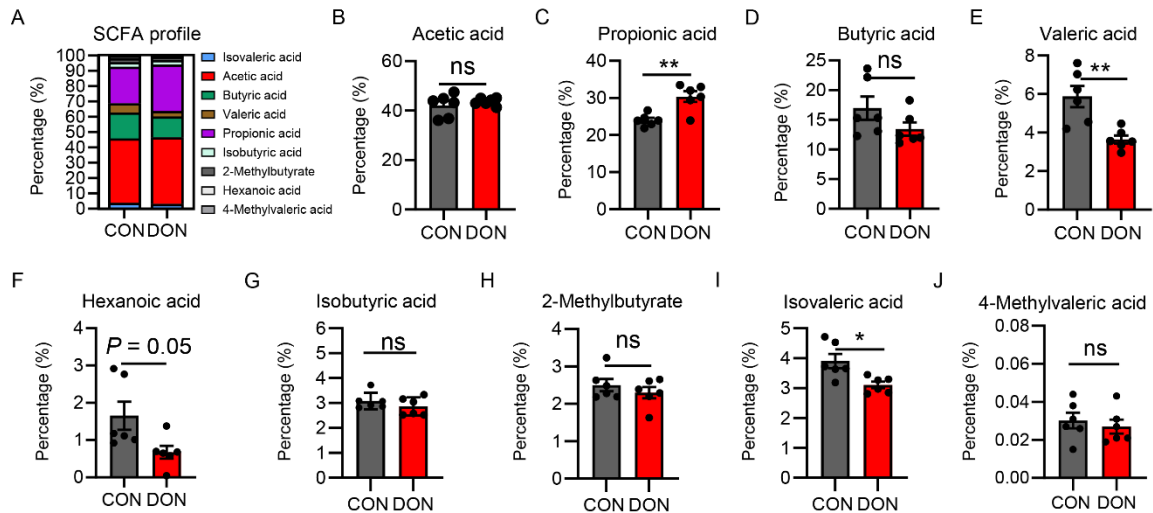
two-tailed Student's t-test (** $P < 0.01$, **** $P < 0.0001$; ns, not significant). ** $P < 0.01$, *** $P < 0.001$ (correlation heatmap significance).



Supplementary Fig. 7. Metatranscriptomic quality control summary. **A** Transcript length distribution in the control and DON groups. **B** Summary of metatranscriptomic read assignment ratio across the CON and DON groups; **C** Bar plot of read assignment comparison in the CON and DON groups. The read assignment ratio was calculated as (total summed unigene counts $\div$ non-rRNA reads) $\times$ 100, representing the cumulative sequencing signal allocated to our assembled unigene catalog after accounting for the fractional distribution of multi-mapping reads between homologous transcripts. Data are mean $\pm$ SEM. Sample size: $n = 4$ per group using the Mann-Whitney U test (ns, $p > 0.05$).



Supplementary Fig. 8. Metatranscriptomic profiling of gut microbial composition and function following DON exposure. A–D Relative abundance of the top transcriptionally active genera in control and DON groups: **A** bacteria; **B** archaea; **C** eukaryotes; **D** viruses. **E** KEGG level 1 functional classification of all annotated transcripts. **F** Clusters of orthologous groups (COG) functional classification. **G** Gene ontology (GO) classification. **H–J** Heatmaps of selected KEGG pathways: **H** Two-component system; **I** Pyruvate metabolism; **J** Glycolysis/Gluconeogenesis in CON and DON groups.



Supplementary Fig. 9. DON exposure alters the relative composition of colonic SCFA profiles in weaning piglets. **A** Stacked bar plot showing the relative percentage composition of individual SCFAs in control (CON) and deoxynivalenol (DON)-exposed groups. **B-J** Bar plots quantifying the relative abundance of individual SCFAs, expressed as a percentage of total SCFAs: **B** acetic acid; **C** propionic acid; **D** butyric acid; **E** valeric acid; **F** hexanoic acid; **G** isobutyric acid; **H** 2-methylbutyrate; **I** isovaleric acid; **J** 4-methylvaleric acid. Data are presented as mean $\pm$ SEM. Sample size: $n = 6$ per group. Statistical significance was determined by unpaired two-tailed Student's *t*-test, comparing DON to CON: * $P < 0.05$, ** $P < 0.01$; ns, not significant.

Supplementary Table 1: Metagenomic sequencing and assembly statistics

Sample	Raw base (G)	Clean base (G)	Clean_GC (%)	Clean_Q20 (%)	Clean_Q30 (%)	Scaftig total length (bp)	Scaftig number	Average length of scaftigs (bp)	N50 (bp)
CON1	10.81	10.72	42.75	99.40	97.41	485 200 307	312 700	1551.65	2239
CON2	10.59	10.49	45.77	99.28	97.12	502 273 344	480 860	1044.53	968
CON3	10.56	10.52	42.52	99.49	97.53	496 375 495	325 798	1523.57	2123
CON4	10.52	10.39	47.05	99.22	96.82	514 811 001	442 466	1163.50	1264
CON5	12.57	12.29	44.34	99.46	97.53	503 217 201	295 342	1703.85	2634
CON6	10.45	10.36	44.39	99.37	97.32	432 334 494	278 896	1550.16	2251
DON1	10.28	10.10	48.19	99.43	97.43	484 594 501	337 414	1436.20	1916
DON2	11.70	11.40	47.20	97.27	97.27	506 982 860	311 626	1626.90	2476
DON3	10.58	10.53	43.64	97.56	97.56	460 206 135	287 188	1602.46	2318
DON4	10.46	10.40	44.30	97.54	97.54	463 348 289	305 882	1514.79	2116
DON5	10.67	10.59	45.22	97.44	97.44	467 322 261	289 373	1614.95	2425
DON6	10.59	10.52	44.39	97.26	97.26	489 101 698	321 565	1521.00	2109

Raw base (G) indicates the total gigabase pairs of unprocessed raw sequencing data generated. Clean base (G) corresponds to the total gigabase pairs retained after quality filtering. Clean_GC (%) represents the percentage of guanine and cytosine nucleotides within quality-filtered clean reads. Clean_Q20 and Clean_Q30 report the proportion of nucleotide bases with Phred quality scores ≥ 20 and ≥ 30 . Scaftigs total length (bp) refers to the cumulative nucleotide length of all assembled scaftigs (contigs and scaffolds). Scaftig number denotes the total count of assembled scaftig sequences recovered. Average length of scaftigs is the mean nucleotide length across all assembled scaftigs per sample. N50 represents the minimum length of the set of longest scaftigs that together account for half of the total cumulative scaftig length.

Supplementary Table 2: Metatranscriptomics sequencing quality metrics

Sample	Total reads	Clean reads	Percentage of clean reads (%)	Clean bases (bp)	GC content (%)	%>Q20	%>Q30
CON1	78 355 178	78 324 532	99.96	11 613 148 216	52.08	98.90	97.36
CON2	91 631 042	91 596 648	99.96	13 602 864 854	51.65	98.91	97.40
CON3	74 325 362	74 296 688	99.96	11 024 680 566	52.17	98.89	97.35
CON4	67 644 974	67 618 744	99.96	10 016 117 306	52.08	98.93	97.44
DON1	77 724 466	77 694 664	99.96	11 500 667 718	51.94	99.01	97.61
DON2	83 829 706	83 799 236	99.96	12 397 640 478	52.00	98.92	97.43
DON3	82 546 956	82 514 794	99.96	12 208 314 038	52.95	98.96	97.49
DON4	80 772 720	80 744 934	99.97	11 914 341 106	52.87	99.03	97.65

Total reads correspond to unprocessed raw sequencing reads before adapter removal and quality filtering. Clean reads denote high-quality sequences retained after all quality control steps. Clean bases correspond to the total number of qualified base pairs derived from filtered clean reads. GC content quantifies the relative proportion of guanine and cytosine nucleotides present within quality-filtered clean reads. Q20 and Q30 values report the proportion of nucleotide bases with Phred quality scores ≥ 20 and ≥ 30 , respectively.

Supplementary Table 3: Transcript assembly and gene catalogue statistics

ID	Number of genes	Total length (bp)	Min_length	Max_length	Average length	N50
Unique_gene	495 002	710 523 456	234	50 372	1 435.40	1 780

Summary of the non-redundant gene catalogue generated by Trinity assembly and CD-HIT clustering (95% identity, 90% coverage). N50 represents the contig length at which 50% of the total assembly length is contained.