

Supplemental materials

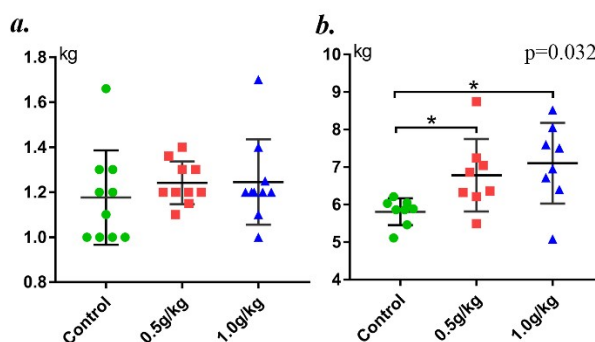


Figure S1 Average birth weight and weaning weight of piglets*

*a. average birth weight, b. average weaning weight. Data were analyzed with one-way ANOVA followed with Dunnett multiple comparisons test.

Table S1 Changes in alpha diversity indices of colonic microbiota from suckling piglets

Indices	Control	0.5g/kg	1.0g/kg	P-value
Observed_species	948.625±21.160	947.500±21.236	976.875±15.140	0.491
Shannon	7.236±0.153	7.186±0.150	7.359±0.148	0.708
Simpson	0.980±0.004	0.979±0.004	0.982±0.004	0.912
Chao1	1035.045±27.098	1090.130±76.531	1056.208±14.913	0.716
ACE	1042.144±24.918	1059.798±41.283	1060.342±14.539	0.882
Goods_coverage	0.997±0.000	0.997±0.000	0.997±0.000	0.385
PD_whole_tree	75.209±1.903	74.508±1.663	77.052±1.372	0.544

Data were analyzed with One-way ANOVA followed by Tukey–Kramer multiple comparison test and presented as means± SEM.

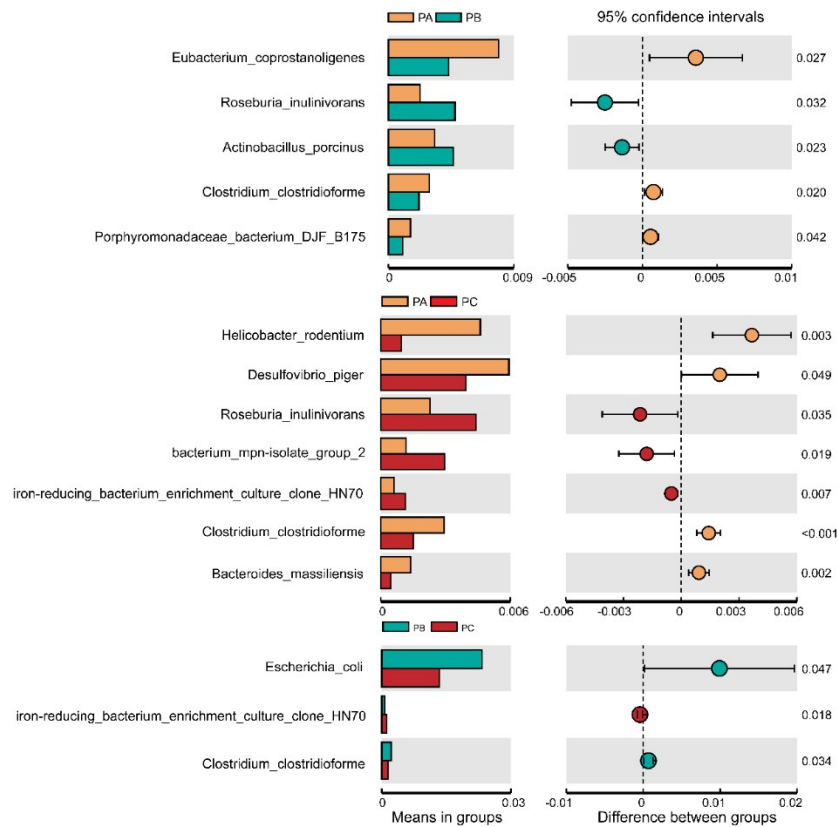


Figure S2 Differences in OTU richness between lysozyme treated groups and control group at species level, Data were analyzed by T-test, pA, control group; pB, 0.5 g/kg lysozyme group; pC, 1.0 g/kg lysozyme.

Table S2 Predicted metabolic functions of colonic microbiota after 14-day lysozyme treatment*

Observation Ids	p-values	Effect size	Control	0.5g/kg	1.0g/kg
DNA repair and recombination proteins	0.007	0.377	2.956 ±0.035	2.982 ±0.032	3.032 ±0.053
Ribosome	0.003	0.417	2.559 ±0.049	2.594 ±0.049	2.674 ±0.070
Pyrimidine metabolism	0.012	0.345	1.946 ±0.027	1.970 ±0.032	2.019 ±0.059
Peptidases	0.009	0.362	1.907 ±0.025	1.926 ±0.024	1.972 ±0.053
Chromosome	0.005	0.399	1.645 ±0.019	1.668 ±0.020	1.702 ±0.042
Amino acid related enzymes	0.000	0.516	1.541 ±0.014	1.560 ±0.016	1.588 ±0.025
Ribosome Biogenesis	0.001	0.508	1.479 ±0.013	1.495 ±0.011	1.512 ±0.015
Two-component system	0.001	0.510	1.477 ±0.050	1.420 ±0.050	1.344 ±0.060
Secretion system	0.000	0.661	1.311 ±0.026	1.271 ±0.025	1.223 ±0.026
DNA replication proteins	0.001	0.475	1.286 ±0.028	1.312 ±0.025	1.352 ±0.033
Function unknown	0.004	0.405	1.212 ±0.032	1.193 ±0.030	1.158 ±0.017
Glycolysis / Gluconeogenesis	0.000	0.540	1.142 ±0.017	1.116 ±0.015	1.099 ±0.018
Oxidative phosphorylation	0.001	0.482	1.132 ±0.026	1.178 ±0.029	1.205 ±0.038
Pyruvate metabolism	0.011	0.350	1.050 ±0.024	1.033 ±0.023	1.004 ±0.030
Alanine, aspartate and glutamate metabolism	0.007	0.376	1.047 ±0.020	1.070 ±0.017	1.086 ±0.023
Homologous recombination	0.002	0.452	1.001 ±0.019	1.012 ±0.017	1.041 ±0.019
Chaperones and folding catalysts	0.003	0.423	0.993 ±0.020	1.027 ±0.030	1.074 ±0.056
Transcription machinery	0.004	0.407	0.990 ±0.045	1.016 ±0.034	1.060 ±0.021

Translation proteins	0.000	0.573	0.964±0.006	0.973±0.006	0.985±0.009
Mismatch repair	0.002	0.457	0.885±0.013	0.896±0.012	0.915±0.015
Peptidoglycan biosynthesis	0.002	0.458	0.876±0.017	0.891±0.015	0.922±0.028
Others	0.004	0.416	0.851±0.012	0.837±0.018	0.809±0.030
DNA replication	0.008	0.372	0.700±0.014	0.708±0.013	0.726±0.014
One carbon pool by folate	0.001	0.487	0.671±0.016	0.688±0.020	0.726±0.032
Terpenoid backbone biosynthesis	0.004	0.411	0.628±0.011	0.635±0.010	0.653±0.016
Lipid biosynthesis proteins	0.000	0.593	0.589±0.007	0.604±0.007	0.614±0.010
Translation factors	0.003	0.427	0.578±0.011	0.587±0.011	0.605±0.016
Cell cycle - Caulobacter	0.000	0.545	0.542±0.005	0.551±0.007	0.568±0.015
Propanoate metabolism	0.004	0.411	0.533±0.018	0.523±0.015	0.501±0.014
Phosphotransferase system (PTS)	0.001	0.480	0.497±0.041	0.443±0.035	0.372±0.075
RNA degradation	0.010	0.356	0.466±0.007	0.473±0.010	0.484±0.013
Nucleotide excision repair	0.004	0.407	0.415±0.009	0.421±0.009	0.435±0.014
Glycerolipid metabolism	0.003	0.426	0.401±0.021	0.382±0.018	0.360±0.019
Photosynthesis proteins	0.001	0.509	0.379±0.009	0.396±0.006	0.398±0.009
Photosynthesis	0.000	0.515	0.377±0.009	0.393±0.006	0.396±0.009
Drug metabolism - other enzymes	0.002	0.437	0.345±0.006	0.353±0.007	0.367±0.016
Cyanoamino acid metabolism	0.000	0.596	0.259±0.011	0.274±0.010	0.289±0.009
Sulfur relay system	0.005	0.397	0.254±0.021	0.245±0.018	0.220±0.014
Benzoate degradation	0.011	0.350	0.223±0.008	0.217±0.010	0.200±0.019
Chloroalkane and chloroalkene degradation	0.008	0.372	0.207±0.018	0.191±0.015	0.177±0.014
Other glycan degradation	0.002	0.439	0.199±0.017	0.221±0.029	0.248±0.020
Tuberculosis	0.002	0.452	0.157±0.002	0.158±0.002	0.162±0.002
Sphingolipid metabolism	0.004	0.413	0.157±0.013	0.167±0.016	0.182±0.007
Phenylpropanoid biosynthesis	0.000	0.615	0.128±0.009	0.140±0.008	0.151±0.005
Lysine degradation	0.004	0.409	0.115±0.005	0.116±0.004	0.107±0.005
Bacterial toxins	0.010	0.357	0.108±0.002	0.104±0.003	0.100±0.006
Glutamatergic synapse	0.006	0.386	0.096±0.003	0.099±0.003	0.101±0.002
Nitrotoluene degradation	0.009	0.359	0.096±0.008	0.090±0.009	0.081±0.007
Glycosphingolipid biosynthesis - globo series	0.004	0.416	0.092±0.008	0.100±0.014	0.116±0.012
Epithelial cell signaling in Helicobacter pylori infection	0.000	0.608	0.091±0.002	0.093±0.002	0.098±0.003
Butirosin and neomycin biosynthesis	0.009	0.363	0.069±0.004	0.069±0.005	0.076±0.004
Lysosome	0.009	0.364	0.067±0.009	0.076±0.016	0.090±0.011
Cell division	0.000	0.516	0.066±0.003	0.070±0.004	0.076±0.004
Zeatin biosynthesis	0.006	0.387	0.058±0.002	0.061±0.003	0.066±0.006
Nucleotide metabolism	0.003	0.432	0.056±0.003	0.053±0.003	0.047±0.006
Ribosome biogenesis in eukaryotes	0.005	0.402	0.051±0.001	0.051±0.001	0.053±0.001
Glycosaminoglycan degradation	0.008	0.366	0.047±0.007	0.054±0.012	0.066±0.012
NOD-like receptor signaling pathway	0.001	0.473	0.046±0.001	0.047±0.001	0.050±0.002
Prostate cancer	0.001	0.503	0.044±0.001	0.046±0.001	0.048±0.002
Proteasome	0.000	0.517	0.044±0.001	0.045±0.001	0.048±0.002
Progesterone-mediated oocyte maturation	0.000	0.528	0.044±0.001	0.045±0.001	0.048±0.002

Antigen processing and presentation	0.000	0.528	0.044 ±0.001	0.045 ±0.001	0.048 ±0.002
Synthesis and degradation of ketone bodies	0.003	0.425	0.041±0.005	0.039±0.004	0.032 ±0.004
Glycosphingolipid biosynthesis - ganglio series	0.008	0.371	0.038 ±0.006	0.045 ±0.011	0.057 ±0.012
Electron transfer carriers	0.002	0.460	0.023 ±0.002	0.021±0.002	0.019 ±0.002
Protein digestion and absorption	0.010	0.355	0.021 ±0.004	0.026 ±0.005	0.033 ±0.010
Penicillin and cephalosporin biosynthesis	0.000	0.569	0.021 ±0.001	0.018 ±0.001	0.016 ±0.002
Styrene degradation	0.009	0.364	0.020 ±0.003	0.018 ±0.002	0.016 ±0.002
Staphylococcus aureus infection	0.003	0.422	0.014 ±0.005	0.010 ±0.003	0.007 ±0.002
Caprolactam degradation	0.005	0.392	0.014 ±0.002	0.015 ±0.002	0.011 ±0.002
Chlorocyclohexane and chlorobenzene degradation	0.007	0.381	0.009 ±0.002	0.008 ±0.002	0.006 ±0.001
Renal cell carcinoma	0.011	0.350	0.009 ±0.001	0.008 ±0.001	0.007 ±0.001
Prion diseases	0.000	0.692	0.004 ±0.000	0.004 ±0.000	0.003 ±0.000
alpha-Linolenic acid metabolism	0.004	0.413	0.004 ±0.001	0.005 ±0.001	0.003 ±0.001
Non-homologous end-joining	0.003	0.423	0.004± 0.000	0.003 ±0.001	0.003 ±0.000
Ubiquitin system	0.009	0.364	0.002 ±0.000	0.002± 0.000	0.002 ±0.000
Various types of N-glycan biosynthesis	0.011	0.350	0.001 ±0.000	0.001 ±0.000	0.001 ±0.000
Betalain biosynthesis	0.008	0.369	0.000 ±0.000	0.000 ±0.000	0.000 ±0.000
Indole alkaloid biosynthesis	0.011	0.350	0.000 ±0.000	0.000 ±0.000	0.000 ±0.000

*Data were analyzed with One-way ANOVA and presented as means± Std.

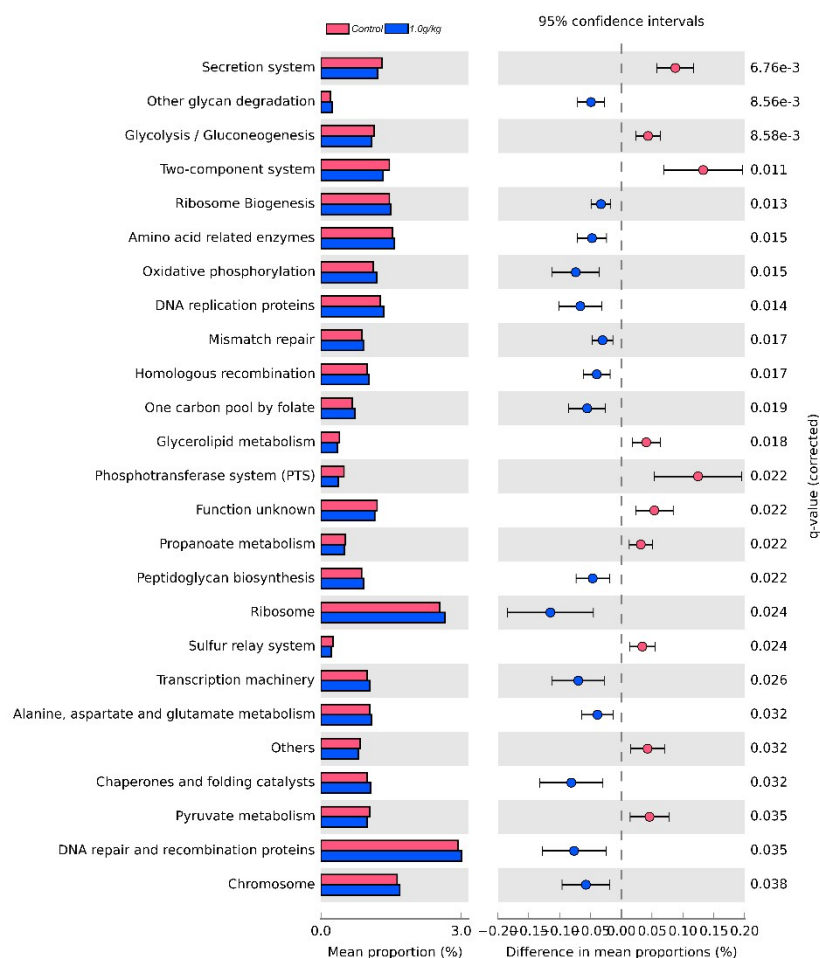


Figure S3 Functional differentiation of colonic microbiota between control group and 1.0g/kg

group