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Supplementary Material

Pioneering gut health improvements in piglets with phytogetic feed additives

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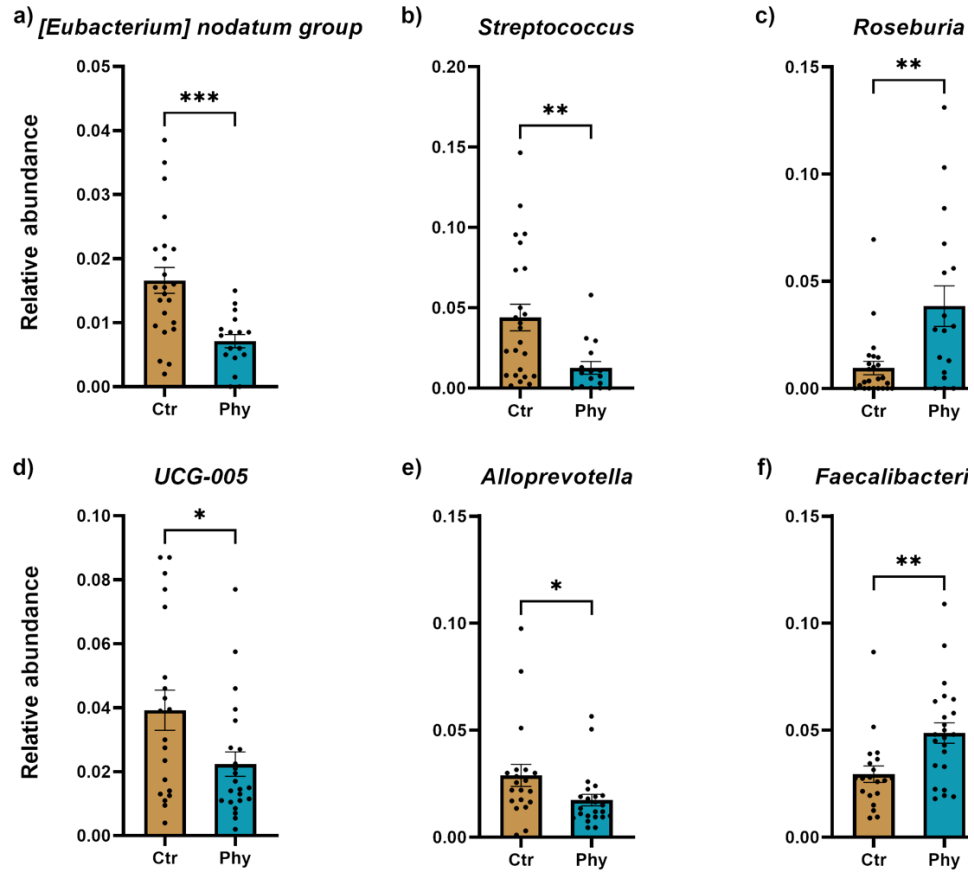
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Supplementary Table S1. Performance data of weaner-to-grower pigs fed with and without phytogetic additives.

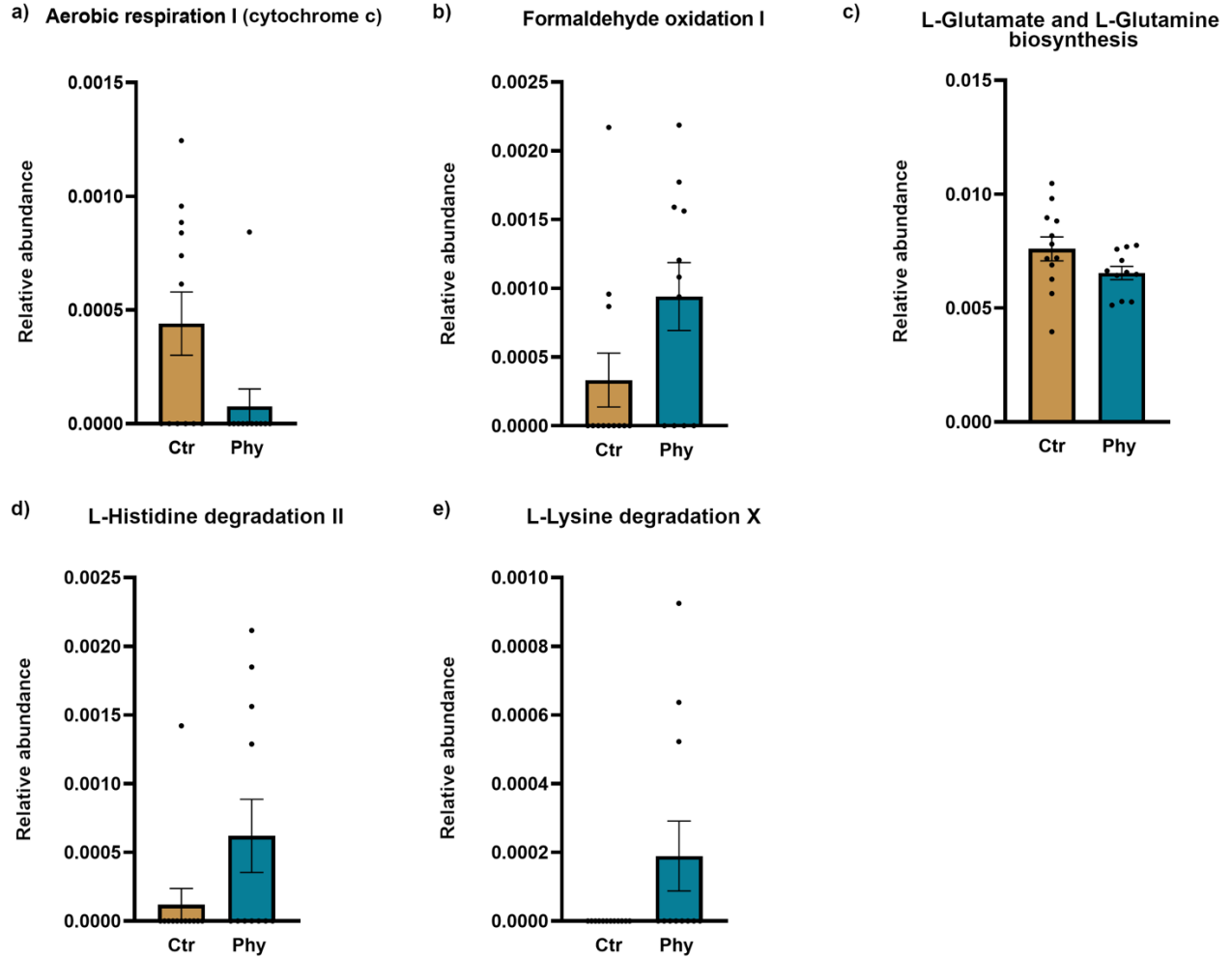
Age	Measure	Control		Treatment	
W3	Average body weight (kg)	6.486		6.218	
	SD	1.4		1.444	
W8	Average body weight (kg)	20.286		20.382	
	SD	3.647		4.752	
		W3	W8	W3	W8
	Maximum body weight (kg)	10.6	29.7	8.9	29.65
	Minimum body weight (kg)	3.6	12.9	3.6	11.35
	25 th percentile	5.4	17.74	5.175	16.98
	75 th percentile	7.35	22.46	7.1	23.15
	Weight gain (kg)	13.80		14.16	

Supplementary Table S2. The SIMPER analysis was conducted on faecal samples at week 8 with contribution of individual genus to the dissimilarity between control and treatment.

Species	Control	Treatment
<i>Prevotella</i>	0.2	0.22
<i>Muribaculaceae</i>	0.08	0.09
<i>Streptococcus</i>	0.04	0.03
<i>Lactobacillus</i>	0.04	0.04
Others	0.1	0.08
<i>Roseburia</i>	0.01	0.03
<i>Clostridium sensu stricto 1</i>	0.03	0.02
<i>UCG-005</i>	0.04	0.03
<i>Faecalibacterium</i>	0.04	0.04
<i>Megasphaera</i>	0.02	0.02
<i>Subdoligranulum</i>	0.05	0.05
<i>Alloprevotella</i>	0.02	0.02
<i>UCG-002</i>	0.02	0.02



Supplementary Fig. S1 Comparative analysis of genus-level relative abundance in faecal samples from male and female piglets at week 8. Panels a) to c) represents genera differentially abundant in male piglets, while panels d) to f) represent those in female piglets when comparing Ctr to Phy groups. a) *[Eubacterium] nodatum group*, b) *Streptococcus*, and c) *Roseburia* show significant differences in males; d) *UCG-005*, e) *Alloprevotella*, and f) *Faecalibacterium* are represented for females. Significance levels are denoted: * $p < 0.05$, ** $p < 0.001$, *** $p < 0.0001$.



Supplementary Fig. S2 Examination of marginally altered metabolic pathways in metagenomic analysis between Ctr and Phy groups. a) Aerobic respiration I (cytochrome), b) Formaldehyde oxidation I, c) L-Glutamate and L-Glutamine biosynthesis, d) L-Histidine degradation II, and e) L-Lysine degradation X. Each bar represents the mean relative abundance of a pathway, with error bars indicating the standard error of the mean.