

1 **Table S1.** Ingredient and chemical composition of the gestation diets

Ingredients	Content, %	Nutrients	Nutrient level
Corn	67.0	Calculated composition	
Soybean meal, dehulled	14.0	GE, MJ/kg	13.28
Wheat bran	15.4	DM, %	88.6
Fish meal	0.6	CP, %	13.6
Soybean oil	-	Ca, %	0.95
Dicalcium phosphate	1.2	Total P, %	0.61
Limestone	0.9	Analyzed composition	
L-Lysine HCl (78%)	-	DM, %	87.4
Salt	0.38	CP, %	12.4
Premix ¹	0.52	Ash, %	5.3
Total	100	EE, %	1.8

2 ¹Premix supplied the following per kilogram of diet: Zn, 90.31 mg as Zn oxide; Mn, 18.01 mg as Mn
3 sulfate; Fe, 53.96 mg as ferrous sulfate; Cu, 5.40 mg as Cu sulfate; Se, 0.30 mg as Na selenite; I, 2.20
4 mg as K iodate; niacin, 55.07 mg; pantothenic acid, 33.04 mg; vitamin A, 11,013 IU; vitamin D, 2,753
5 IU; vitamin E, 55 IU; riboflavin, 9.9 mg; vitamin K, 4.41 mg; vitamin B 12, 0.06 mg; choline, 495 mg;
6 pyridoxine, 1.65 mg; folic acid, 1.65 mg; thiamine, 1.01 mg.

7 **Table S2.** The number of reads for 16S rRNA sequencing

Groups	Raw Reads	Clean Reads	Effective Reads
NG1	79966	78830	75125
NG2	79962	78947	72641
NG3	80189	78930	72217
NG4	80007	78939	70402
NG5	77639	76566	72680
NG6	79943	78749	73614
NG7	78562	78658	71186
NG8	78498	78716	72432
NG9	79568	78498	73357
NG10	79926	78594	74552
LG1	80064	78875	73108
LG2	80425	79295	72648
LG3	79710	78692	72203
LG4	79925	78210	71143
LG5	80132	76957	73564
LG6	80254	77598	74120
LG7	80551	79142	72984
LG8	80356	78859	73049
LG9	79963	77691	71268
LG10	79662	76135	72254

8 Abbreviations represented: NG: normal blood glucose; LG: low blood glucose.

9 **Table S3.** List of primers used for RT-qPCR analysis

Genes	Forward primer (5' to 3' direction)	Reverse primer (5' to 3' direction)
PGC-1 α	ATCGCAGTCGCAACATTACA	TTGGTTGGCTTTATGAGGAGG
GCN5	GTCTTCTGTGCCGTCACCTCAA	GCTCTTGGGCACCTTGATGTCT
PEPCK	ATGCCTCCTCAGCTGCATAATGGTC	CTTTCGATCCTGGCCACATC
G6P	GAGGAAGGAATGAACATTCT	TACGGGCGTTGTCCAAACAG
β -actin	CGTTGGCTGGTTGAGAATC	CGGCAAGACAGAAATGACAA

- 10 Abbreviations represented: PGC-1 α , peroxisome proliferative activated receptor-g co-activator 1; GCN5,
11 general control non-repressed protein 5; PEPCK, phosphoenolpyruvate carboxykinase; G6P, glucose-6-
12 phosphatase.

13 **Table S4.** Primer sequences

Target bacteria	Source	Identifier
Lactobacillus	ATCC	1578
Clostridium_sensu_stricto_1	ATCC	1485
Clostridium_sensu_stricto_3	ATCC	1485
Faecalibacterium	ATCC	216851
Parabacteroides	ATCC	375288
[Eubacterium]_hallii_group	ATCC	1730
Bifidobacteriaceae	ATCC	31953
Lachnospiraceae_AC2044_group	ATCC	186803
Streptococcaceae	ATCC	1300

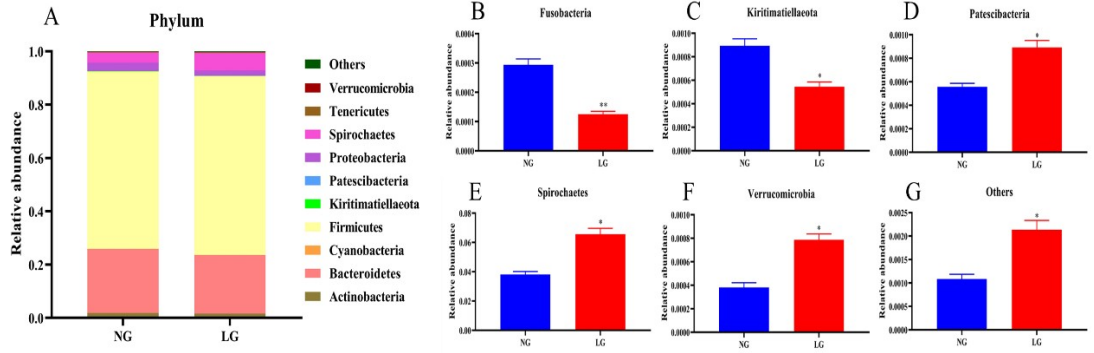
14 **Table S5.** Name, type, dilution, and source of primary antibodies

Antibody	Isotype	Dilution	Source
PGC-1 α	Rabbit	1:1000	Abcam (Cambridge, MA, USA)
GCN5	Rabbit	1:1000	Abcam (Cambridge, MA, USA)
p-GCN5	Rabbit	1:1000	Abcam (Cambridge, MA, USA)
PEPCK	Rabbit	1:1000	Abcam (Cambridge, MA, USA)
G6P	Rabbit	1:1000	Abcam (Cambridge, MA, USA)
β -actin	Rabbit	1:2500	Abcam (Cambridge, MA, USA)
Secondary Antibody			
HRP labelled Antibody	Goat anti rabbit	1:10,000	Santa Cruz (Santa Cruz, CA, USA)

15 Abbreviations represented: PGC-1 α , peroxisome proliferative activated receptor-g co-activator 1;

16 GCN5, general control non-repressed protein 5; p-GCN5: phosphorylation of general control non-

17 repressed protein 5; PEPCK, phosphoenolpyruvate carboxykinase; G6P, glucose-6-phosphatase.

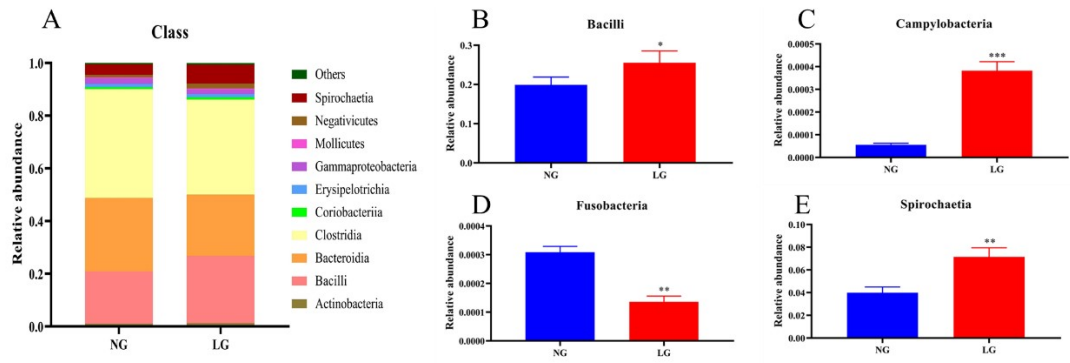


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19 **Fig S1.** Low fasting blood glucose levels shaped colonic microbiota at the phylum level in late-pregnancy

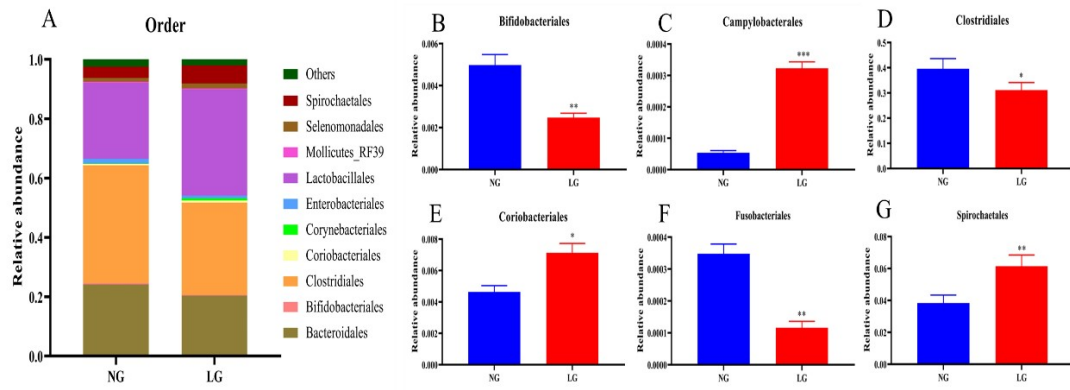
20 sows. Relative abundance of the top 10 genera in each group (A) and the significant relative abundance

21 of microbiota in each group (B-G). Data are means of 10 sows per treatment, *: $P < 0.05$, **: $P < 0.01$.



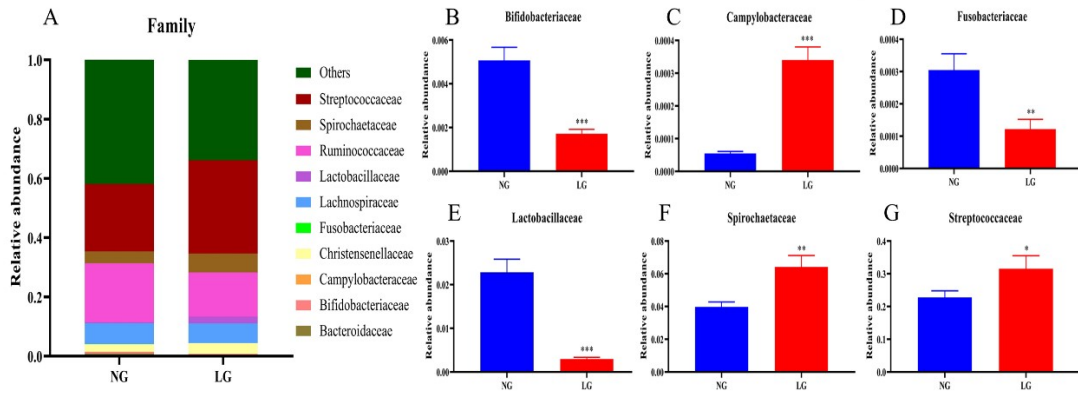
22

23 **Fig S2.** Low fasting blood glucose levels shaped colonic microbiota at the class level in late-pregnancy
 24 sows. Relative abundance of the top 10 genera in each group (A) and the significant relative abundance
 25 of microbiota in each group (B-E). Data are means of 10 sows per treatment, *: $P < 0.05$, **: $P < 0.01$, ***:
 26 $P < 0.001$.



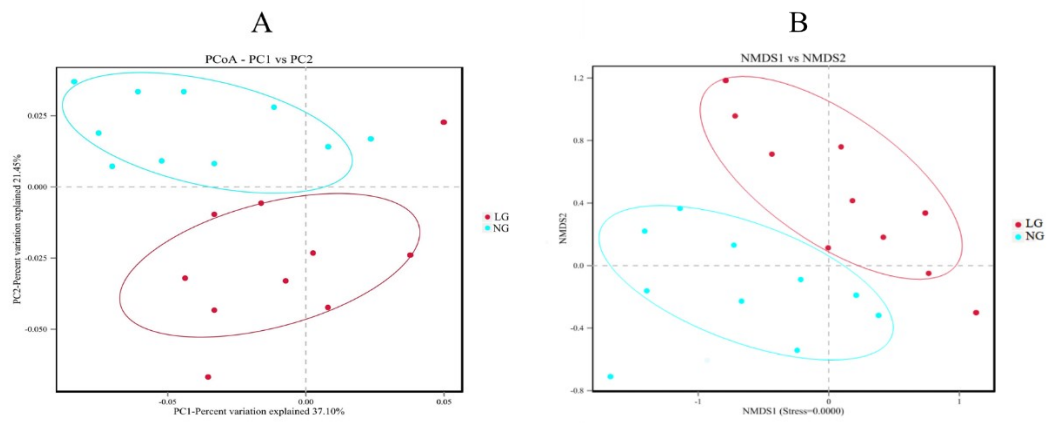
27

28 **Fig S3.** Low fasting blood glucose levels shaped colonic microbiota at the order level in late-pregnancy
 29 sows. Relative abundance of the top 10 genera in each group (A) and the significant relative abundance
 30 of microbiota in each group (B-G). Data are means of 10 sows per treatment, *: $P < 0.05$, **: $P < 0.01$, ***:
 31 $P < 0.001$.



32

33 **Fig S4.** Low fasting blood glucose levels shaped colonic microbiota at the family level in late-pregnancy
 34 sows. Relative abundance of the top 10 genera in each group (A) and the significant relative abundance
 35 of microbiota in each group (B-G). Data are means of 10 sows per treatment, *: $P < 0.05$, **: $P < 0.01$, ***:
 36 $P < 0.001$.



37

38 **Fig S5.** Principal coordinates analysis of beta-diversity analysis based on Bray Curtis distances of 86
 39 genera differentially enriched in late-pregnancy sows. A: PCoA; B: NMDS analysis. Data are means of
 40 10 sows per treatment.