TABLE S1 Composition of diets fed to sows during gestation and lactation (fresh weight basis, %)

	Gestation		**Lactation**	
Ingredient[a]	**Non-GM**	**GM**	**Non-GM**	**GM**
Maize	86.55	86.55	74.42	74.42
Soybean meal (non-GM)	10.33	10.33	19.30	19.30
Soybean oil	-	-	3.02	3.02
L-Lysine HCl	0.16	0.16	0.25	0.25
DL-Methionine	-	-	0.10	0.10
L-Threonine	-	-	0.06	0.06
Vitamin and mineral premix[b]	0.10	0.10	0.10	0.10
Salt	0.40	0.40	0.40	0.40
Di-calcium phosphate	1.36	1.36	1.29	1.29
Limestone flour	1.10	1.10	1.06	1.06
Analysed chemical composition				
Dry matter	88.40	87.80	89.50	88.60
Crude protein	11.80	11.00	15.60	15.00
Acid hydrolyzed fat	3.00	3.20	5.90	6.00
Crude fibre	1.70	1.60	1.60	1.90
Ash	4.10	4.30	4.60	4.30
Lysine	0.64	0.68	1.01	0.96
Ca[c]	7.60	7.60	7.50	7.50
P[c]	6.10	6.10	6.20	6.20
Digestible energy, MJ of DE/kg[c]	13.80	13.80	14.50	14.50

[a] Non-GM; non-GM near isogenic maize; GM; genetically modified Bt MON810 maize.

[b] Premix provided per kg of complete diet: Cu from copper sulphate, 15 mg; Fe from ferrous sulphate monohydrate, 70 mg; Mn from manganese oxide, 62 mg; Zn from zinc oxide, 80 mg, I from potassium iodate, 0.6 mg; Se from sodium selenite, 0.2 mg; retinyl acetate, 3.44 mg; cholecalciferol, 25 μg; DL-alpha-tocopheryl acetate, 100 mg; vitamin K, 2 mg; vitamin $B_{12,}$ 15 μg; riboflavin, 5 mg; nicotinic acid, 12 mg; pantothenic acid, 10 mg; choline chloride, 500 mg; vitamin $B_{1,}$ 2 mg; and vitamin $B_{6,}$ 3 mg.

[c] Calculated values.

TABLE S2 Composition of experimental diets fed to offspring from weaning for 115 days (fresh weight basis, %)

	Starter (d 0 – 7)		**Link (d 8 – 30)**		**Grower (d 31 – 70)**		**Finisher 1 (d 71 – 100)**		**Finisher 2 (d 101 – 115)**	
Ingredient[a]	**Non-GM**	**GM**	**Non-GM**	**GM**	**Non-GM**	**GM**	**Non-GM**	**GM**	**Non-GM**	**GM**
Maize	27.33	27.33	38.88	38.88	65.31	65.31	73.33	73.33	79.05	79.05
Soybean meal (non-GM)	24.00	24.00	25.00	25.00	28.64	28.64	22.76	22.76	17.35	17.35
Lactofeed 70[b]	25.00	25.00	20.00	20.00	0	0	0	0	0	0
Immunopro 35[c]	12.50	12.50	9.00	9.00	0	0	0	0	0	0
Soybean oil	8.00	8.00	4.00	4.00	2.37	2.37	0.06	0.06	0	0
L-Lysine HCl	0.30	0.30	0.30	0.30	0.36	0.36	0.43	0.43	0.49	0.49
DL-Methionine	0.25	0.25	0.20	0.20	0.14	0.14	0.14	0.14	0.14	0.14
L-Threonine	0.12	0.12	0.12	0.12	0.15	0.15	0.17	0.17	0.19	0.19
L-Tryptophan	0.10	0.10	0.10	0.10	0.05	0.05	0.07	0.07	0.08	0.08
Vitamin/mineral premix	0.30[d]	0.30[d]	0.30[d]	0.30[d]	0.10[e]	0.10[e]	0.10[e]	0.10[e]	0.10[e]	0.10[e]
Mycosorb[f]	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
Salt	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30
DiCal Phos	0.50	0.50	0.50	0.50	1.19	1.19	1.13	1.13	0.90	0.90
Limestone flour	1.10	1.10	1.10	1.10	1.19	1.19	1.26	1.26	1.15	1.15
Myco Curb[g]	0	0	0	0	0	0	0.05	0.05	0.05	0.05
Analyzed chemical composition										
Dry matter	91.4	91.0	90.9	90.5	89.2	88.7	87.5	87.7	87.4	88.2
Crude protein	20.2	21.2	19.8	20.4	19.7	20.1	17.1	17.2	15.1	15.3
Acid hydrolyzed fat	10.1	9.9	6.8	7.0	5.4	5.2	3.1	3.4	2.9	3.0
Crude fiber	1.7	1.4	1.5	1.3	2.1	2.1	2.1	1.8	1.8	1.8
Ash	6.0	5.9	5.9	5.8	4.8	4.8	5.2	5.6	4.8	4.4
Lysine	1.47	1.46	1.46	1.47	1.33	1.34	1.30	1.27	1.12	1.14
DE, MJ/kg[h]	16.33	16.33	15.38	15.38	14.50	14.50	14.00	14.00	13.99	13.99

[a] Non-GM; non-GM near isogenic maize; GM; genetically modified Bt MON810 maize.

[b] Lactofeed 70 contains 70% lactose, 11.5% protein, 0.5% oil, 7.5% ash and 0.5% fibre (Volac, Cambridge, UK).

[c] Immunopro 35 contains whey protein powder - protein 35% (Volac, Cambridge, UK).

[d] Premix provided per kg of complete diet: Cu, 155 mg; Fe, 90 mg; Mn, 47 mg; Zn, 120 mg, I, 0.6 mg; Se, 0.3 mg; retinyl acetate 2.1 mg; cholecalciferol, 25 μg; DL-alpha-tocopheryl acetate, 100 mg; vitamin K, 4 mg; vitamin $B_{12,}$ 15 μg; riboflavin, 2 mg; nicotinic acid, 12 mg; pantothenic acid, 10 mg; choline chloride, 250 mg; vitamin $B_{1,}$ 2 mg; vitamin $B_{6,}$ 3 mg.

[e] Premix provided per kg of complete diet: Cu, 15 mg; Fe, 24 mg; Mn, 31 mg; Zn, 80 mg, I, 0.3 mg; Se, 0.2 mg; retinyl acetate 0.7 mg; cholecalciferol, 25 μg; DL-alpha-tocopheryl acetate, 40 mg; vitamin K, 4 mg; vitamin $B_{12,}$ 15 μg; riboflavin, 2 mg; nicotinic acid, 12 mg; pantothenic acid, 10 mg; vitamin $B_{1,}$ 2 mg; vitamin $B_{6,}$ 3 mg.

[f] Mycosorb is an organic mycotoxin adsorbent (Alltech, Dunboyne, Co. Meath, Ireland).

[g] Myco Curb is a mould inhibitor (Kemin Europa N. V. Herentals, Belgium).

[h] Calculated values.

TABLE S3 Fecal bacterial counts from sows fed a GM maize diet during gestation and lactation[a]

	Treatment[b]			
Day	**Non-GM**	**GM**	**pooled SEM**	***P*-value**
	Enterobacteriaceae			
day 110 of gestation	7.44	7.68	0.132	0.37
day 28 of lactation	6.69	6.98	0.132	0.28
	Lactobacillus			
day 110 of gestation	7.69	7.59	0.103	0.51
day 28 of lactation	8.29	8.32	0.183	0.93
	Total anaerobes			
day 110 of gestation	8.67	8.66	0.111	0.92
day 28 of lactation	8.23	8.37	0.154	0.58

[a] Data are presented as least squares means ($\log_{10}$ CFU g^{-1}). Variability present at day 0 of gestation has been accounted for by including day 0 counts as covariates in the statistical model.

[b] Non-GM; non-GM near isogenic maize; GM; genetically modified Bt MON810 maize.

TABLE S4 Full outline of fecal microbiota from sows at day 110 of gestation

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Phylum			
Firmicutes	47.4	82.7	62.9
Spirochaetes	6.7	22.9	15.9
Bacteroidetes	7.5	20.9	14.2
Proteobacteria	1.5	11.0	3.0
Lentisphaerae	0.3	4.1	1.9
Fibrobacteres	0.0	3.3	0.8
Planctomycetes	0.0	1.0	0.5
uncultured *Bacteroidetes*	0.0	1.2	0.3
Synergistetes	0.0	0.4	0.0
Actinobacteria	0.0	0.2	0.0
Verrucomicrobia	0.0	0.2	0.0
Deferribacteres	0.0	0.0	0.0
uncultured *Lentisphaerae*	0.0	0.0	0.0
Family			
Lachnospiraceae	18.0	37.6	27.3
Ruminococcaceae	14.1	32.5	24.9
Spirochaetaceae	6.7	22.7	15.9
Rikenellaceae	1.9	11.2	3.5
Clostridiaceae	1.4	3.9	2.6
Porphyromonadaceae	0.5	4.3	1.9
Prevotellaceae	0.7	3.8	1.8
Peptostreptococcaceae	0.8	2.8	1.7
Veillonellaceae	0.4	1.6	0.9
Succinivibrionaceae	0.0	8.0	0.8
Fibrobacteraceae	0.0	3.3	0.8
uncultured *Rikenellaceae*	0.2	2.6	0.7
Eubacteriaceae	0.3	0.9	0.5
Streptococcaceae	0.0	3.9	0.4
Desulfovibrionaceae	0.1	1.1	0.4
uncultured *Lachnospiraceae*	0.0	1.0	0.4
Peptococcaceae	0.0	0.8	0.3
Planctomycetaceae	0.0	0.9	0.3
Victivallaceae	0.0	1.4	0.3
Erysipelotrichaceae	0.0	1.0	0.3
Bacteroidaceae	0.0	0.9	0.3
Enterobacteriaceae	0.0	1.0	0.2
Lactobacillaceae	0.0	0.8	0.2
Rhodospirillaceae	0.0	0.4	0.0
Neisseriaceae	0.0	0.0	0.0
Synergistaceae	0.0	0.4	0.0
Anaeroplasmataceae	0.0	0.8	0.0
Campylobacteraceae	0.0	0.2	0.0
Helicobacteraceae	0.0	0.2	0.0
Clostridiales family XI incertae sedis	0.0	0.2	0.0
Alcaligenaceae	0.0	0.2	0.0

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Verrucomicrobiaceae	0.0	0.0	0.0
Deferribacteraceae	0.0	0.0	0.0
Coriobacterineae	0.0	0.0	0.0
Oxalobacteraceae	0.0	0.0	0.0
uncultured *Ruminococcaceae*	0.0	0.4	0.0
uncultured *Succinivibrioaceae*	0.0	0.3	0.0
uncultured *Rhodospirrillaceae*	0.0	0.2	0.0
uncultured *Erysipelotrichaceae*	0.0	0.0	0.0
Uncultured family XIII incertae sedis	0.0	0.2	0.0
Genus			
Treponema	6.7	22.4	15.8
uncultured *Ruminococcus*	3.0	11.2	6.8
Clostridium	0.8	3.1	2.0
Parabacteroides	0.7	4.2	1.9
Prevotella	0.7	3.8	1.8
Ruminococcus	0.5	3.7	1.5
Ruminococcaceae incertae sedis	0.5	2.3	1.1
Peptostreptococcaceae incertae sedis	0.5	1.9	1.1
Lachnospiraceae incertae sedis	0.6	2.0	1.0
Anaerobiospirillum	0.0	8.0	0.8
Phascolarctobacterium	0.4	1.4	0.7
uncultured *Planctomycetes*	0.0	1.0	0.4
Streptococcus	0.0	3.9	0.4
Desulfovibrio	0.0	1.1	0.4
Turicibacter	0.0	1.0	0.3
Bacteroides	0.0	0.9	0.3
Enterobacteriaceae-associated genera	0.0	0.9	0.2
Anaerotruncus	0.0	0.4	0.2
Fibrobacter	0.0	3.0	0.2
Lactobacillus	0.0	0.8	0.2
Oscillospira	0.0	0.8	0.2
Sarcina	0.0	0.5	0.1
Thalassospira	0.0	0.4	0.0
Microvirgula	0.0	0.0	0.0
Paludibacter	0.0	0.6	0.0
Dethiosulfovibrio	0.0	0.5	0.0
Coprococcus	0.0	0.5	0.0
Eubacterium	0.0	0.0	0.0
Anaeroplasma	0.0	1.1	0.0
Victivallis	0.0	0.5	0.0
Spirochaeta	0.0	0.3	0.0
Campylobacter	0.0	0.2	0.0
Quinella	0.0	0.0	0.0
Helicobacter	0.0	0.2	0.0
Sutterella	0.0	0.2	0.0

	Overall values		
	5th percentile	95th percentile	median relative abundance
Anaerovibrio	0.0	0.2	0.0
Akkermansia	0.0	0.0	0.0
Blautia	0.0	0.2	0.0
Acetitomaculum	0.0	0.2	0.0
Mucispirillum	0.0	0.0	0.0

TABLE S5 Full outline of fecal microbiota of pigs at weaning (~28 days of age)

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Phylum			
Firmicutes	19.5	75.8	54.0
Proteobacteria	5.0	57.0	22.0
Bacteroidetes	6.2	35.4	18.6
Spirochaetes	0.0	16.9	1.0
Synergistetes	0.0	9.0	0.4
Lentisphaerae	0.0	2.5	0.3
Planctomycetes	0.0	1.9	0.2
Fibrobacteres	0.0	0.3	0.0
Actinobacteria	0.0	0.7	0.0
Verrucomicrobia	0.0	0.8	0.0
Deferribacteres	0.0	0.4	0.0
Fusobacteria	0.0	9.8	0.0
Chlamydiae	0.0	0.2	0.0
Euryarchaeota	0.0	0.1	0.0
Family			
Ruminococcaceae	5.4	26.8	17.5
Lachnospiraceae	4.0	42.1	17.0
Succinivibrionaceae	0.0	55.7	15.1
Veillonellaceae	1.4	12.7	4.8
Prevotellaceae	0.2	14.4	3.5
Rikenellaceae	0.6	13.1	3.2
Bacteroidaceae	0.0	20.0	2.9
Porphyromonadaceae	0.2	7.7	1.6
Enterobacteriaceae	0.0	13.6	1.3
Desulfovibrionaceae	0.1	6.3	1.2
Spirochaetaceae	0.0	16.9	1.0
Lactobacillaceae	0.0	7.3	0.8
Synergistaceae	0.0	9.0	0.4
Erysipelotrichales incertae sedis	0.0	8.3	0.3
Clostridiaceae	0.0	2.4	0.3
Victivallaceae	0.0	1.6	0.2
Planctomycetaceae	0.0	1.9	0.2
Eubacteriaceae	0.0	0.8	0.2
Alcaligenaceae	0.0	0.8	0.2
Peptostreptococcaceae	0.0	1.5	0.2
Peptococcaceae	0.0	0.8	0.0
Streptococcaceae	0.0	0.6	0.0
Erysipelotrichaceae	0.0	0.2	0.0
Rhodospirillaceae	0.0	0.7	0.0
Neisseriaceae	0.0	0.0	0.0
Fibrobacteraceae	0.0	0.3	0.0
Campylobacteraceae	0.0	1.8	0.0
Helicobacteraceae	0.0	0.5	0.0
Clostridiales family XI incertae sedis	0.0	0.0	0.0
Verrucomicrobiaceae	0.0	0.6	0.0

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Deferribacteraceae	0.0	0.5	0.0
Coriobacterineae	0.0	0.5	0.0
Oxalobacteraceae	0.0	0.0	0.0
Moraxellaceae	0.0	0.0	0.0
Leuconostocaceae	0.0	0.0	0.0
Bifidobacteriaceae	0.0	0.0	0.0
Fusobacteriaceae	0.0	9.8	0.0
Enterococcaceae	0.0	0.2	0.0
Aeromonadaceae	0.0	0.0	0.0
Staphylococcaceae	0.0	0.0	0.0
Chlamydiaceae	0.0	0.2	0.0
Methanobacteriaceae	0.0	0.1	0.0
Actinomycineae	0.0	0.1	0.0
Genus			
Anaerobiospirillum	0.0	55.7	15.1
Prevotella	0.2	14.4	3.5
Bacteroides	0.0	20.0	2.9
Phascolarctobacterium	0.9	5.4	2.4
Lachnospiraceae incertae sedis	0.0	7.5	1.8
Parabacteroides	0.2	7.6	1.6
ucultured *acterium*	0.2	8.0	1.4
Anaerovibrio	0.0	6.3	1.2
Desulfovibrio	0.2	4.2	1.1
Treponema	0.0	16.9	1.0
Enterobacteriaceae-associated genera	0.0	13.5	1.0
Ruminococcaceae incertae sedis	0.1	1.9	0.8
uncultured *Ruminococcus*	0.0	3.4	0.8
Lactobacillus	0.0	7.3	0.8
Anaerotruncus	0.0	2.7	0.4
Subdoligranulum	0.0	2.2	0.4
Ruminococcus	0.0	1.6	0.4
Megasphaera	0.0	3.8	0.4
uncultured *Planctomycetes*	0.0	1.9	0.2
Sutterella	0.0	0.8	0.2
Blautia	0.0	0.9	0.2
Dethiosulfovibrio	0.0	4.9	0.2
Clostridium	0.0	1.0	0.1
Oscillospira	0.0	0.0	0.0
Peptostreptococcaceae incertae sedis	0.0	1.0	0.0
Streptococcus	0.0	0.6	0.0
Turicibacter	0.0	0.0	0.0
Thalassospira	0.0	0.7	0.0
Microvirgula	0.0	0.0	0.0
Paludibacter	0.0	0.1	0.0
Fibrobacter	0.0	0.3	0.0
Coprococcus	0.0	0.4	0.0

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Eubacterium	0.0	0.1	0.0
Victivallis	0.0	0.4	0.0
Spirochaeta	0.0	0.0	0.0
Campylobacter	0.0	1.8	0.0
Helicobacter	0.0	0.5	0.0
Akkermansia	0.0	0.6	0.0
Acetitomaculum	0.0	0.1	0.0
Mucispirillum	0.0	0.5	0.0
Catabacter	0.0	0.1	0.0
Leuconostoc	0.0	0.0	0.0
Oribacterium	0.0	0.4	0.0
Acidaminococcus	0.0	2.5	0.0
Faecalibacterium	0.0	1.0	0.0
Bifidobacterium	0.0	0.0	0.0
Fusobacterium	0.0	9.8	0.0
Enterococcus	0.0	0.2	0.0
Catenibacterium	0.0	0.4	0.0
Lachnospira	0.0	0.7	0.0
Solobacterium	0.0	0.1	0.0
Bilophila	0.0	1.8	0.0
Alistipes	0.0	0.9	0.0
Butyricimonas	0.0	0.1	0.0
Succiniclasticum	0.0	1.0	0.0
Peptococcus	0.0	0.6	0.0
Gemella	0.0	0.0	0.0
Cloacibacillus	0.0	2.7	0.0
Roseburia	0.0	0.3	0.0
Shuttleworthia	0.0	0.1	0.0
uncultured rumen bacterium	0.0	0.0	0.0
uncultured *Clostridiales* bacterium	0.0	0.0	0.0
Mitsuokella	0.0	0.4	0.0
Chlamydia	0.0	0.2	0.0
Methanobrevibacter	0.0	0.1	0.0
Odoribacter	0.0	0.0	0.0
Parasporobacterium-Sporobacterium	0.0	0.2	0.0
Hydrogenoanaerobacterium	0.0	0.1	0.0
Parvimonas	0.0	0.0	0.0
uncultured *Lachnospiraceae* bacterium	0.0	0.2	0.0
Anaerovorax	0.0	0.0	0.0
Mogibacterium	0.0	0.0	0.0
Dysgonomonas	0.0	0.0	0.0

TABLE S6 Full outline of fecal microbiota of pigs at day 100 post-weaning

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Phylum			
Firmicutes	37.0	77.5	58.5
Bacteroidetes	7.0	24.6	16.1
Spirochaetes	2.2	27.8	13.3
Proteobacteria	2.0	37.5	4.1
Lentisphaerae	0.3	4.7	1.3
Planctomycetes	0.0	2.9	0.6
Fibrobacteres	0.0	1.1	0.1
Synergistetes	0.0	0.3	0.0
Actinobacteria	0.0	0.2	0.0
Verrucomicrobia	0.0	0.1	0.0
Deferribacteres	0.0	0.2	0.0
Fusobacteria	0.0	0.0	0.0
Chlamydiae	0.0	0.0	0.0
Family			
Ruminococcaceae	14.7	33.8	21.9
Lachnospiraceae	10.6	45.5	16.1
Spirochaetaceae	2.2	27.8	13.3
Prevotellaceae	1.7	15.8	5.6
Rikenellaceae	0.9	13.5	4.4
Veillonellaceae	0.3	8.1	2.5
Succinivibrionaceae	0.1	37.1	1.7
Porphyromonadaceae	0.3	8.8	1.5
Clostridiaceae	0.2	5.2	1.2
Streptococcaceae	0.0	11.1	1.0
Lactobacillaceae	0.0	6.2	0.9
Peptostreptococcaceae	0.1	3.0	0.8
Planctomycetaceae	0.0	2.9	0.6
Victivallaceae	0.0	3.0	0.5
Desulfovibrionaceae	0.0	1.6	0.3
Peptococcaceae	0.0	0.5	0.3
Eubacteriaceae	0.0	0.6	0.2
Fibrobacteraceae	0.0	1.1	0.1
Rhodospirillaceae	0.0	0.5	0.1
Enterobacteriaceae	0.0	0.7	0.0
Bacteroidaceae	0.0	0.2	0.0
Erysipelotrichaceae	0.0	0.2	0.0
Neisseriaceae	0.0	0.1	0.0
Synergistaceae	0.0	0.3	0.0
Anaeroplasmataceae	0.0	0.6	0.0
Helicobacteraceae	0.0	0.2	0.0
Alcaligenaceae	0.0	0.5	0.0
Deferribacteraceae	0.0	0.2	0.0
Coriobacterineae	0.0	0.1	0.0
Oxalobacteraceae	0.0	0.0	0.0
Bifidobacteriaceae	0.0	0.0	0.0
Fusobacteriaceae	0.0	0.0	0.0

	Overall values		
	5th percentile	95th percentile	median relative abundance
Erysipelotrichales incertae sedis	0.0	0.3	0.0
Chlamydiaceae	0.0	0.0	0.0
Methanobacteriaceae	0.0	0.0	0.0
Genus			
Treponema	2.2	27.8	13.1
Prevotella	1.7	15.8	5.6
uncultured *Ruminococcus*	1.4	9.5	3.5
uncultured bacterium	0.5	5.0	2.4
Phascolarctobacterium	0.3	5.1	1.8
Anaerobiospirillum	0.1	37.1	1.7
Lachnospiraceae incertae sedis	0.3	3.8	1.4
Clostridium	0.1	4.4	1.0
Streptococcus	0.0	11.1	1.0
Parabacteroides	0.3	8.6	0.9
Lactobacillus	0.0	6.2	0.9
Ruminococcus	0.3	3.3	0.7
Ruminococcaceae incertae sedis	0.1	1.6	0.7
uncultured *Planctomycetes*	0.0	2.9	0.6
Peptostreptococcaceae incertae sedis	0.0	2.5	0.5
Oscillospira	0.0	1.8	0.5
Desulfovibrio	0.0	1.6	0.3
Anaerotruncus	0.0	0.8	0.2
Faecalibacterium	0.0	1.5	0.2
Subdoligranulum	0.0	0.7	0.2
Oribacterium	0.0	0.6	0.2
Anaerovibrio	0.0	1.2	0.2
Fibrobacter	0.0	1.1	0.1
Megasphaera	0.0	2.1	0.1
Victivallis	0.0	0.5	0.1
Blautia	0.0	0.9	0.1
Paludibacter	0.0	1.8	0.1
Peptococcus	0.0	0.4	0.1
Enterobacteriaceae-associated genera	0.0	0.7	0.0
Bacteroides	0.0	0.2	0.0
Sarcina	0.0	0.2	0.0
Turicibacter	0.0	0.2	0.0
Thalassospira	0.0	0.5	0.0
Microvirgula	0.0	0.1	0.0
Dethiosulfovibrio	0.0	0.3	0.0
Coprococcus	0.0	0.6	0.0
Eubacterium	0.0	0.0	0.0
Anaeroplasma	0.0	0.6	0.0
Spirochaeta	0.0	0.1	0.0

	Overall values		
	5th percentile	**95th percentile**	**median relative abundance**
Helicobacter	0.0	0.2	0.0
Sutterella	0.0	0.5	0.0
Acetitomaculum	0.0	0.7	0.0
Mucispirillum	0.0	0.2	0.0
Catabacter	0.0	0.1	0.0
Acidaminococcus	0.0	0.5	0.0
Bifidobacterium	0.0	0.0	0.0
Fusobacterium	0.0	0.0	0.0
Dorea	0.0	0.4	0.0
Catenibacterium	0.0	1.0	0.0
Lachnospira	0.0	0.1	0.0
Solobacterium	0.0	0.2	0.0
Butyricimonas	0.0	0.0	0.0
Cloacibacillus	0.0	0.0	0.0
Roseburia	0.0	0.1	0.0
Shuttleworthia	0.0	0.1	0.0
Mitsuokella	0.0	0.1	0.0
Chlamydia	0.0	0.0	0.0
Parasporobacterium-Sporobacterium	0.0	0.0	0.0
Mogibacterium	0.0	0.1	0.0
Butyrivibrio	0.0	0.2	0.0
Butyrivibrio-Pseudobutyrivibrio	0.0	0.0	0.0
Dialister	0.0	0.1	0.0

TABLE S7 Full outline of cecal microbiota of pigs at day 115 post-weaning

	Overall values		
Phylum	**5th percentile**	**95th percentile**	**median relative abundance**
Firmicutes	32.3	71.5	54.9
Bacteroidetes	14.2	35.0	23.1
Proteobacteria	2.4	35.6	11.5
Spirochaetes	0.3	20.8	3.9
Lentisphaerae	0.0	2.7	0.4
Planctomycetes	0.0	1.3	0.2
Fibrobacteres	0.0	0.4	0.0
Synergistetes	0.0	0.3	0.0
Actinobacteria	0.0	0.0	0.0
Verrucomicrobia	0.0	5.0	0.0
Deferribacteres	0.0	0.0	0.0
Fusobacteria	0.0	0.9	0.0
Chlamydiae	0.0	0.0	0.0
Family			
Ruminococcaceae	8.2	29.9	18.1
Prevotellaceae	4.3	30.1	13.7
Lachnospiraceae	7.1	24.0	11.7
Veillonellaceae	3.6	27.0	9.0
Succinivibrionaceae	0.0	29.2	4.7
Spirochaetaceae	0.3	20.8	3.9
Peptostreptococcaceae	0.6	9.1	3.3
Rikenellaceae	0.8	7.1	2.3
Porphyromonadaceae	0.4	11.3	2.1
Clostridiaceae	0.0	4.7	1.7
Desulfovibrionaceae	0.0	2.1	0.6
Enterobacteriaceae	0.0	7.2	0.6
Streptococcaceae	0.0	2.8	0.6
Peptococcaceae	0.0	1.2	0.5
Alcaligenaceae	0.0	1.4	0.5
Eubacteriaceae	0.0	1.1	0.4
Erysipelotrichaceae	0.0	1.0	0.3
Lactobacillaceae	0.0	4.4	0.3
Planctomycetaceae	0.0	1.3	0.2
Bacteroidaceae	0.0	2.4	0.0
Rhodospirillaceae	0.0	0.9	0.0
Neisseriaceae	0.0	7.4	0.0
Fibrobacteraceae	0.0	0.4	0.0
Victivallaceae	0.0	0.7	0.0
Synergistaceae	0.0	0.3	0.0
Anaeroplasmataceae	0.0	0.6	0.0
Campylobacteraceae	0.0	0.9	0.0
Helicobacteraceae	0.0	4.6	0.0
Verrucomicrobiaceae	0.0	5.0	0.0
Deferribacteraceae	0.0	0.0	0.0
Fusobacteriaceae	0.0	0.9	0.0
Erysipelotrichales incertae sedis	0.0	0.6	0.0

Genus			
Prevotella	4.3	30.0	13.7
Anaerobiospirillum	0.0	29.2	4.7
Phascolarctobacterium	1.4	9.7	4.1
Treponema	0.3	20.8	3.9
uncultured *Ruminococcus*	0.5	6.1	2.7
Peptostreptococcaceae incertae sedis	0.5	7.1	2.6
Anaerovibrio	0.6	7.3	2.6
Lachnospiraceae incertae sedis	1.1	5.6	2.2
Parabacteroides	0.3	11.2	2.1
Clostridium	0.0	4.6	1.6
uncultured bacterium	0.3	4.2	1.3
Ruminococcaceae incertae sedis	0.4	1.6	1.0
Ruminococcus	0.0	8.7	0.8
Faecalibacterium	0.0	5.2	0.8
Oscillospira	0.0	3.8	0.7
Desulfovibrio	0.0	2.1	0.6
Streptococcus	0.0	2.8	0.6
Sutterella	0.0	1.4	0.5
Subdoligranulum	0.0	2.6	0.3
Turicibacter	0.0	1.0	0.3
Lactobacillus	0.0	4.4	0.3
Megasphaera	0.0	2.5	0.3
Peptococcus	0.0	0.8	0.3
*Enterobacteriaceae-*associated genera	0.0	5.0	0.3
uncultured *Planctomycetes*	0.0	1.3	0.2
Anaerotruncus	0.0	0.6	0.2
Blautia	0.0	1.1	0.1
Bacteroides	0.0	2.4	0.0
Sarcina	0.0	0.2	0.0
Thalassospira	0.0	0.8	0.0
Microvirgula	0.0	7.4	0.0
Paludibacter	0.0	0.4	0.0
Fibrobacter	0.0	0.4	0.0
Dethiosulfovibrio	0.0	0.3	0.0
Coprococcus	0.0	1.0	0.0
Eubacterium	0.0	0.5	0.0
Anaeroplasma	0.0	0.6	0.0
Victivallis	0.0	0.4	0.0
Campylobacter	0.0	0.9	0.0
Helicobacter	0.0	4.6	0.0
Akkermansia	0.0	5.0	0.0
Acetitomaculum	0.0	0.4	0.0
Mucispirillum	0.0	0.0	0.0
Oribacterium	0.0	0.8	0.0
Acidaminococcus	0.0	2.9	0.0

Fusobacterium	0.0	0.9	0.0
Dorea	0.0	0.0	0.0
Catenibacterium	0.0	0.7	0.0
Lachnospira	0.0	0.3	0.0
Solobacterium	0.0	0.6	0.0
Roseburia	0.0	0.2	0.0
Shuttleworthia	0.0	0.2	0.0
Mitsuokella	0.0	0.4	0.0
Chlamydia	0.0	0.0	0.0
Butyrivibrio	0.0	0.2	0.0
Dialister	0.0	0.0	0.0
Deltaproteobacteria	0.0	0.0	0.0
Oscillibacter	0.0	0.1	0.0

TABLE S8 The effect of maternal feeding of GM maize on the fecal and cecal microbiota of offspring[a]

Sow trt[b]	**Non-GM**	**GM**	***P* - value**	***N*[c]**
Feces				
Weaning (~28 days of age)				
Family				
Ruminococcaceae#	12.0 (2.9 - 26.5)	18.5 (11.1 - 33.4)	0.01	20;20
Lachnospiraceae†	15.1 (12.1 - 18.5)	20.2 (16.6 - 24.3)	0.04	20;20
Clostridiaceae#	0.1 (0 - 3.1)	0.6 (0 - 2.4)	0.03	10;18
Victivallaceae#	0.1 (0 - 1.3)	0.3 (0 - 1.6)	0.03	11;19
Genus				
Subdoligranulum#	0.2 (0 - 1.9)	0.6 (0 - 2.6)	0.03	13;18
Day 100 pw[d]				
Genus				
Ruminococcus#	0.9 (0.3 - 4.1)	0.6 (0.2 - 1.8)	0.05	18;20
Cecum				
Enterobacteriaceae#	1.1 (0 - 24.1)	0.5 (0 - 1.6)	0.03	16;17

[a] Data are presented as treatment means (with 95% confidence intervals) for data analyzed using parametric tests (†) or medians (with 5-95th percentiles) for data analyzed using non-parametric tests (#).

[b] Sows were fed a non-GM or a GM maize-based diet during gestation and lactation.

[c] *n* – number of animals in which the bacterial taxon was present (non-GM vs GM).

[d] pw - post-weaning.

TABLE S9 Effects of feeding a GM maize-based diets to pigs from weaning for 115 days on fecal and cecal microbiota[a]

Offspring trt[b]	**Non-GM**	**GM**	***P* - value**	***N***[c]
Feces				
Weaning (~28 days of age)				
Family				
Rikenellaceae[#]	1.4 (0.5 - 13.4)	4.0 (1.0 - 13.1)	0.03	20;20
Day 100 pw[d]				
Genus				
Oscillospira[#]	0.6 (0.2 - 2.9)	0.3 (0 - 1.8)	0.01	19;17
Faecalibacterium[#]	0.3 (0 - 1.7)	0.2 (0 - 1.5)	0.03	13;12
Thalassospira[#]	0.1 (0 - 0.5)	0 (0 - 0.6)	0.03	12;3
Cecum				
Anaerotruncus[#]	0 (0 - 0.5)	0.3 (0 - 1.0)	0.02	9;12

[a] Data are presented as treatment means (with 95% confidence intervals) for data analyzed using parametric tests (†) or medians (with 5-95th percentiles) for data analyzed using non-parametric tests ([#]).

[b] Sows were fed a non-GM or a GM maize-based diet during gestation and lactation.

[c] *n* – number of animals in which the bacterial taxon was present (non-GM vs GM).

[d] pw - post-weaning.

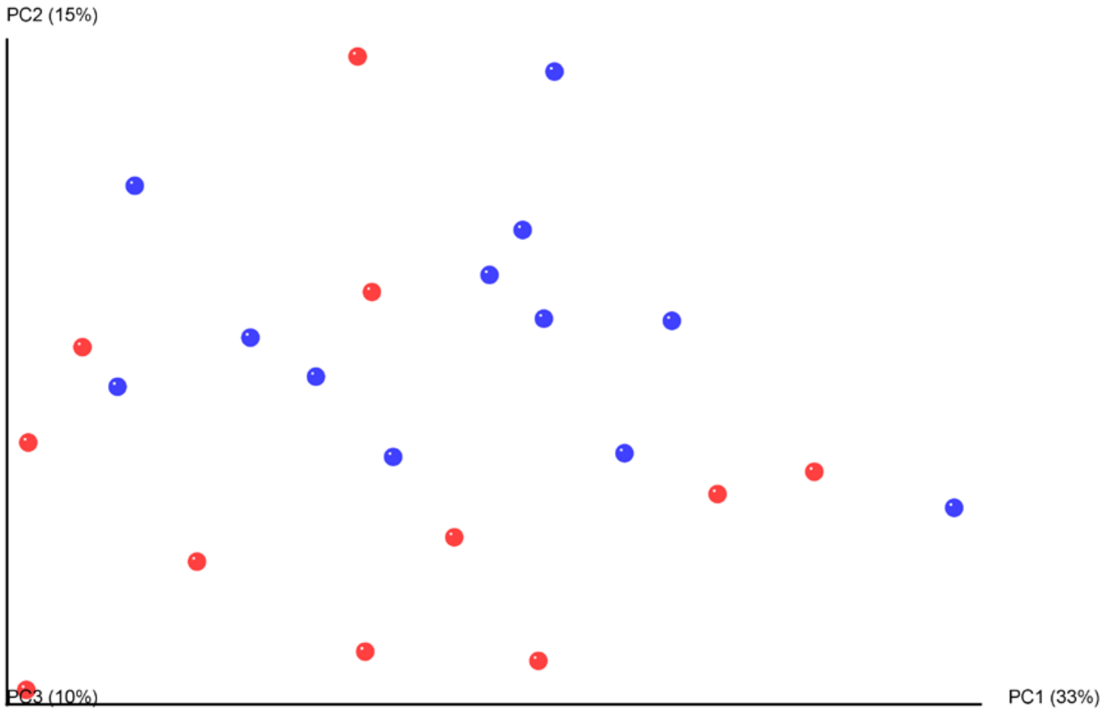

FIG S1 Unweighted beta diversity at day 110 of gestation in the feces of sows fed a non-GM (blue) or a GM (red) maize-based diet.

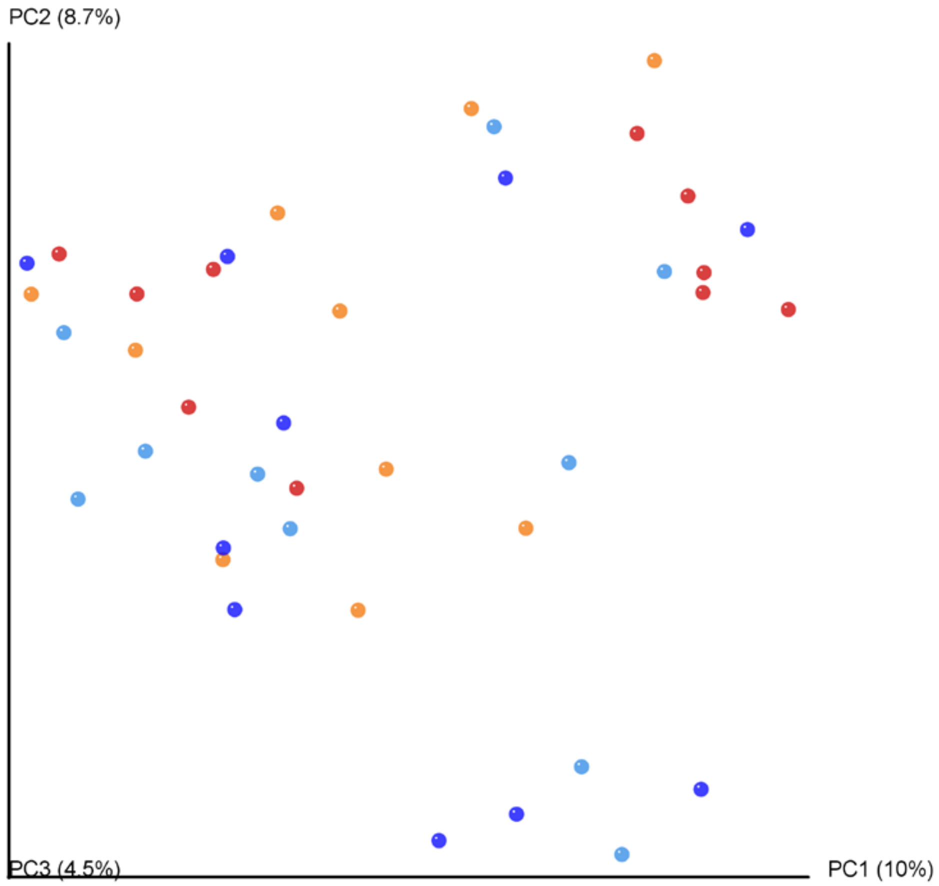

FIG S2 Unweighted beta diversity at weaning in feces of pigs fed a non-GM or a GM maize-based diet for 115 days within sow treatments (non-GM/non-GM – blue; non-GM/GM – light blue; GM/non-GM – orange; GM/GM – red).

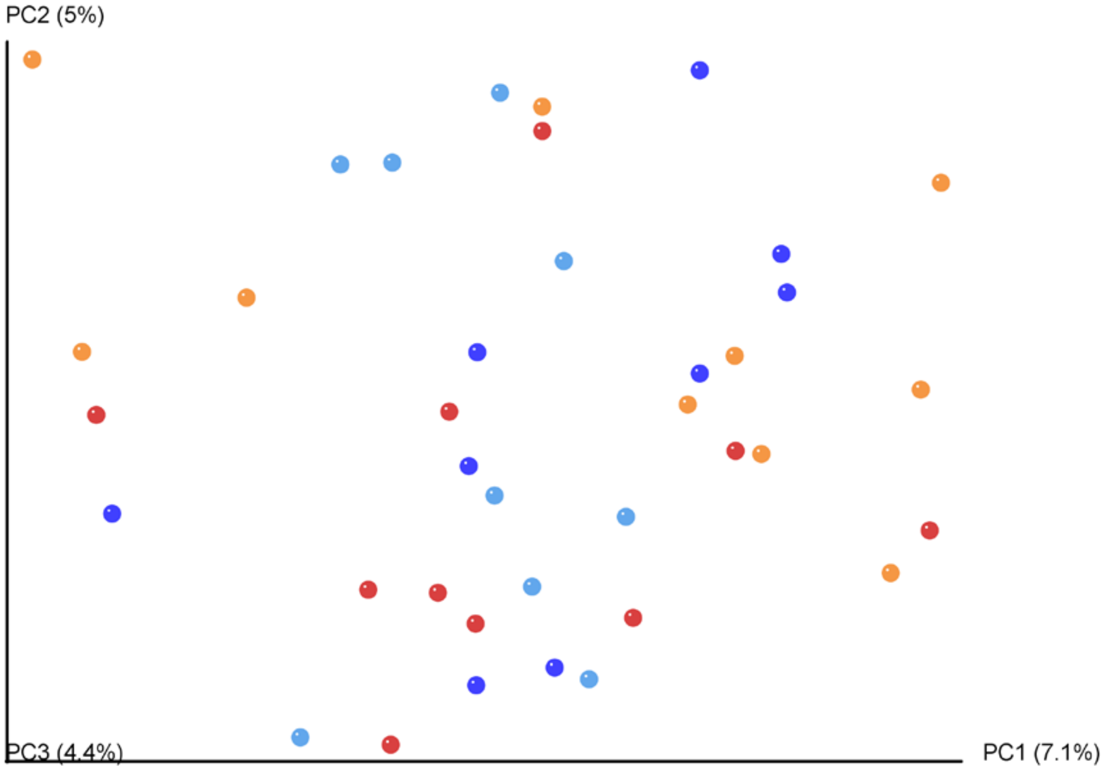

FIG S3 Unweighted beta diversity at day 100 post-weaning in feces of pigs fed a non-GM or a GM maize-based diet for 115 days within sow treatments (non-GM/non-GM – blue; non-GM/GM – light blue; GM/non-GM – orange; GM/GM – red).

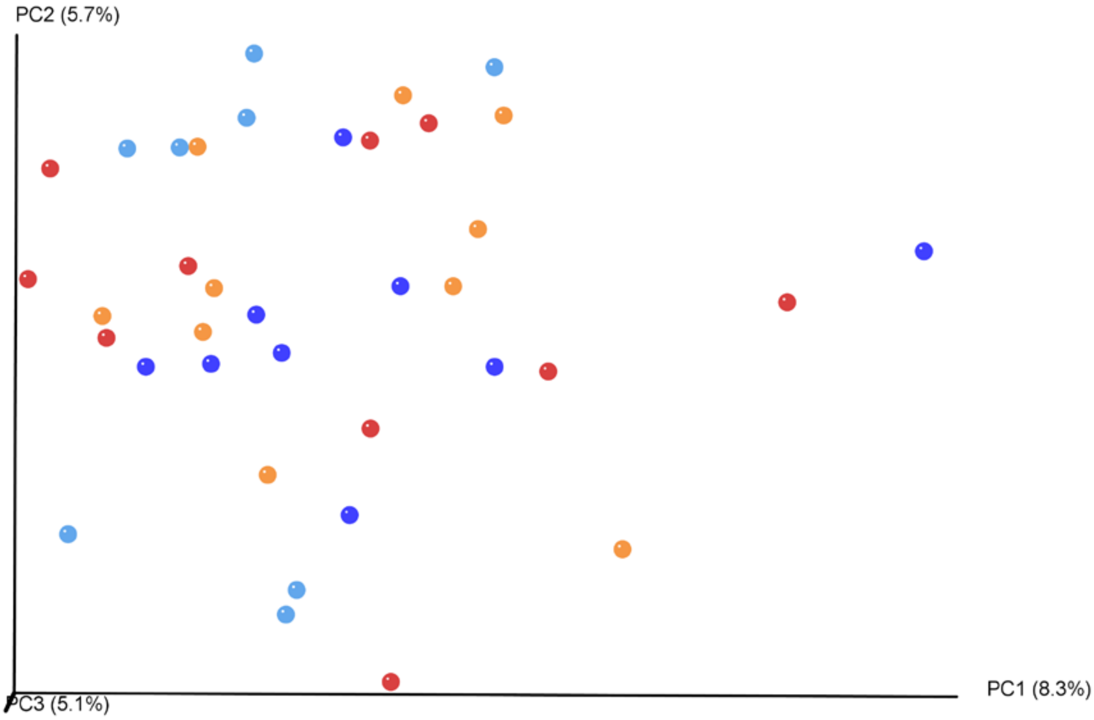

FIG S4 Unweighted beta diversity at day 115 post-weaning in cecal digesta of pigs fed a non-GM or a GM maize-based diet for 115 days within sow treatments (non-GM/non-GM – blue; non-GM/GM – light blue; GM/non-GM – orange; GM/GM – red).