1   **Supplemental material**

2

3   **Supplemental table 1:** Analysis of similarities (ANOSIM; 0: similar, 1: no similarity) of DGGE

4   banding patterns between microbial populations of rats fed diets containing low amylose maize
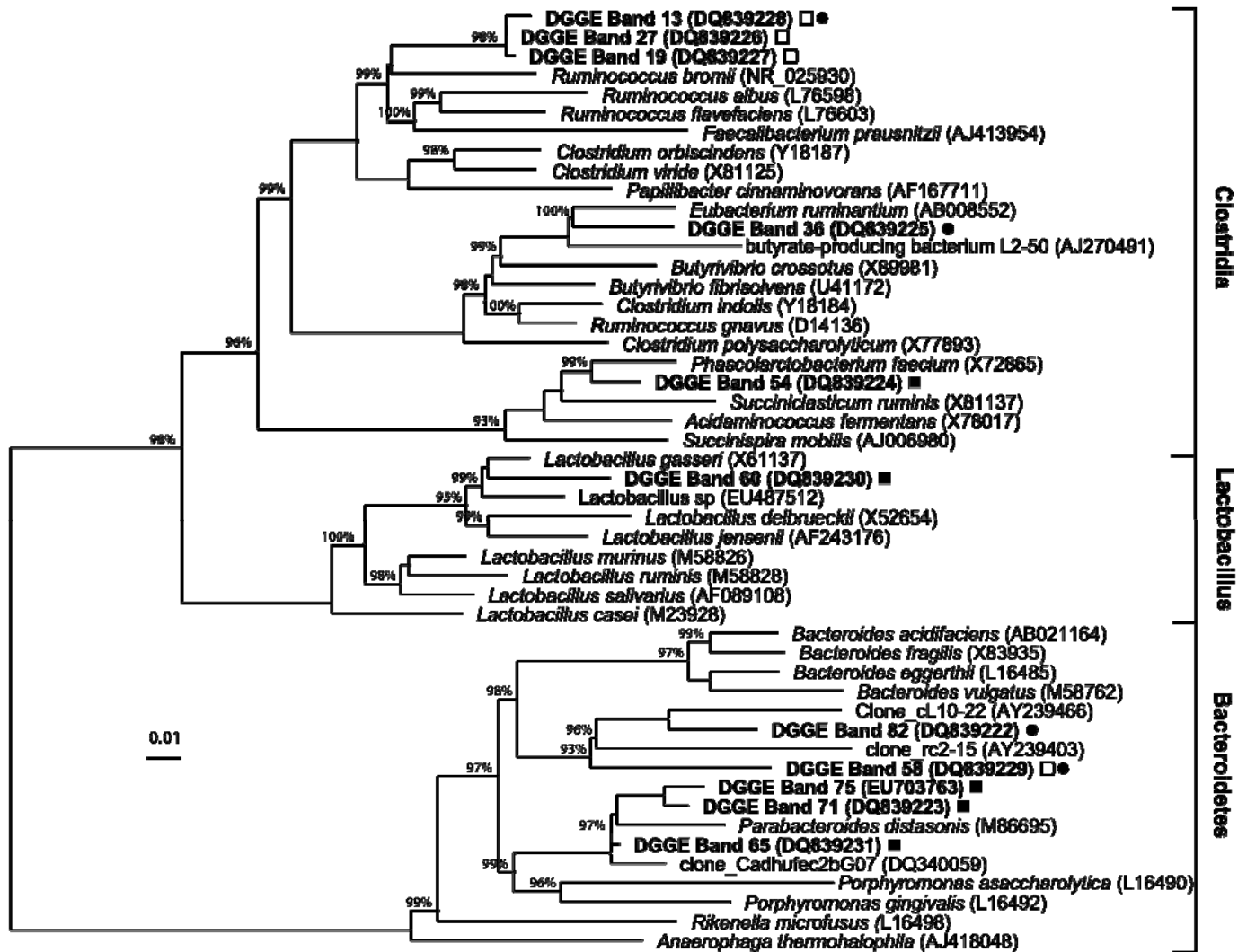
5   starch (LAMS), LAMS with 3% tributyrin (LAMST), high amylose maize starch (HAMS) and

6   butyrylated HAMS (HAMSB) over the course of the study. Shaded cells are significant ($P<0.01$). #

7   Sampled for sequence analysis of key DGGE bands.

Week:	0	4	7	11	15	19	21	#27	29	31
LAMS vs LAMST	0.058	-0.057	0.73	0.017	0.186	-0.035	0.275	0.176	0.148	0.36
LAMS vs HAMS	0.044	0.218	0.522	0.509	0.515	0.578	0.719	0.897	0.829	0.583
LAMS vs HAMSB	0.103	0.484	0.838	0.808	0.715	0.866	0.757	0.924	0.992	0.864
LAMST vs HAMS	0.104	0.174	0.358	0.467	0.642	0.733	0.657	0.693	0.928	0.492
LAMST vs HAMSB	0.282	0.417	0.752	0.699	0.753	0.915	0.707	0.785	1.000	0.878
HAMS vs HAMSB	-0.068	0.411	0.499	0.465	0.646	0.785	0.794	0.968	0.976	0.822

8

DGGE Band 13 (DQ639228) □ ●
99%
DGGE Band 27 (DQ639226) □
DGGE Band 19 (DQ639227) □
99%
Ruminococcus bromii (NR_025930)
99%
Ruminococcus albus (L76598)
100%
Ruminococcus flavefaciens (L76603)
Faecalibacterium prausnitzii (AJ413954)
99%
98%
Clostridium orbiscindens (Y18187)
Clostridium viride (X81125)
Papillibacter cinnaminovorans (AF167711)
100%
Eubacterium ruminantium (AB008552)
DGGE Band 36 (DQ639225) ●
99%
butyrate-producing bacterium L2-50 (AJ270491)
Butyrivibrio crossotus (X89981)
98%
Butyrivibrio fibrisolvens (U41172)
100%
Clostridium indolis (Y18184)
Ruminococcus gnavus (D14136)
Clostridium polysaccharolyticum (X77893)
96%
99%
Phascolarctobacterium faecium (X72865)
DGGE Band 54 (DQ639224) ■
Succiniclasticum ruminis (X81137)
93%
Acidaminococcus fermentans (X78017)
Succinispira mobilis (AJ006980)
98%
Lactobacillus gasseri (X61137)
99%
DGGE Band 60 (DQ639230) ■
95%
Lactobacillus sp (EU487512)
99%
Lactobacillus delbrueckii (X52654)
Lactobacillus jensenii (AF243176)
100%
Lactobacillus murinus (M58826)
98%
Lactobacillus ruminis (M58828)
Lactobacillus salivarius (AF089108)
Lactobacillus casei (M23928)

99%
Bacteroides acidifaciens (AB021164)
97%
Bacteroides fragilis (X83935)
Bacteroides eggerthii (L16485)
98%
Bacteroides vulgatus (M58762)
Clone_cL10-22 (AY239466)
96%
DGGE Band 82 (DQ639222) ●
93%
clone_rc2-15 (AY239403)
DGGE Band 58 (DQ639229) □●
DGGE Band 75 (EU703763) ■
97%
DGGE Band 71 (DQ639223) ■
97%
Parabacteroides distasonis (M86695)
DGGE Band 65 (DQ639231) ■
99%
clone_Cadhufec2bG07 (DQ340059)
96%
Porphyromonas asaccharolytica (L16490)
Porphyromonas gingivalis (L16492)
99%
Rikenella microfusus (L16498)
Anaerophaga thermohalophila (AJ418048)

0.01

Clostridia

Lactobacillus

Bacteroidetes

10 **Supplemental figure 1**:16S rRNA gene based phylogenetic tree of DGGE band phylotypes extracted from the week 27 gel. Branching points

11 with >90% bootstrap support have values shown at nodes. The scale bar indicates 0.01 changes per nucleotide. Diets to which the bands were

12 specific are indicated: LAMS/LAMST ●, HAMS □, HAMSB ■.

13

14
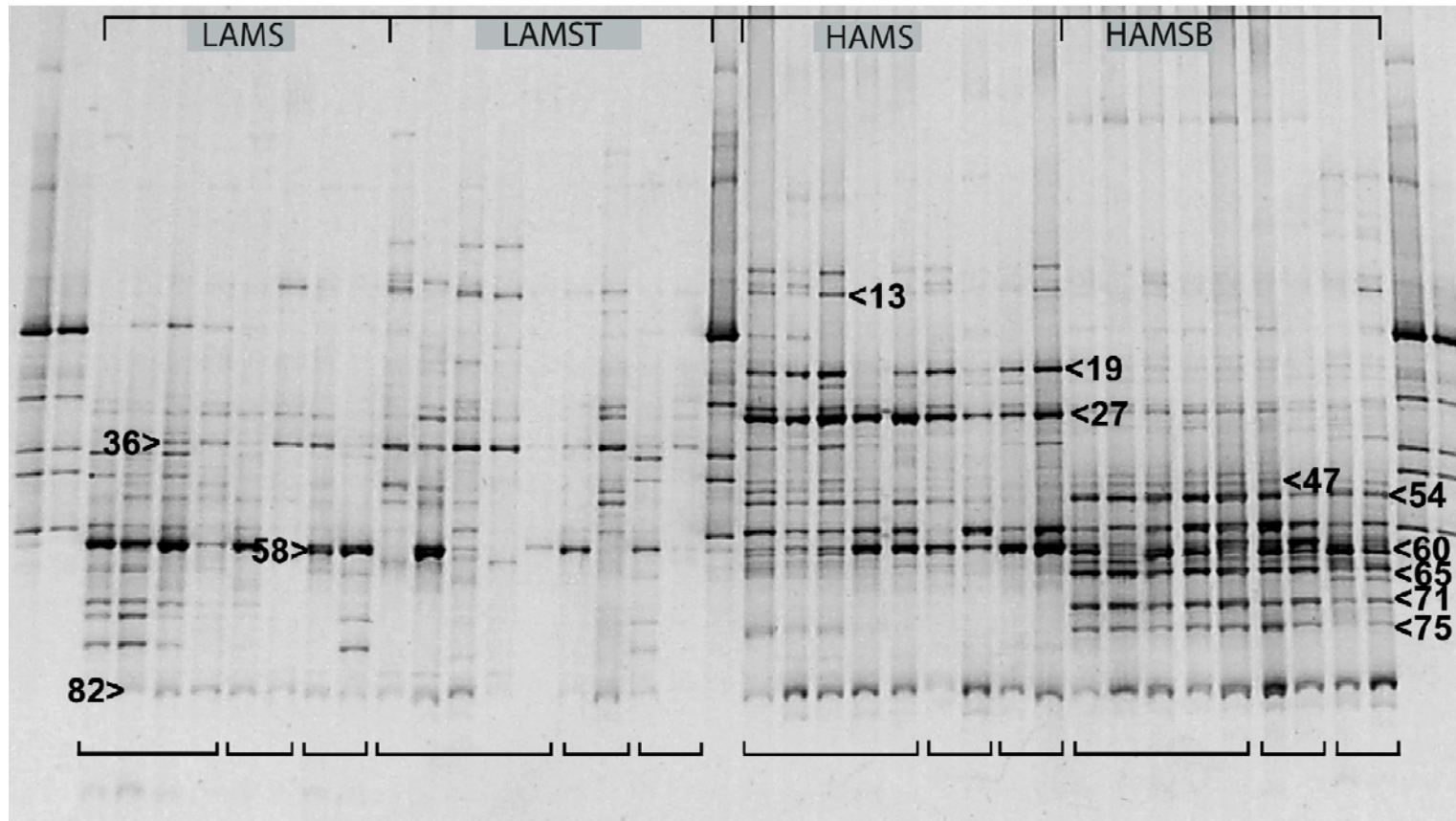
Supplemental figure 2: DGGE gel of samples at week 27. Diet groups are shown at the top of the gel, whilst samples from animals in the same

cage are indicated by brackets at the base of the gel. Key bands that were sequenced are labelled on the gel.