**Additional files**

**Additional file 1.** (.xls) Statistical analysis of bacterial growth (OD600nm), pH of the digestive liquids and the non-gaseous fermentation products. The STATISTICA (version 10.0) computer software (StatSoft, Inc.) was used. All variables were examined for normality and homogeneity of variance. Tukey's HSD (honestly significant difference) test was applied after ANOVA analysis to compare statistical significance among the variables in experiments. Statistical signiﬁcance was considered at p < 0.05.

**Additional file 2.** (.xls) Detailed taxonomic composition (genus level) of the microbial communities selected in batch experiment based on hypervariable V4 region of the 16S rRNA gene, sequenced on MiSeq platform (Illumina).

**Additional file 3.** (.pdf) Alpha Diversity (a. Shannon, b. Simpson) of the microbial communities selected in time in the static batch experiments for each collection day, except day 0, which is an inoculation day. The lower and upper hinges represent the first and third quartiles respectively. The whiskers extends to the largest and lowest values. The middle line represents the median value.

**Additional file 4.** (.xls)Detailed characteristics of the digestive liquids from the batch experiments – data used for preparation of Figures 3, 4 and Table 2. The samples from which the material was taken for WGS are marked in yellow.

**Additional file 5.** (.pdf) Taxonomic composition of the microbial communities from the selected samples (see Table 4) based on WGS analysis: a. phylum level, b. class level, c. family level, d. genus level.

Only the top 10 most dominant lineages are shown, the remaining lineages and the unclassified sequences are grouped into other. For detailed taxonomic assignments see Additional File 6.

**Additional file 6.** (.xls) Detailed taxonomic composition of the microbial communities from the selected samples (see Table 4) based on WGS analysis: phylum, class, order, family, genus, species.

**Additional file 7.** (.xls) Detailed calculations for Figure 6 based on taxonomic assignments in Additional File 6.