



## **FEED-A-GENE**

**Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems**

### **Deliverable D5.1**

## **Rules to use information from the gut microbiota to improve feed efficiency**

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# 1. Summary

## Objectives

As many studies have shown, the gut microbiota plays an important role in the metabolism, nutrition, and immune system of monogastric animals. This suggests that microbial communities inhabiting the gastrointestinal tract could also influence feed efficiency.

The objective of this deliverable was to evaluate the genetic effects influencing the composition of the gut microbiota as affected by a wide range of environmental conditions and physiological factors (i.e., maternal transmission, feeding regime, farm management, presence of antibiotics in the feed, sex, heat, and humidity). The aim was to propose criteria and methodologies to use variability in gut microbiota as a heritable trait affecting feed efficiency.

## Rationale:

Results obtained in this deliverable rely on the analysis of five experimental designs conducted in rabbits and pigs and performed by INRA and IRTA:

- A factorial design conducted at INRA allowed disentangling the maternal transmission of gut microbiota (neonatal environment) from the direct genetic effect of the animal in a cross-fostering trial between and within rabbit lines selected (INRA G10) or not (INRA G0) for feed efficiency (300 rabbits per line in three batches).
- The interaction between feeding regime (i.e., *ad libitum* or restricted) and the genetic control of the gut microbiota composition was studied in relation to post-weaning growth and feed efficiency in a rabbit line (451 Caldes kits) selected by IRTA for high average daily gain after weaning.
- The relationship between microbiota composition and apparent digestibility coefficients was evaluated in 60 castrated male pigs from Duroc, Large White, and Pietrain breeds raised in the experimental facility of INRA. Pigs were fed alternatively a low-fiber (LF) and a high-fiber (HF) diet during four successive 3-week periods from 11 to 23 weeks of age.
- The impact of climate and heat challenge on microbiota composition was evaluated in female and castrated male pigs from a backcross design between Large White and Creole breeds. A total of 522 and 531 genetically-related pigs were raised either under a temperate or tropical climate, respectively, from 11 to 23 weeks of age. In the temperate climate, the pigs were exposed to an acute heat stress (HS) of 29°C during 3 weeks.
- Sex and diet effects and association between feed efficiency and faecal microbial composition were investigated in 160 commercial three-breed crossbred pigs from Topigs Norsvin.

All animals were genotyped and their faeces (pigs) or caecal content (rabbits) were collected.

The microbial composition, diversity and richness of gut microbiota was characterized by means of Illumina sequencing of 16S rRNA gene amplicons (V4-V5 hypervariable regions) in a MiSeq platform. Raw paired-ended sequences were processed with QIIME/QIIME2 software by discarding the low quality and the chimeric sequences. Filtered sequences were assembled into contigs and then clustered into OTUs (Operational Taxonomic Units; contigs sharing a 97% of similarity)/ASVs (Amplicon Sequence Variants; contigs sharing a 99% of similarity). The OTU/ASV table was filtered at sample (discarding those with less than 5,000 filtered contigs) and OTU/ASV (discarding those with less than 0.01% counts across all samples) levels. This table was normalized using the Cumulative Sum Scaling (CSS) normalization yielding the normalized abundances of 931/792 OTUs/ASVs. The taxonomic affiliation was

obtained using the RDP train set 15 with the utax algorithm (pigs and INRA rabbits) or the Greengenes reference database gg\_13\_5\_otus/99 (IRTA rabbits).

Differences in caecal microbial composition, diversity, and richness were assessed from a univariate perspective (i.e., bootstrap analysis of variance fitting a model with a factor combining the farm where the animal was raised, the batch, the feeding regime, and the presence or absence of antibiotics in rabbit feed) and from a multivariate perspective using: (1) Principal Variance Component Analysis, (2) sparse Partial Least Squares - Discriminant Analysis (sPLS-DA) and (3) machine learning algorithms (Support Vector Machine) selecting a certain number of OTUs/ASVs that allow the best discrimination of samples according to a given factor.

Kruskal-Wallis tests, glm methodologies, or generalized Friedman rank sum tests with replicated blocked (package muStatsv1.7.0) were used to point out OTUs with significant abundancy differences between conditions (i.e., sex, temperature, diet, maternal effect, and line effect).

Genetic determinism of the caecal microbiota of rabbits (IRTA) has been assessed by fitting two mixed models (i.e., a genetic model and another model without the additive genetic effect) for 14 representative traits of rabbit caecal microbiota (i.e., the relative abundances of 8 phyla, 4  $\alpha$ -diversity indexes and the first 2 principal components computed from the relative abundance phyla table). To test the existence of a genetic determinism of caecal microbiota, different model choice criteria were used: (1) Deviance Information Criterion (DIC) and (2) Bayes Factor (BF). Variance components were computed (gibbs2f90) for the 14 traits. In INRA rabbits, the variance components (i.e., linear animal mixed model) and QTL analyses (i.e., fixed effect test of each of the 161 033 SNP) were performed using the GEMMA software.

Prediction of growth and feed efficiency traits from microbiota data were evaluated using Partial Least Square Regression method (PLSR).

The relationships between OTUs and the zootechnical traits were characterized by the maximal information coefficient (MIC) index and the background noise was estimated by the maximal value of random permutations.

Mixed linear models were used to estimate jointly host genetic effects and microbiota effect on growth and feed efficiency traits.

**Teams involved:**

INRA, IRTA, TOPIGS

**Species and production systems considered:** rabbits and pigs in all European countries

## 2. Introduction

The gut microbiota is deeply involved in the physiology of its host through the regulation of digestion, metabolism, and immunity and, consequently, it could play a role in feed efficiency. The recent development of sequencing technologies (i.e., 16S sequences clustered into Operational Taxonomic Units) allows the description of this complex ecosystem in livestock species. Different factors have been demonstrated to influence the composition and functions of the gut microbiota, including maternal transmission, environment (i.e., diet composition and quantity, humidity, and heat), age, and physiological status. Specific datasets based on controlled genetic and non-genetic factors, or using crossfostering, are needed to better evaluate the relative contribution of each effect (i.e., host genetics and microbiota).

From month 1 to 48, data from five experimental designs were analysed to estimate the effect of genetic and non-genetic factors on the diversity and the composition of the gut microbiota in pigs and rabbits. Specific statistical methods were used to study the genetic determinism (i.e., heritability and quantitative trait loci (QTL)) of the composition of the microbiota. Regression and machine learning models were applied for the prediction of growth and feed efficiency traits from microbiota data.

## 3. Results

### 3.1 Factors influencing gut microbiota composition

#### INRA RABBITS

The zootechnical parameters varied between the three batches of the trial, with the rabbits of the first batch having the most favorable feed conversion ratio (FCR), essentially due to a reduced feed intake. The performance of the second and third batches were similar to each other (Figure 1). A linear model taking into account the foster dam, the biological mother, the sex, and the batch was used to test the different effects. The richness of the microbial communities of the kits decreased during the experiment (Figure 1), and this effect was even more significant when kits originating from dams that were treated with an antibiotic (baytril) during the second batch were excluded ( $P=10^{-6}$ ). The batch effect (i.e., the fact that the rabbits were grown in three consecutive batches) was also significant for the Simpson diversity (Table 1). In parallel to the decrease in richness, the global composition of the gut microbiota drifted during the experiment (Figure 2). The observations were independent from the sex of the rabbit.

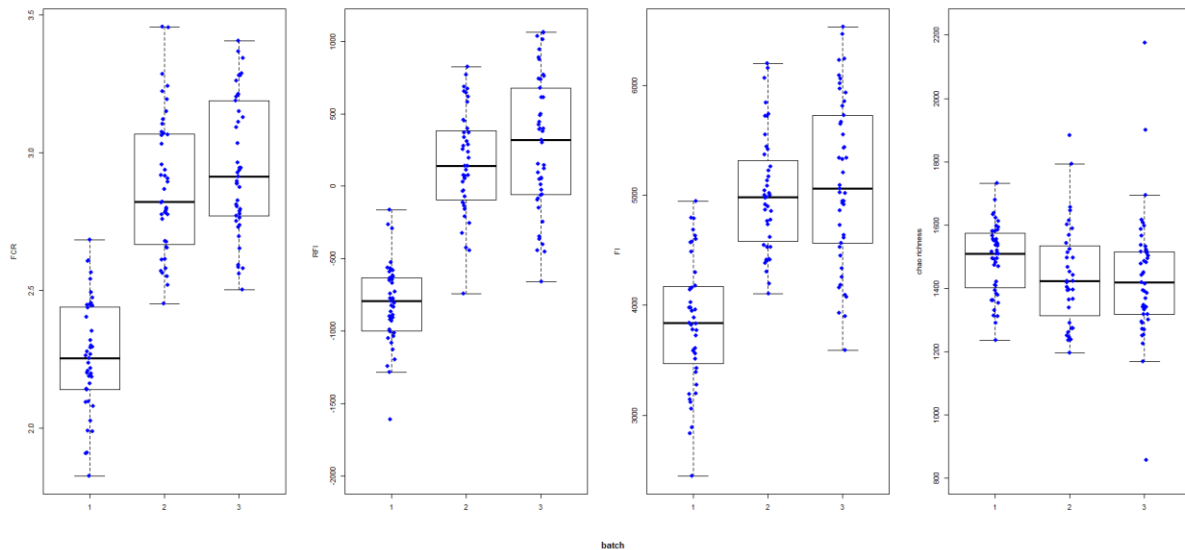


Figure 1. From left to right: impact of the batch on residual feed intake (RFI), feed intake, FCR, and richness of the gut microbes.

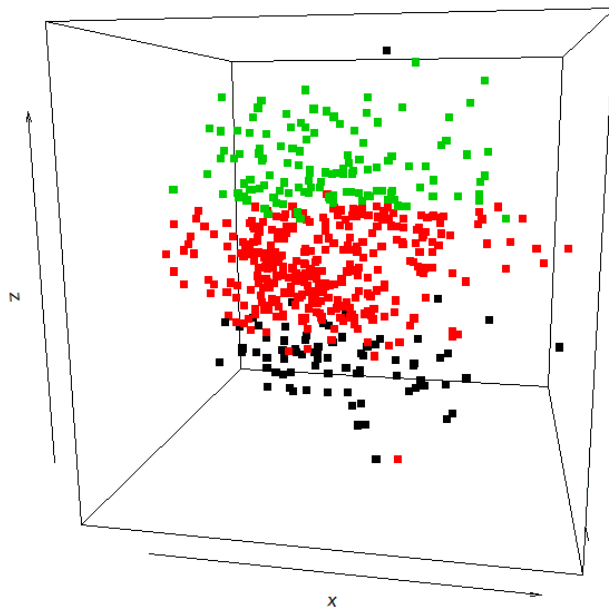


Figure 2. PCA projection capturing 8% of the variability of the microbial data. The first batch is represented in black, the second batch in red, and the third batch in green.

The microbial diversity in the gut of the rabbits at slaughter was higher in the rabbits fostered by G10 dams, independently of their genetic background. The neonatal environment and the genetic background interplayed on the Shannon index, as rabbits from the G10 line had a lower Shannon index only when fostered by a dam from the G00 line ( $P=0.0039$ ). The Gini-Simpson index exhibited the same pattern with less diversity in the G10 kits when focusing on rabbits fostered by G00 dams ( $P=0.019$ ) (Table 1).

*Table 1. Shannon, Simpson and Chao diversity (Richness) indexes tested with linear models including the effects of sex, batch, kit and foster dam lines and their interaction.*

		Foster dam line	Kit line	Foster dam x kit	1 (N=162)	Batch 2 (N=177)	3 (N=187)	Sex M	F
Richness	FosterG00-GenetG00	1517			1542	1522	1493	1487	1559
	FosterG00-GenetG10	1496			1559	1491	1444	1507	1487
	FosterG10-GenetG00	1555			1623	1547	1504	1559	1550
	FosterG10-GenetG10	1542			1582	1535	1511	1549	1533
	P-value	0.034	0.32	0.8	0.0002			0.72	
Shannon	FosterG00-GenetG00	5.31			5.32	5.30	5.31	5.29	5.34
	FosterG00-GenetG10	5.23			5.23	5.18	5.26	5.23	5.22
	FosterG10-GenetG00	5.37			5.41	5.35	5.36	5.36	5.38
	FosterG10-GenetG10	5.37			5.39	5.34	5.38	5.40	5.33
	P-value	0.012	0.0008	0.02	0.43			0.76	
Simpson	FosterG00-GenetG00	0.984			0.984	0.985	0.984	0.984	0.984
	FosterG00-GenetG10	0.982			0.982	0.981	0.984	0.982	0.982
	FosterG10-GenetG00	0.985			0.985	0.985	0.985	0.985	0.985
	FosterG10-GenetG10	0.985			0.98	0.985	0.986	0.986	0.984
	P-value	0.33	0.004	0.051	0.08			0.34	

Interestingly, the four groups had a different variance, which depended only on the neonatal environment ( $P=0.00328$ ; Figure 3), with higher variability of the microbiota in rabbits weaned in the environment provided by the G00 foster dams.

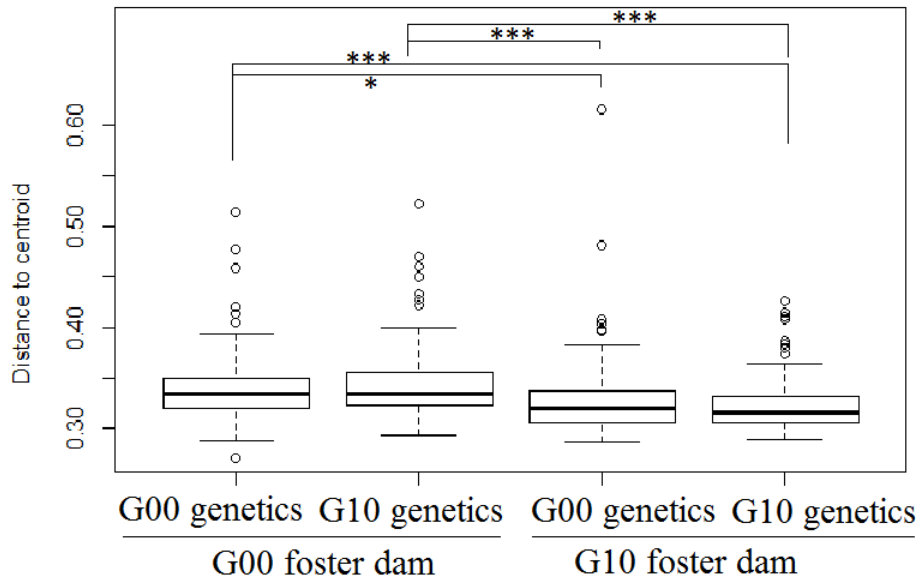


Figure 3. Variance of the distance to the centroid of the microbiota composition for each combination of foster dam line x kit line.

The rare OTUs were filtered out before further analyses, thereby reducing the number of tests from 9,041 to 1,053 OTUs after rarefying at 12,228 sequences per sample, which represents 95% of the sequences. The neonatal environment had the strongest impact on the microbiota: 254 OTUs were affected by the foster dam line, 10 of which were also impacted by the genetic background of the kit. The latter impacted only 41 OTUs. Most of these OTUs (i.e., 93% in total, 90% of the OTUs affected by the kit line and 87% of the OTUs affected by the foster dam line) could not be reliably classified at the genus level. The 10 OTUs affected by both the dam line and the kit line were either unclassified (5 OTUs), or belonged to the *Alistipes* (1 OTU), the *Bacteroides* (2 OTU), and the *Butyrivibrio* (2 OTUs) genera.

Perhaps unsurprisingly considering that 285 species were affected by the kit genetic background and the dam environment, the DAPC projection showed four groups discriminated by the dam environment and kit genetic line ( $P < 0.0001$ ; Figure 4).



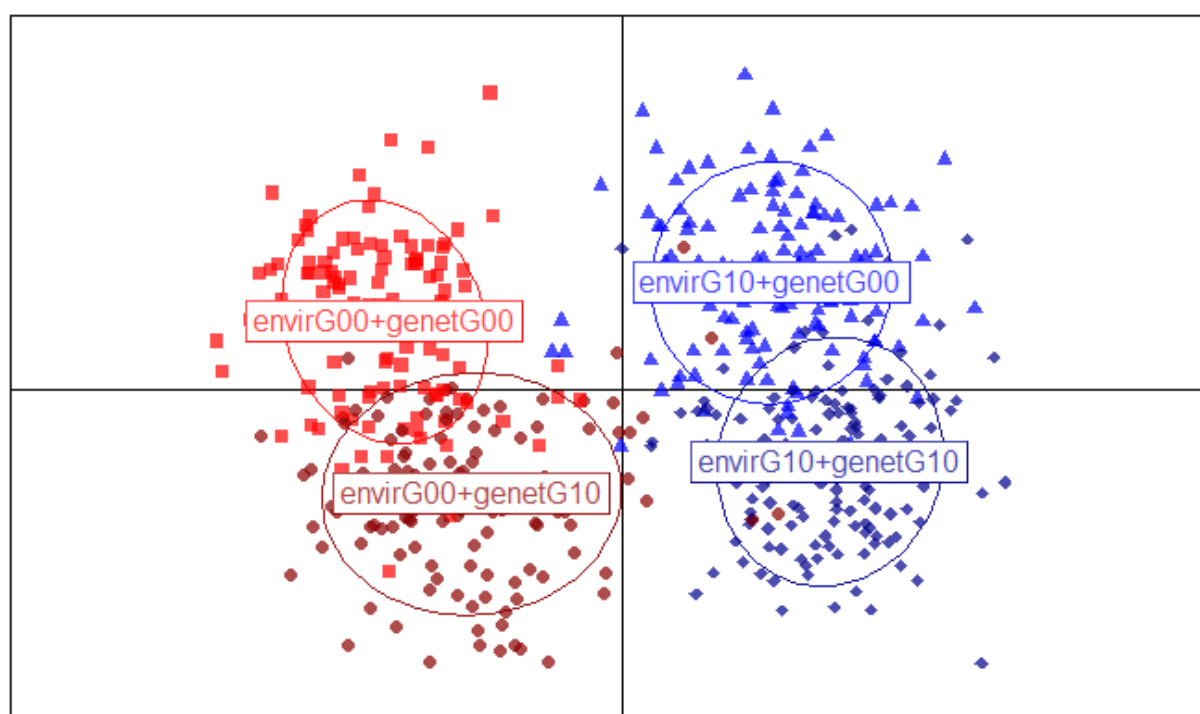


Figure 4. DAPC projection using 150 principal components: 97.4% of the variability of the initial dataset was captured in the principal components, while the DA projection represented 88% of that variability. The neonatal environment from the foster dam (envirG00 or envirG10) was combined with the genetic line of the kit (genetG00 or genetG10).

## IRTA RABBITS

Bootstrap analyses of variance were performed to study the effect of different factors (i.e., the farm where the animal was raised, whether it was fed *ad libitum* or under restriction, and whether it received a diet supplemented with antibiotics or without antibiotics) on microbial composition (i.e., relative abundance of bacteria at different taxonomic levels summarized in ASV) and  $\alpha$ -diversity indexes of IRTA rabbits caecal microbiota.

Univariate analyses revealed that 450 out of the 844 ASVs were differentially represented between farms, nine between feeding regimes (*ad libitum* vs restricted), and 157 between diets with and without antibiotics (Annexes 1, 2, and 3).

All  $\alpha$ -diversity indexes reached different magnitudes in the two farms (Table 2). The Chao1 and Shannon indexes, and the number of observed ASVs were different between gut microbial populations of rabbits fed with antibiotics and that from those not taking antibiotics (Table 3).

Table 2.  $\alpha$ -diversity indexes differentially represented between IRTA rabbits raised in two different farms.

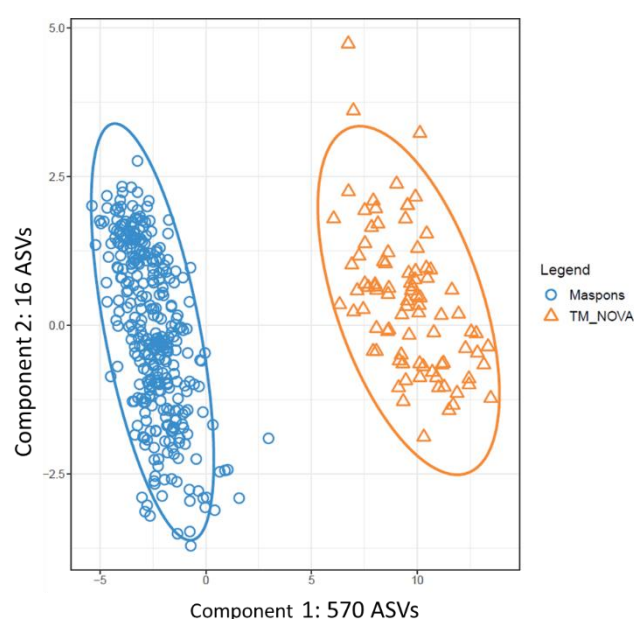
$\alpha$ -diversity index	Difference between farms	SE	P <sub>FDR</sub>
Observed ASVs	74.22	10.70	0.00
Chao1	76.66	11.38	0.00
Shannon	0.43	0.07	0.00
Inverse Simpson	16.18	3.53	0.00

*Table 3.  $\alpha$ -diversity indexes differentially represented between IRTA rabbits fed without antibiotics and with antibiotics.*

$\alpha$ -diversity index	Difference between diets	SE	P <sub>FDR</sub>
Observed ASVs	37.68	17.15	0.05
Chao1	37.42	18.25	0.05
Shannon	0.27	0.11	0.05

The sPLS-DA analyses, which select (based on a lasso penalty) ASVs that best discriminate the samples according to a tested factor, revealed that:

1. For farm comparisons, 570 ASVs were selected in component 1 as differentially represented between farms, which explained 3.9% of the total variability of the microbiota composition (Figure 5). Further univariate analyses indicated that 398 of these 570 ASVs were differentially represented between farms.



*Figure 5. sPLS-DA representing samples of animals raised in the Maspons farm (blue) and in the TM\_NOVA farm (orange).*

2. For feeding regimens comparisons: 160 ASVs were selected in component 1 as differentially represented between feeding regimes in the Maspons farm. These ASV only explained 0.95% of total variance (Figure 6). Further univariate analyses also indicated that five of these 160 ASVs were differentially represented between feeding regimes in the Maspons farm. In total, the univariate analyses indicated declared only seven ASVs as differentially represented between feeding regimens, i.e. two that did not contribute to the sPLS-DA first axis and five that did.

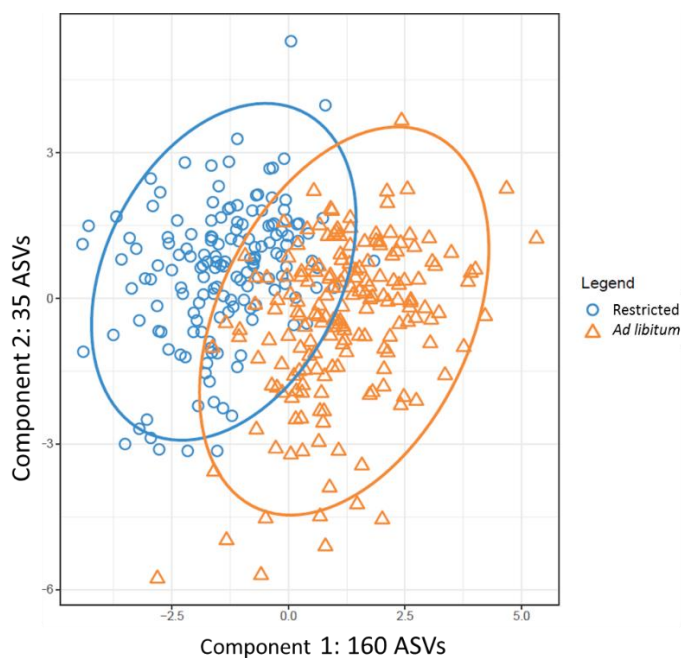


Figure 6. sPLS-DA representing samples of animals fed under restriction (blue) and ad libitum (orange) in the Maspons farm.

- For the combination of antibiotics and feed regime effects: 635 ASVs were retained for component 1 (2.61% of total variance) and 170 ASVs for component 2 (2.11% of total variance), which allowed the discrimination of samples according to the combination of two factors: presence or not of antibiotics in the diet, and feeding regime (i.e., restricted vs *ad libitum*) of animals raised in the TM\_NOVA farm (Figure 7). Further univariate analyses declared 63 of these 805 ASVs differentially represented between feeding regimes and diets combinations within the TM\_NOVA farm. In this case, 67 ASVs were identified as differentially affected by feeding regimes and diets combinations using univariate analysis.

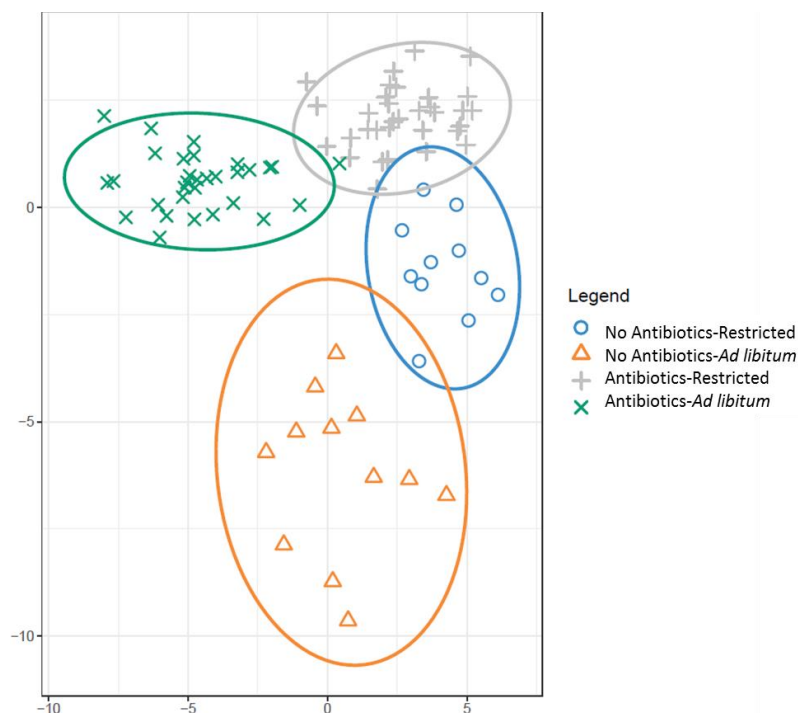


Figure 7: sPLS-DA representing samples of animals fed under restriction without antibiotics (blue), fed ad libitum without antibiotics (orange), fed under restriction with antibiotics (gray) and fed ad libitum with antibiotics (green) in the TM\_NOVA farm.

In general, important differences were observed between sPLS-DA and univariate analyses in the number of ASVs declared as different depending on the tested factors: the number of ASVs discriminant in the sPLS-DA was always larger than those significant with the univariate analyses. However, nearly all the ASVs selected from the univariate methods were selected in the sPLS-DA. Nevertheless, the low percentage of total variance that the different components of the sPLS-DA explained was surprising, with a maximum of 3.9% for the largest percentage.

The Support Vector Machine (SVM) algorithm provided another multivariate perspective to classify samples according to the feeding regime based on the OTUs abundances (i.e., in this analysis, sequences were pre-processed using the QIIME software) as predictors. After ranking OTUs in an unbiased Random Forest algorithm based on conditional inference, subsets of 50, 100, 150, and 200 most informative OTUs were used for classification of test sets. The classification quality and the stability of the results in all test sets improved with increased number of predictors (OTUs), but differences were not significant (Figure 8). The best classification was obtained with the subset of 200 OTUs, with 91% chances of exact classification of the samples. Using the whole set of OTUs as predictors degraded the classification quality due to the effect of non-informative OTUs (89% of good prediction). Five out of the 10 OTUs that contributed the most to the classification were overrepresented in caecal samples of animals fed *ad libitum*, and all were assigned to the order *Clostridiales* ( $P > 0.80$ ). The other five OTUs were overrepresented in samples of animals that were restrictedly fed. Four were assigned to the same order *Clostridia*.

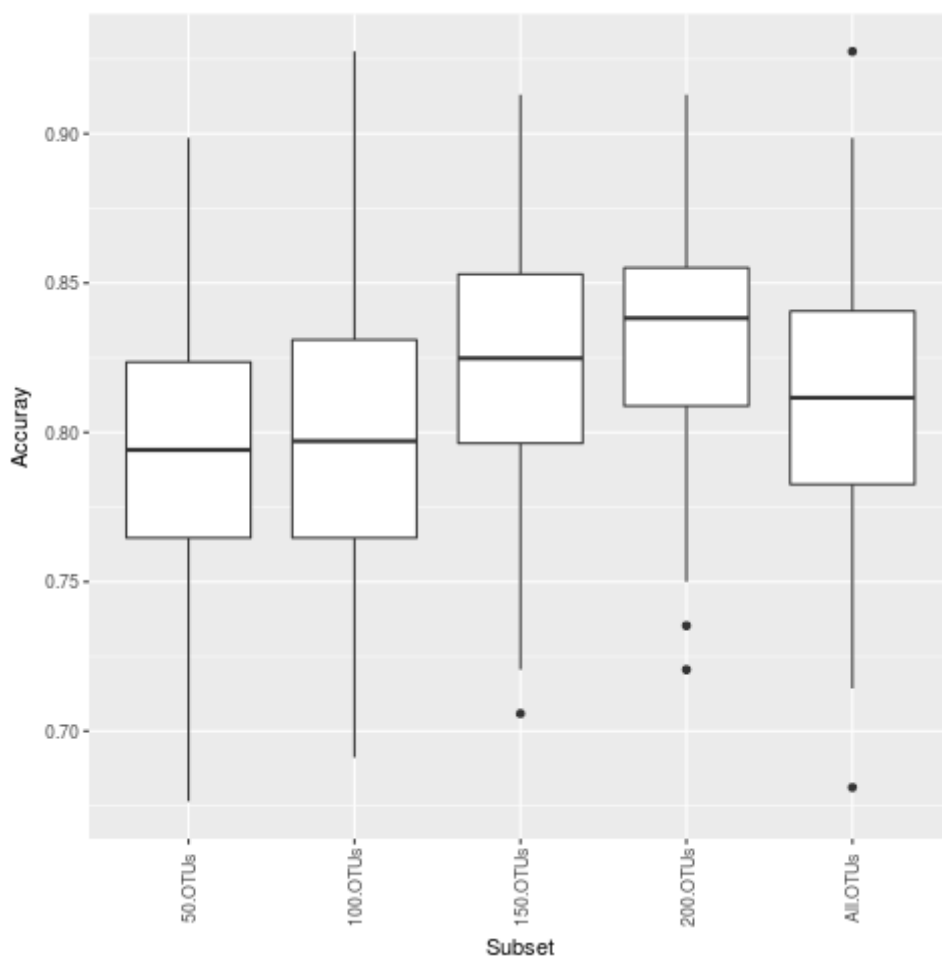


Figure 8. Classification accuracies with different subset sizes of OTUs predictors.

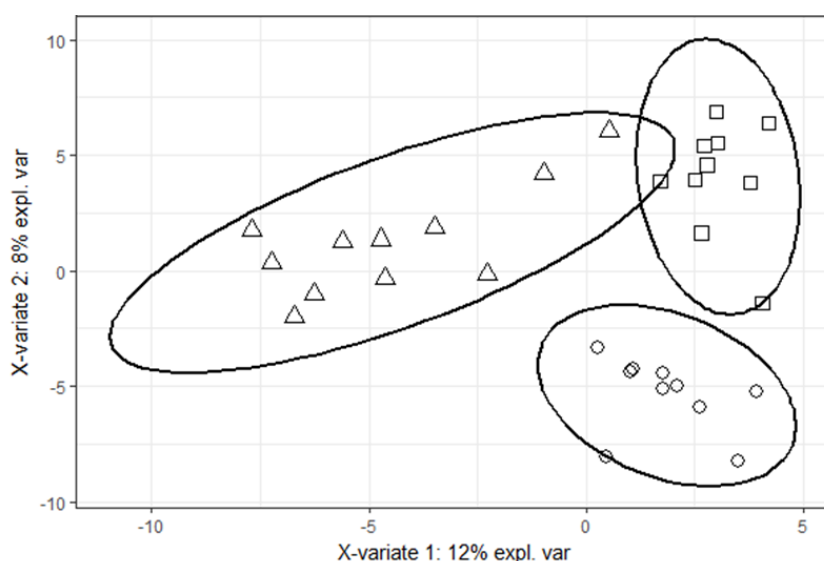
The method and input data used in the machine learning procedure were different from those of the univariate analyses and the sPLS-DA. Specifically, 97% of the OTUs obtained with the

QIIME software were used for the machine learning classification, whereas 99% of the ASVs obtained with QIIME2 software were employed in the other analyses. The machine learning classification was applied to records from the Maspons farm only.

### INRA PIGS - EFFECT OF DIETARY FIBRE CONTENT, BREED, AND AGE

Using a principal variance component analysis, the variance of the composition of the faecal microbiota was explained by the diet (32% of the total variance), test period (21%), and breed (1.5%).

In pigs fed the low-fibre (LF) diet, at the end of the first period, faecal microbiota composition was used in a sparse partial least square discriminant analysis (sPLS-DA) to discriminate the pigs according to their breed, with 13.9% misclassification error-rate and 200 OTUs (Figure 9). However, once fed a high-fibre (HF) diet, the sPLS-DA was unable to discriminate pigs from the different breeds, suggesting that an exposure to the HF diet eliminates the difference between breeds.



*Figure 9. Score plot of two-component sPLS-DA model showing faeces samples clustering according to breed, with the percentage of variance captured for each principal component ( $\Delta$ : Duroc,  $\square$ : Large-White,  $\circ$ : Pietrain), for the animals fed the low-fibre diet during period 1. According to the cross-validation permutation test, the misclassification error-rate was 14%.*

Irrespective of the breed and the period, the dietary significantly influenced the composition of the microbiota composition (Figure 10). In a general linear model (GLM) analysis, 1,641 out of 2,041 OTUs were different between the LF and HF diets. In a sPLS-DA, 31 OTUs were used to discriminate pigs according to their diet with a 3.9% error-rate, and could be used as biomarkers of the dietary treatment.

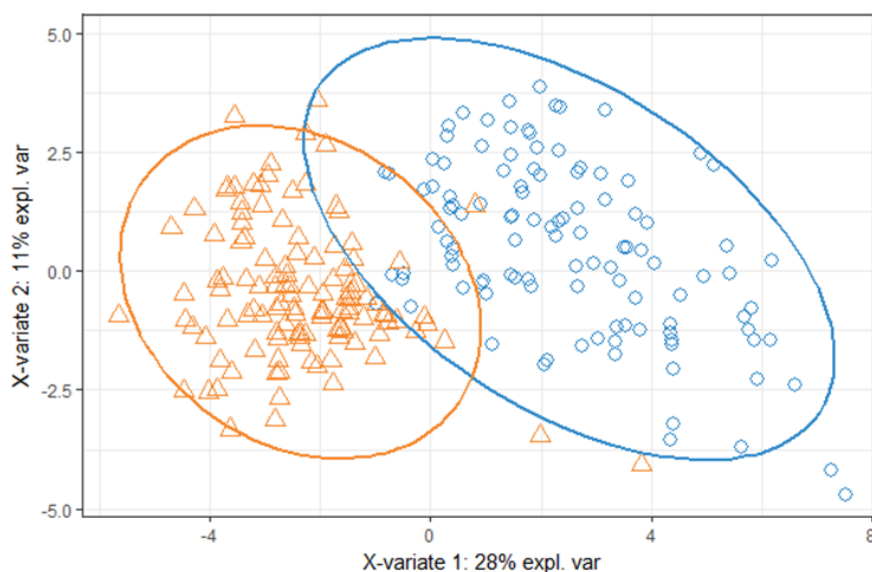


Figure 10. Score plot of a two-component sPLS-DA model showing faecal sample clustering according to the diet, with the percentage of variance captured for each principal component ( $\Delta$ : Low-fibre diet,  $\circ$ : High-fibre diet). According to the cross-validation permutation test, the misclassification error rate was 3.9%.

This discrimination was not affected by the previous diet or previous switches of diets, illustrating the resilience of the biomarkers.

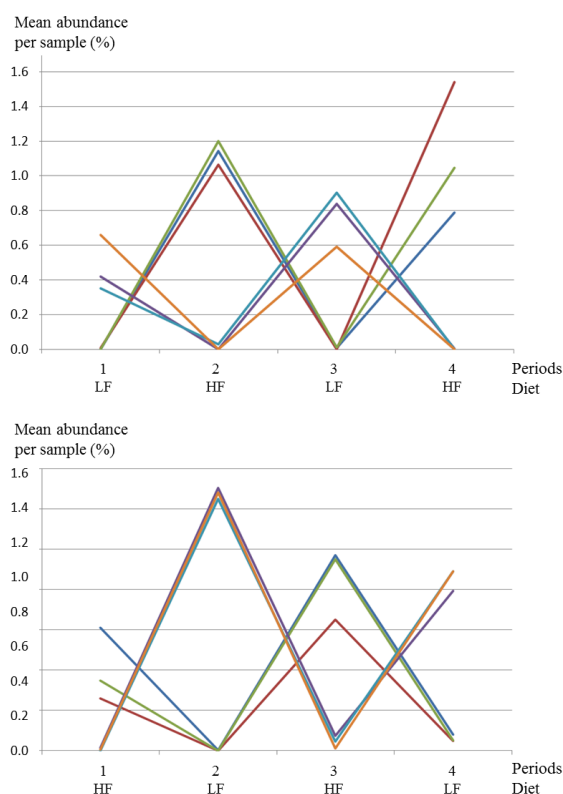


Figure 11. Variation of the relative abundancy of predictive OTUs of diet effect. The three most contributive OTUs from the low-fibre diet (LF) (OTU 514: purple, OTU 1140: light blue, OTU 923: orange) and the high-fibre diet (HF) (OTU 792: dark blue, OTU 689: red, OTU 1940:



green) were extracted from the sPLS-DA analysis using their contributions to the first principal component.

The relationship between microbiota composition and digestibility coefficients was tested using Pearson correlations (Figure 12). In the LF diet, 83 and 65 OTUs were correlated with the digestibility coefficients of N and energy, respectively ( $P < 0.05$ ), and 49 and 37 OTUs were correlated with the digestibility coefficients of cellulose and hemicellulose, respectively. The significant correlation coefficients ranged from 0.29 to 0.36 for positive correlations (0.31 on average), and from -0.29 to -0.45 for negative correlations (-0.34 on average). In the HF diet, no OTUs were found that correlated with digestibility coefficients.

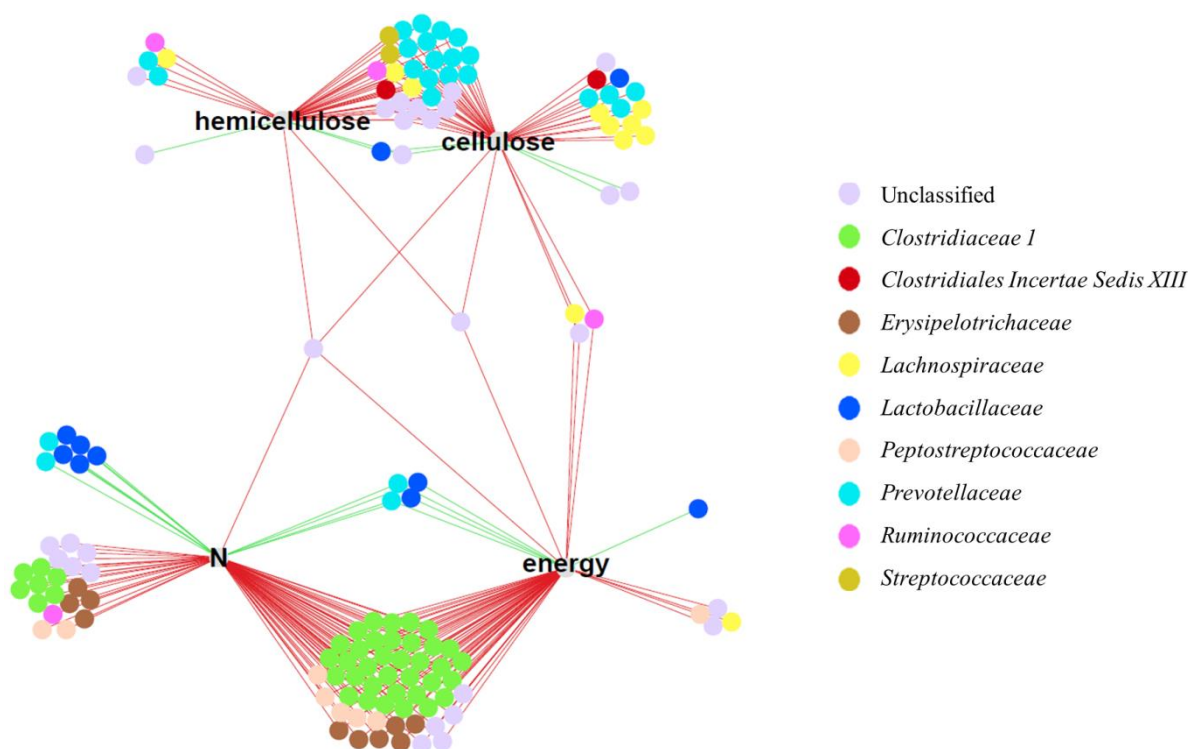


Figure 12. Correlated OTUs (represented by dots colored according to the taxonomical family of the corresponding bacteria) to digestibility coefficients (energy, N, hemicellulose, and cellulose) in pigs fed the low-fibre diet (Pearson correlations). The negative and positive correlations are represented by red and green lines, respectively.

*Clostridiaceae 1* (*Clostridium sensu stricto* and unclassified at genus level), *Erysipelotrichaceae* (*Turicibacter*), and *Peptostreptococcaceae* (*Clostridium XI*) were negatively correlated with energy and nitrogen digestibility coefficients, whereas *Lachnospiraceae* (*Blautia*, *Coprococcus* and *Dorea* genera) were negatively correlated with the digestibility of energy, cellulose, or hemicellulose. Two OTUs belonging to *Clostridiales Incertae Sedis XIII* and four *Streptococcus* were negatively correlated with the digestibility of cell wall components. *Ruminococcaceae* negatively correlated with cellulose, hemicellulose, nitrogen, and energy digestibility.

*Prevotellaceae* (mainly *Prevotella* genus) were negatively correlated with the digestibility of cell wall components, except for six unclassified *Prevotellaceae*, which were positively correlated with energy and nitrogen digestibility.

*Lactobacillaceae* were positively correlated with nitrogen, energy, cellulose, and hemicellulose digestibility, except one negatively correlated with cellulose digestibility. The only genus represented in this family was *Lactobacillus*.

## INRA PIGS - EFFECT OF ACUTE AND CHRONIC HEAT STRESS ON THE COMPOSITION OF MICROBIOTA

The microbiota composition was evaluated in female and castrated male pigs from a backcross design between Large White and Creole breeds from faeces collected at 23 weeks of age in two climates (abbreviated TEMP23 and TROP23 for temperate and tropical climates, respectively) and at 26 weeks of age in the temperate climate (TEMP26).

Using a principal component analysis, the variance of the faecal microbiota composition was explained by the environment (TEMP23, TEMP26, TROP23; 20% of the total variance), sire family (3.9%), batch (3.2%), and sex (0.8%). Irrespective of the environment, the microbiota composition was dominated by *Firmicutes* and *Bacteroidetes* phyla (91.7, 88.3, and 87.5% for TEMP23, TEMP26, and TROP23, respectively). The relative abundance of *Firmicutes*, *Proteobacteria* and *Spirochaetes* was greater ( $P<0.05$ ) in the tropical climate than in the temperate climate. The relative abundance of *Actinobacteria* and *Bacteroidetes* was greater ( $P<0.05$ ) in TEMP23 compared to TEMP26 and TROP23 environments.

The diversity of the microbiota was not affected by heat stress, but the microbiota composition differed significantly. Generalized linear models (GLM) analyses highlighted 182 OTUs that differed in abundance between TEMP23 and TEMP26 and corresponded to two biological pathways, and 1,296 OTUs that differed in abundance between TEMP23 and TROP23 and corresponded to 20 pathways. From these comparisons, we could extract OTUs systematically more abundant in hot conditions (either in the tropical climate or after a heat challenge in the temperate climate) (Figure 13). These 78 OTUs belonged mainly to *Prevotellaceae* family (41% of the OTUs) and *Lachnospiraceae* family (18%). In contrast, 37% of the 43 OTUs that were always more abundant under TEMP23 came from the *Clostridiaceae* 1 family and 5% from *Peptostreptococcaceae* family.

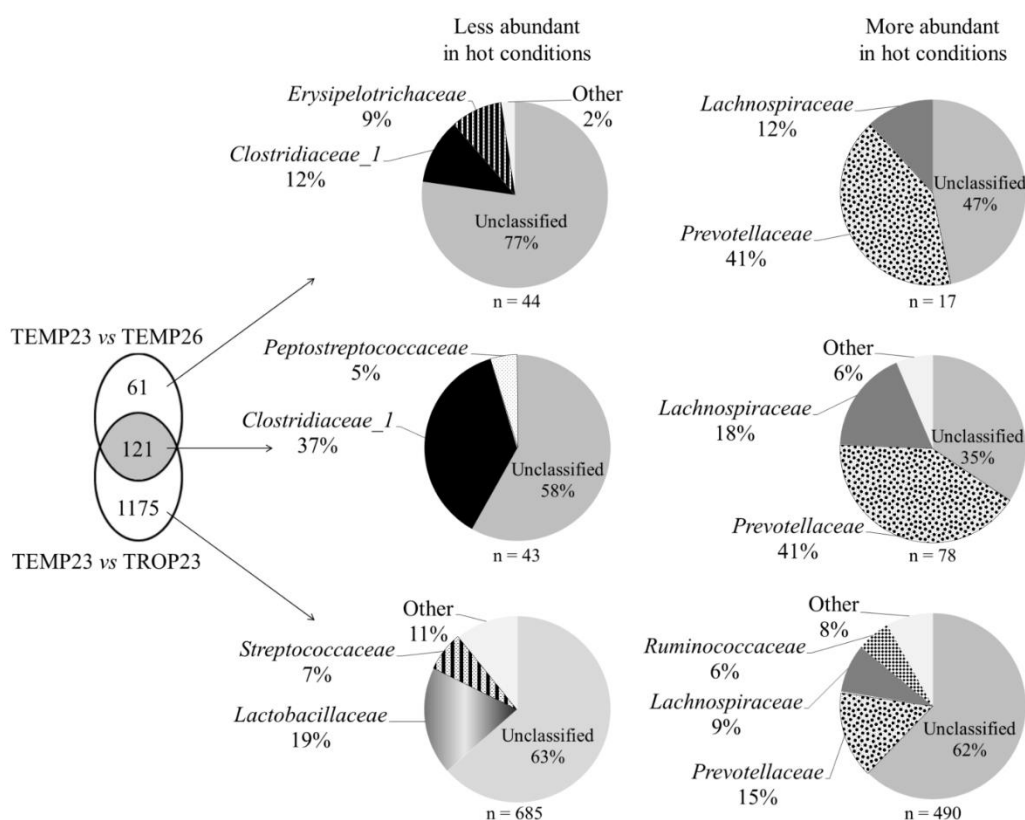


Figure 13: Venn plot representation of the OTUs differentially abundant in a GLM analysis, aggregated at the family level, between TEMP23 vs. TEMP26, and between TEMP23 vs. TROP23.



The pathways overrepresented in TEMP23 compared to TROP23 were related to metabolism (i.e., biosynthesis of isoflavonoid, steroid hormone and betalain; Figure 14). In contrast, the 17 pathways overrepresented in TROP23 were related to human diseases, metabolism, genetic information processing, cellular processes and organismal systems. The comparison between TEMP23 and TEMP26 pointed out that the steroid hormone biosynthesis pathway was overrepresented in TEMP23, and the G protein-coupled receptor pathway was overrepresented in TEMP26.

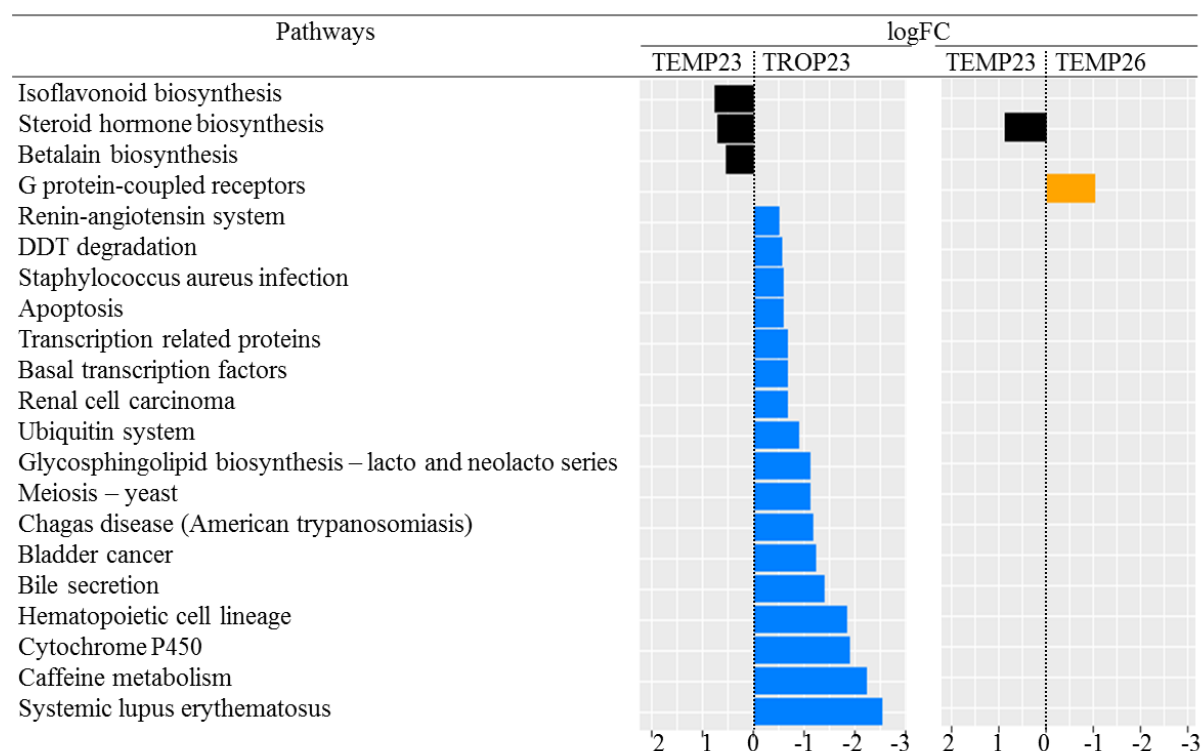
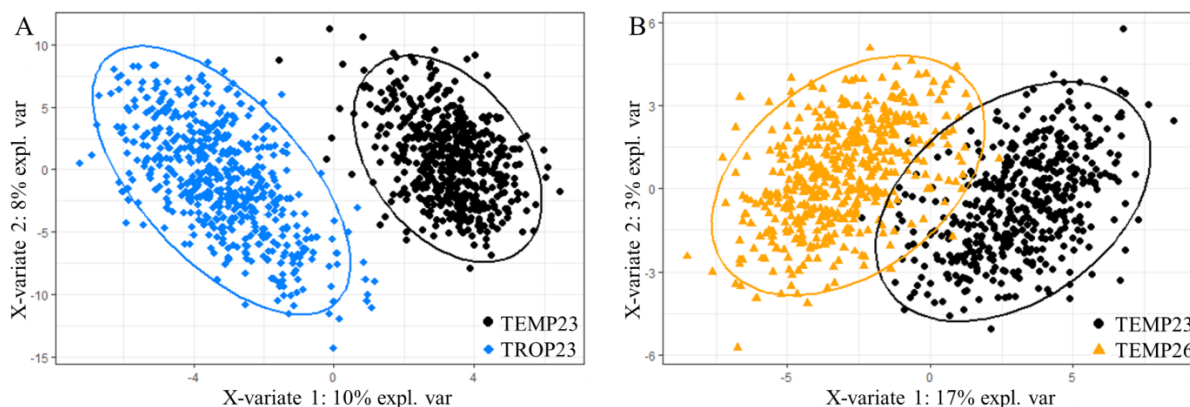


Figure 14. Functional pathways differentially abundant between the temperate climate at 23 wk (TEMP23) and 26 wk of age (TEMP26), and the tropical climate at 23 wk of age (TROP23). Log2 fold changes (logFC) resulted from a two-by-two comparison using a GLM analysis (false discovery rate < 0.05).

Pigs raised under two different environments were discriminated using microbiota information in a sparse partial least square discriminant analysis (sPLS-DA; Figure 15). The discrimination of the pigs under temperate and tropical climates involved 125 OTUs and a misclassification error-rate of 0.2%. Between 23 and 26 weeks of age, in the temperate climate, pigs were discriminated using 62 OTUs and 7.1% error-rate. Every OTU selected in the sPLS-DA was previously found as differentially abundant in the GLM analyses.



**Figure 15.** Score plot of two-component sPLS-DA models showing faeces samples clustering according to the environment (TEMP23: under temperate climate at 23 wk of age; TEMP26: under temperate climate after a 3-week heat challenge; TROP23: under tropical climate at 23 wk of age), with percentage of variance captured by each principal component. According to the cross-validation permutation test, the misclassification error-rates with two components are 0.2 and 7.1% in models 1 (panel A) and 2 (panel B), respectively.

The microbiota composition of all pigs at 23 weeks of age clustered into two enterotypes dominated either by *Turicibacter*, *Sarcina*, and *Clostridium sensu stricto* (enterotype 1 abbreviated E1), or by *Lactobacillus* (E2). According to an ANOVA analysis, the alpha diversity of the samples in E2 was greater ( $P < 0.05$ ) compared to the samples in E1 based on the number of OTUs (2,589 vs 2,742 OTUs in TEMP23, 2,600 vs 2,698 OTUs in TROP23, respectively) and the Shannon index (7.18 vs 7.25 in TEMP23, 7.14 vs 7.18 in TROP23, respectively).

From the ANOVA analysis of the effect of enterotypes on production and thermoregulation traits recorded during the growth period in both climates, whatever the trait, the interaction between the enterotypes and the climates was not significant ( $P > 0.05$ ). Pigs in E1 were 3.3 kg heavier at wk 11 compared to pigs in E2 ( $P < 0.05$ ). However, the two enterotypes did not differ for the body weight recorded at 23 wk of age. The two enterotypes did not differ in ADG, ADFI, or FCR recorded between 11 and 23 wk of age. Regarding the thermoregulation traits, skin temperature at 23 wk of age was 0.3°C greater in E2 compared to E1 (i.e., 34.9 vs 35.2°C, respectively;  $P < 0.05$ ), and the rectal temperature did not differ between the two enterotypes (i.e., 39.3 vs 39.4°C, respectively;  $P = 0.11$ ). During the acute heat stress challenge, the rise in rectal temperature from wk 23 to 24 was greater in pigs from E2 than in those from E1 (i.e., 0.34 vs 0.25°C, respectively,  $P < 0.05$ ). On For the long-term response between wk 23 and 26, the variation in rectal temperature remained 0.05°C greater ( $P < 0.05$ ) in E2 compared to E1.

When pigs were exposed to an acute heat stress in the temperate climate, the repartition in the two enterotypes changed. Among the 241 pigs belonging to E1 in wk 23, 199 (82.6%) remained in the same enterotype in wk 26 and 42 (17.4%) switched from E1 to E2 in wk 26. In contrast, 123 pigs remained in E2 from wk 23 to wk 26 when 122 switched from E2 to E1. The performance and thermoregulation responses of pigs switching from one enterotype to another one, evaluated by ANOVA, did not differ from those of pigs that remained stable in their enterotype before and after heat stress. In particular, growth performance and variation in rectal temperature after heat stress did not differ between pig that switched or not.

## TOIGS NORSVIN PIGS- EFFECT AND SEXE, ASSOCIATION WITH FEED EFFICIENCY

The aim of this study was to investigate the association between feed efficiency and faecal microbial composition in commercial grower-finisher pigs. In addition, two factors affecting feed efficiency were studied for their effect on the faecal microbiome: diet composition and sex. In this study, 160 three-breed cross pigs (synthetic boar x (Large White x Landrace)) were used,

81 males and 79 females, coming from 20 litters. Two different diets were fed to the pigs, a diet based on corn/soybean meal (CS) as typically fed to commercial grower-finisher pigs in the America's and a diet based on wheat/barley/by-products (WB) as typically fed in Europe.

The faecal microbiome was characterized by 16S ribosomal DNA sequencing and clustered by OTUs. Results were subjected to a discriminant approach combined with principal component analysis (DAPC) to test the association of microbiota abundance with a number of factors: diet, sex, and feed efficiency extremes.

The relative abundance of microbes in the faeces was clearly different between the animals fed the two different diets. At the phylum level, only two phyla were sufficient to distinguish the diets: *Bacteroidetes* and *Proteobacteria*. At the class level, the classes *Gammaproteobacteria*, *Spirochaetes*, and *Bacteroidia* were sufficient to distinguish the animals fed the CS diet from the animals fed the WB diet. Two genera, *Ruminococcus* and *Blautia* were also sufficient to distinguish the groups. Finally at the OTU level, two OTUs were sufficient (Figure 16), namely OTU 33 and OTU 16, for discrimination. For both OTUs, the most likely bacterium was *Butyricicoccus pullicaecorum*.

In contrast to the diets, the differences between the relative abundances of microbes in the faeces between male and female pigs were of lower magnitude. At the phyla level, there was no separation between the two sexes, and at the class level the analysis needed 22 out of 45 classes to reach a significant difference. However, when looking at the genera level, there was a highly significant distinction between the male and female pigs. The main class differing between the sexes was *Methanobacteria*. The microbial abundance in the faeces of the sexes was clearly separated at the OTU level as well (Figure 16). The most important OTU for sex separation was the same as for diet, OTU 16, which was associated with *Butyricicoccus pullicaecorum*.

As there was a strong effect of diet and sex on the faecal microbiome, for evaluation of the effect of the composition of faecal microbiota on feed efficiency, the 25% pigs with the highest and the 25% with the lowest individual feed efficiency per diet and sex (20 animals per combination) were retained. This resulted in four groups: male pigs fed the CS diet (MCS), female pigs fed the CS diet (FCS), male pigs fed the WB diet (MWB), and female pigs fed the WB diet (FWB). The high and low feed efficient pigs could only be separated in the MWB group, at phylum level and based on two phyla, which were both more abundant in the high feed efficiency pigs. The MWB and MCS could be separated at class level, and at genera level the analysis only showed a significant separation between the high and low feed efficient animals in FCS and MWB. At the OTU level, there was only a separation for the MWB and FWB (Figure 16). In total, 17 OTUs were necessary to discriminate the MWB, and seven OTUs to distinguish the FWB. Three of the OTUs required for discriminating high and low feed efficiency pigs were common for the male and female pigs. Strikingly, the effects of two of those OTUs had different directions in male and female pigs.

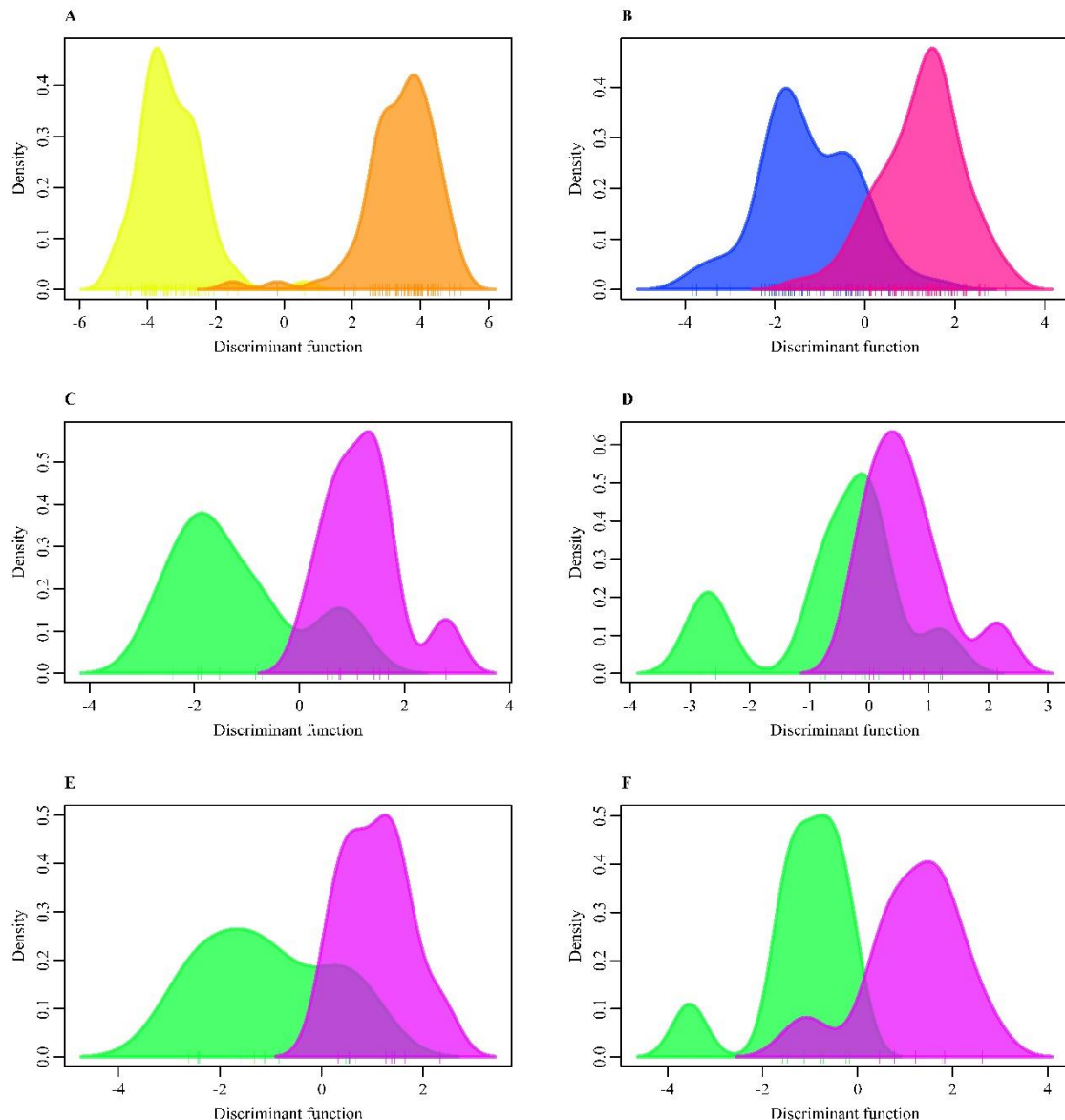


Figure 16. Gaussian kernel density estimation of the discriminant function as result of the discriminant analysis of principle components for tested groups based on operational taxonomic units. A) Diet. Yellow = corn/soybean meal diet, orange = wheat/barley/by-products diet. B) Sex. Blue = male pigs, pink = female pigs. C-F) Feed efficiency. Green = high feed efficiency, purple = low feed efficiency. C) Male pigs fed a corn/soybean meal diet, D) Female pigs fed a corn/soybean meal diet, E) Male pigs fed a wheat/barley/by-products diet, F) Female pigs fed a wheat/barley/by-products diet. Adapted from Verschuren et al. (2018).

## 3.2 Genetic determinism of microbiota composition

### 3.2.1 Heritability

#### IRTA RABBITS

Bayes Factors (BF) and Deviance Information Criterion (DIC) were used as model choice criteria to test the existence of a host genetic determinism on 14 representative traits of rabbit caecal microbiota (Tables 4 and 5). Both criteria pointed out the existence of a host control on the relative abundance of phyla *Euryarcheota*, *Proteobacteria*, and *Tenericutes*, on all  $\alpha$ -diversity indexes, and on PC2 ( $BF > 3.16$  and  $DIC_{ng} - DIC_g > 7$ ). The punctual estimates of

heritability of these eight traits, except the relative abundance of phylum *Tenericutes*, showed values greater than 0.10. However, the probability of the heritability value being equal to or greater than 0.10 ranged between 0.42 and 0.67, resulting in a low evidence of the genetic model. The large estimation errors for heritability might lie in the low number of data used.

Table 4. Descriptive statistics for the studied traits in IRTA rabbits.

Trait	Mean	Standard deviation	Range
<i>Euryarcheota</i>	0.002	0.003	0.020
<i>Actinobacteria</i>	0.015	0.006	0.051
<i>Bacteroidetes</i>	0.067	0.028	0.210
<i>Cyanobacteria</i>	0.009	0.005	0.031
<i>Firmicutes</i>	0.759	0.040	0.252
<i>Proteobacteria</i>	0.016	0.008	0.050
<i>Tenericutes</i>	0.071	0.015	0.100
<i>Verrucomicrobia</i>	0.016	0.006	0.043
Observed OTUs	469.384	82.403	469.000
Chao1	565.021	102.015	606.914
Shannon	5.031	0.324	2.235
Inverse Simpson	69.729	20.683	110.787
PC1	3.30E-16	2.025	14.365
PC2	-1.85E-16	1.197	6.636

Table 5. Parameters estimates, mean (standard deviation) of marginal posterior distributions, and model choice criteria in IRTA rabbits.

Trait	$h^2$	$P$ ( $h^2 \geq 0.1$ )	$c^2$	$l^2$	$DIC_{ng} - DIC_g$	BF <sub>(g/ng)</sub>
<i>Euryarcheota</i>	0.13 (0.08)	0.55	0.03 (0.03)	0.10 (0.06)	10.90	1267.75
<i>Actinobacteria</i>	0.10 (0.08)	0.41	0.03 (0.03)	0.09 (0.05)	6.95	20.91
<i>Bacteroidetes</i>	0.09 (0.08)	0.36	0.03 (0.03)	0.15 (0.07)	6.09	1.26
<i>Cyanobacteria</i>	0.11 (0.08)	0.47	0.05 (0.04)	0.11 (0.06)	9.62	3.06
<i>Firmicutes</i>	0.09 (0.08)	0.38	0.02 (0.02)	0.05 (0.04)	6.28	8.29
<i>Proteobacteria</i>	0.11 (0.10)	0.42	0.06 (0.04)	0.15 (0.07)	11.97	11.76
<i>Tenericutes</i>	0.08 (0.07)	0.32	0.12 (0.06)	0.04 (0.04)	7.92	11.42
<i>Verrucomicrobia</i>	0.08 (0.07)	0.29	0.04 (0.03)	0.11 (0.05)	3.72	280.06
Observed OTUs	0.17 (0.13)	0.63	0.07 (0.04)	0.19 (0.08)	30.71	62630.02
Chao1	0.18 (0.13)	0.67	0.07 (0.04)	0.18 (0.08)	35.17	25719.38
Shannon	0.11 (0.09)	0.47	0.04 (0.03)	0.10 (0.06)	10.30	1319.49
Inverse Simpson	0.11 (0.08)	0.45	0.05 (0.03)	0.04 (0.03)	9.07	78.26
PC1	0.09 (0.08)	0.35	0.04 (0.03)	0.13 (0.06)	5.94	22.76
PC2	0.11 (0.08)	0.48	0.04 (0.03)	0.14 (0.07)	9.87	1458.26

$h^2$ : heritability;  $P$  ( $h^2 \geq 0.10$ ): probability of  $h^2$  being equal to or greater than 0.10;  $c^2$ : percentage of total phenotypic variance explained by the cage effect;  $l^2$ : percentage of total phenotypic variance explained by the litter effect; DIC: Deviance Information Criterion; BF: Bayes Factor.

## INRA RABBITS

A total of 866 OTUs were obtained after normalization by Total Sum Scaling (TSS), for 510 rabbits. The most probable taxonomy was retrieved with uchiime, a program that detects chimeric sequences. These OTUs were individually tested with an animal linear mixed model including the fixed effect of the contemporary group ( $n=3$  levels) and of the sex ( $n=21$  levels),



and the random effect of the animal structured by a pedigree relationship matrix: from this analysis the variance components for each OTU were estimated, giving access to estimations of their heritability. The phenotypic standard deviations of the OTUs ranged from 0.51 to 3.69 (on the normalized scale) with most OTUs having phenotypic standard deviations between 1 and 2 (Figure 17).

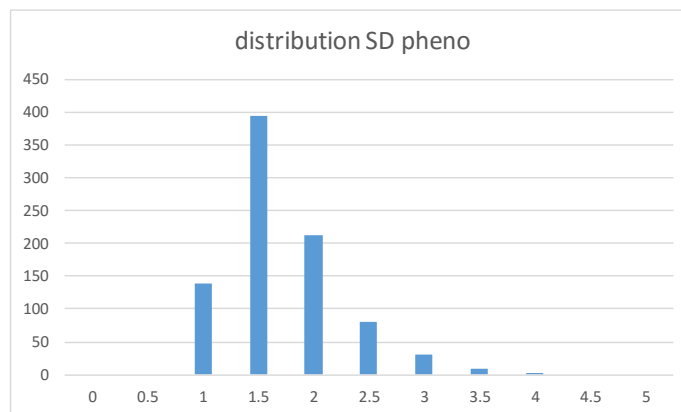


Figure 17. Distribution of the phenotypic standard deviations of the 866 analysed OTUs.

Because some of the OTUs had inadequate distributions or very low genetic determinism, 320 OTUs (37%) had a very low genetic variance component. The remaining 546 OTUs had  $h^2$  ranging from 0.00027 to 0.48, i.e., from null to relatively high heritability. The average  $h^2$  was 0.10, with a standard deviation of 0.08 (Figure 18).

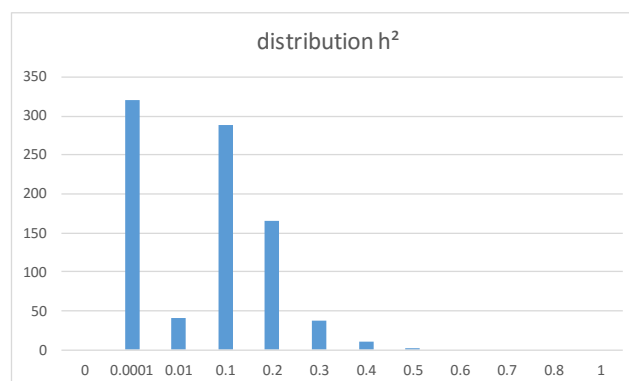


Figure 18. Distribution of the heritability estimates obtained for 546 OTUs.

These estimates fall in the usual ranges reported in the literature (Camarinha-Silva et al, 2017; Lu et al., 2018; González-Recio et al., 2018). They indicate a reasonable genetic control of the rabbit caecal microbiote by the host.

### 3.2.2 Genome-Wide Association Studies

#### INRA RABBITS

The 866 OTUs were individually evaluated, testing the fixed effect of each of the 161,033 SNP (with  $MAF < 0.005$ ) one after the other, the SNP genotypes being coded as 0, 1, or 2 (0=homozygous for the minor allele, 1=heterozygote, 2=homozygous for the major allele).

To account for the multiple tests performed in the GWAS, only  $-\log_{10}(P\text{-value}) > 5$  were considered as significant. Among the 866 tested OTUs, 326 had significant results for at least 1 SNP. Only 58 (18%) had no estimate for  $h^2$  (see paragraph 3.2.1), and the average  $h^2$  of these OTUs was slightly higher than for all the OTUs ( $0.11 \pm 0.07$ , Figure 19).

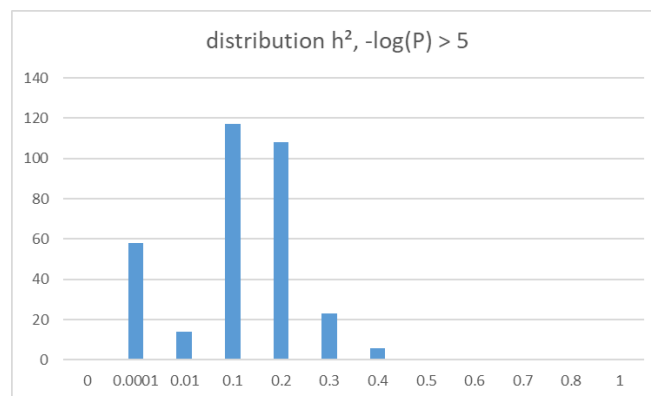


Figure 19. Distribution of the heritability estimates obtained for the 326 OTUs with significant signals in the genome wide association studies.

From 6 (chromosome 6) to 40 (chromosomes 2 and 3) OTUs had at least 1 SNP with  $-\log_{10}(P)$  higher than 5 on each chromosome. Because the rabbit sequence is relatively recent, an important proportion of the SNPs do not yet have a known position, and 107 OTUs also had significant signals on SNPs with unknown position (chromosome 23 in the following). Among the 326 OTUs with significant SNPs, only 214 had significant SNPs on at least two different chromosomes, which matches the 112 OTUs found with only one SNP with  $-\log_{10}(P) > 5$  (Figure 20).

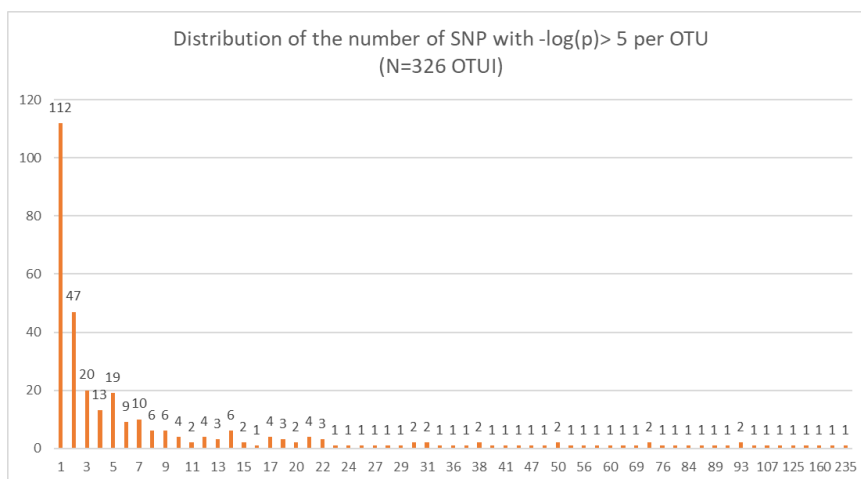


Figure 20. Number of OTUs depending on the number of significant SNPs detected.

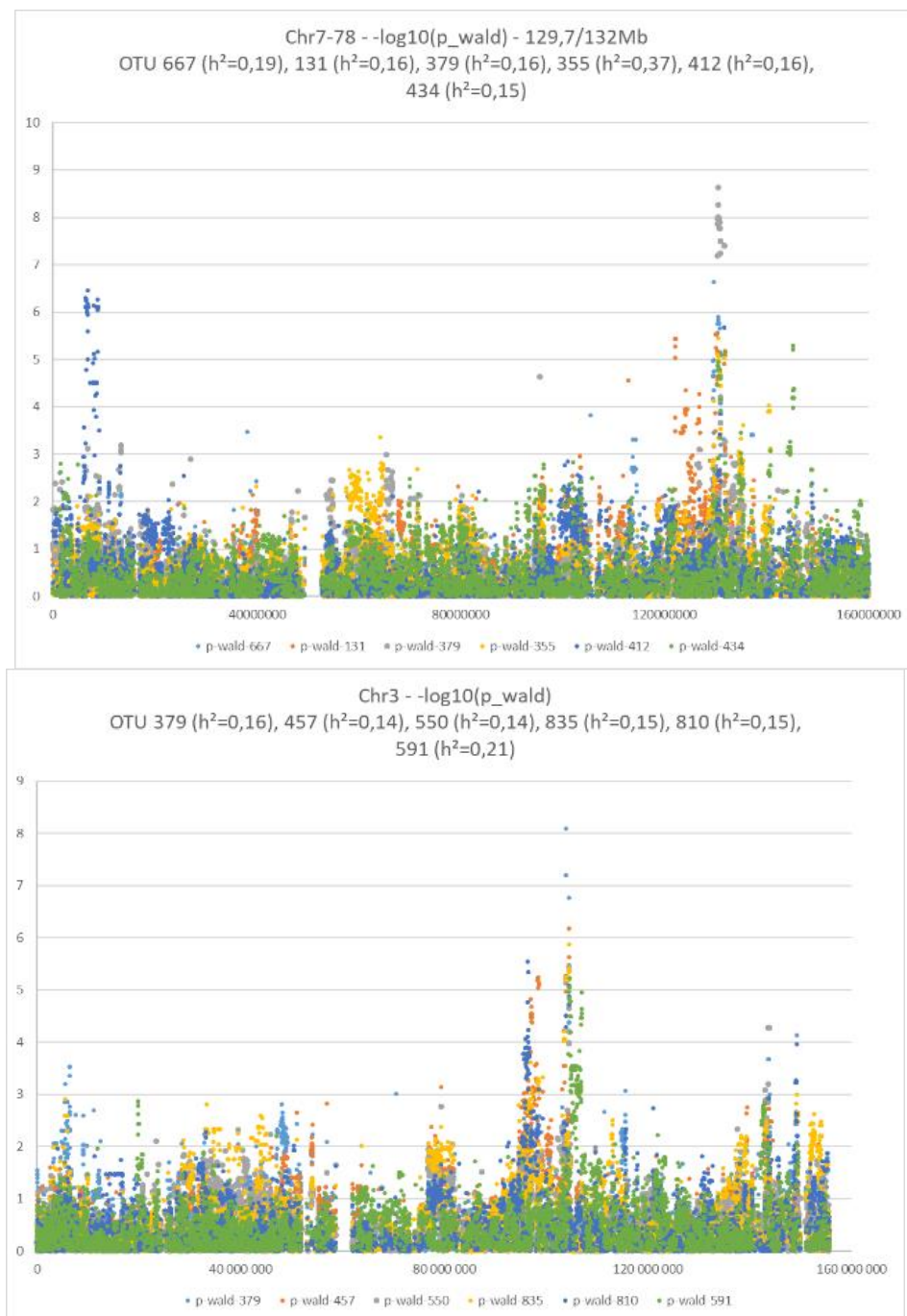
To produce an overview of the results, we will describe specifically: 1). Some of the OTUs with the highest number of significant SNPs, 2). Some regions with accumulation of significant SNPs from different OTU, and 3). The OTUs with the most significant signals ( $P$ -values  $< 1.15 \times 10^{-9}$ , which accounts for the fact that at each OTU level signals with  $P$ -values  $< 10^{-6}$  can be considered as significant, but given that 866 OTUs are analysed, the safest threshold corresponds to  $10^{-6} / 866 = 1.15 \times 10^{-8}$ ).

#### QTL regions associated with multiple OTU abundancies

In the following section, isolated signals (i.e., only one SNP with  $-\log_{10}(P) > 5$  for a given OTU in a region) were not considered. In addition, signals on SNPs that were not localized were ignored.

The QTL regions were defined as groups of SNP for which significant SNPs were found within distances of 1 Mb. A total of 184 QTL regions were identified, spanning from 5 kb to 4.38 Mb, with an average size of 725 kb. Most of the regions (128) were specific to one OTU, whereas 37 had signals for two OTUs, 9 for three OTUs, 7 (on chromosome 1, 2 (2 regions), 7, 12 (2

regions), and 20) for four OTUs, and 3 (on chromosome 3, 7, and 8) for six OTUs. The Manhattan plots obtained for the three chromosomes significant for six OTUs in the same regions are given in Figure 21.





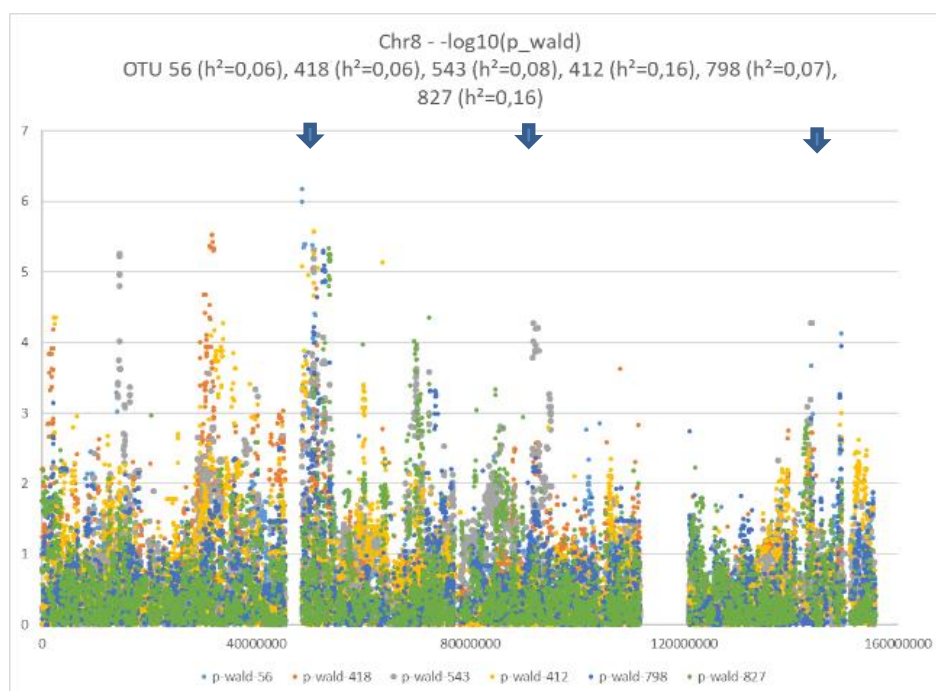


Figure 21. Three chromosomes with six OTUs showing significant signals in the same region.

For these three QTL regions, the taxonomy of the involved OTUs was examined, but no particular homogeneity in the identification suggested a baseline to propose biological hypotheses for these QTL actions. Similarly, genes were searched in the regions identified based on the position of the peaks using the Ensembl database ([https://www.ensembl.org/Oryctolagus\\_cuniculus/](https://www.ensembl.org/Oryctolagus_cuniculus/)). For the chromosome 3 peak, no gene is reported in the region, but the *MMP16* gene is located 0.1 Mb downstream. In contrast, in the chromosome 7 region 20 genes are mapped, and 17 are listed in the chromosome 8 region, but with no clear connection with gut/digestive functions.

Because a significant QTL was found for residual feed intake on chromosome 18 at about 48 Mb, the significant signals in this region were examined. One region spanning from 49.2 to 50.0 Mb was identified as affecting two OTUs (Figure 22). The taxonomy results indicated a most probable link to the *Clostridiales* order ( $P=1$ ). The most likely family (Table 6) was *Lachnospiraceae* ( $P=1$ ), and both OTUs could belong to the *Ruminococcus2* genus, with  $P=0.53$  and  $P=0.73$ . Given that the Manhattan plots are very similar for these two OTUs, they may correspond to the same microbiota, counted as two different OTUs in the initial table.

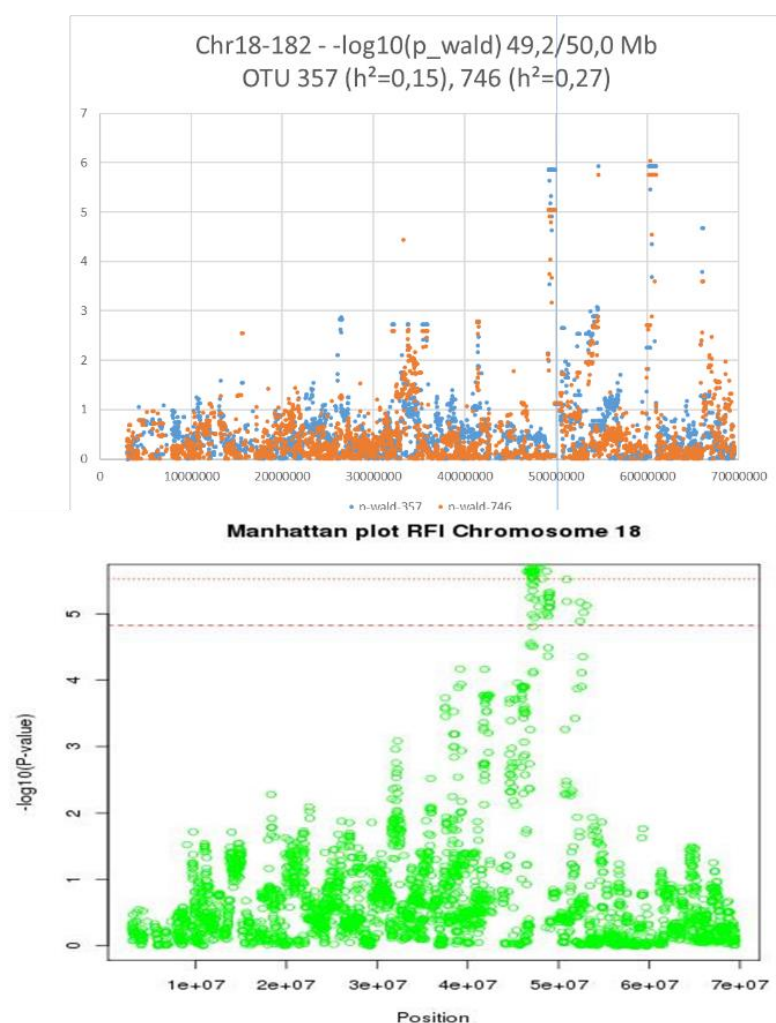


Figure 22. Significant regions in the neighborhood of the signals reported on residual feed intake (RFI) in the same rabbit population.

Table 6. Taxonomy assignments of the two OTUs with significant signals in the neighborhoods of the RFI peak, and associated probabilities

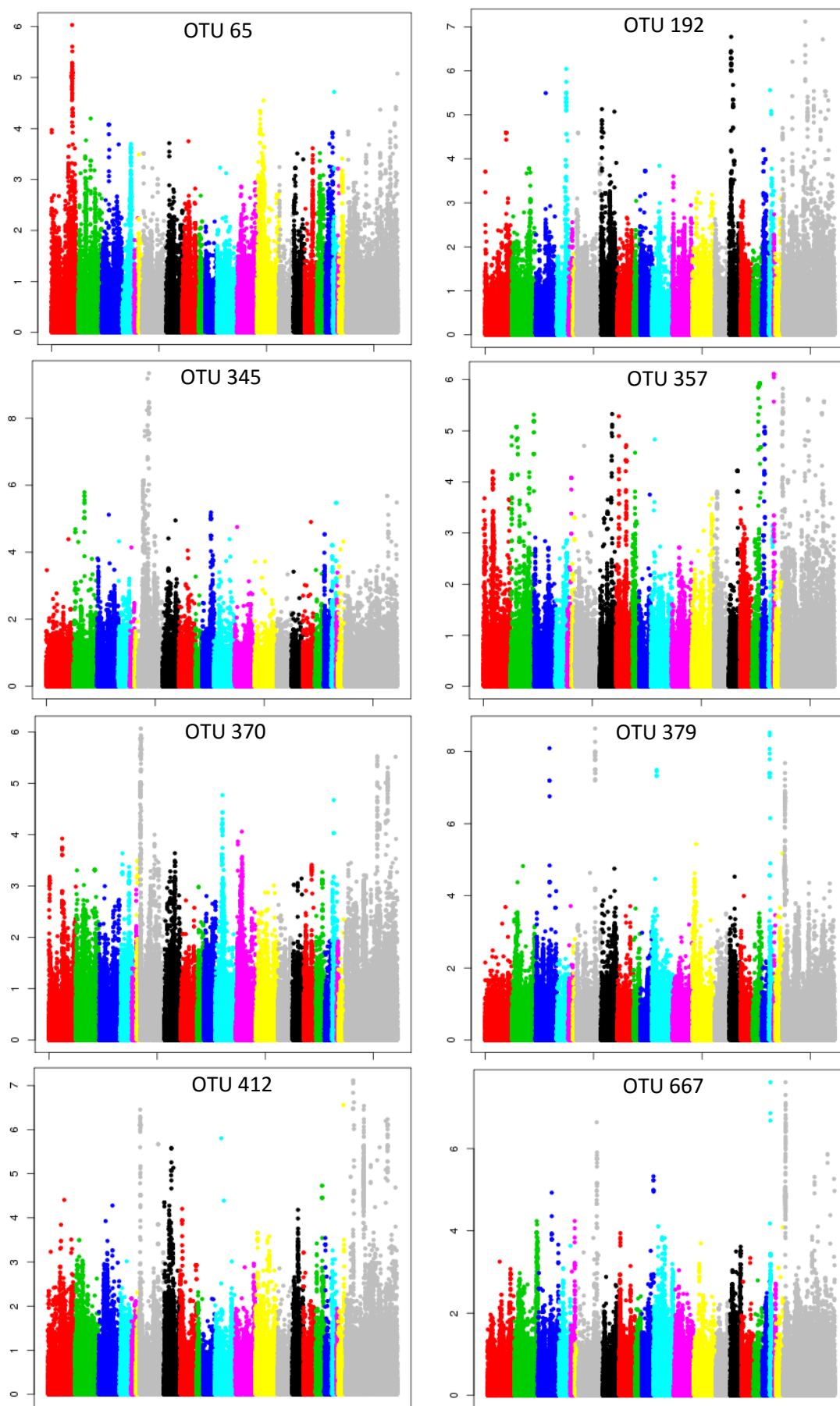
OTU>OTU name; domain	Phylum	Class	Order	Family	Genus
357>New.Reference OTU1958; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Lachnospiraceae (1.00)	Ruminococcus2 (0.73)
746>New.Reference OTU4370; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Lachnospiraceae (1.00)	Ruminococcus2 (0.53)

Among the OTUs found in these signals, the heritabilities are according to the general distribution reported previously: most are around 0.13-0.16, with some lower or higher values.

#### OTUs with the largest number of significant SNPs

Eleven OTUs had 92 and more SNPs with significant signals (Figure 23). The distribution of their *P*-values in the genome is given in Figure 23. The heritabilities of these OTUs ranged from 0.10 to 0.25.

Among these 11 OTUs, six were assigned with  $P > 0.80$  to the *Firmicutes* phylum, two belonging to the *Lachnospiraceae* family, two to the *Ruminococcaceae* family, and one was assigned to the *Bacteroidetes* phylum (family *Bacteroidaceae*). The others did not have a clear taxonomy assignment (Table 7).



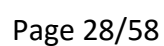


Table 7. Taxonomy assignments of the 11 OTUs with highest number of significant signals, and associated probabilities

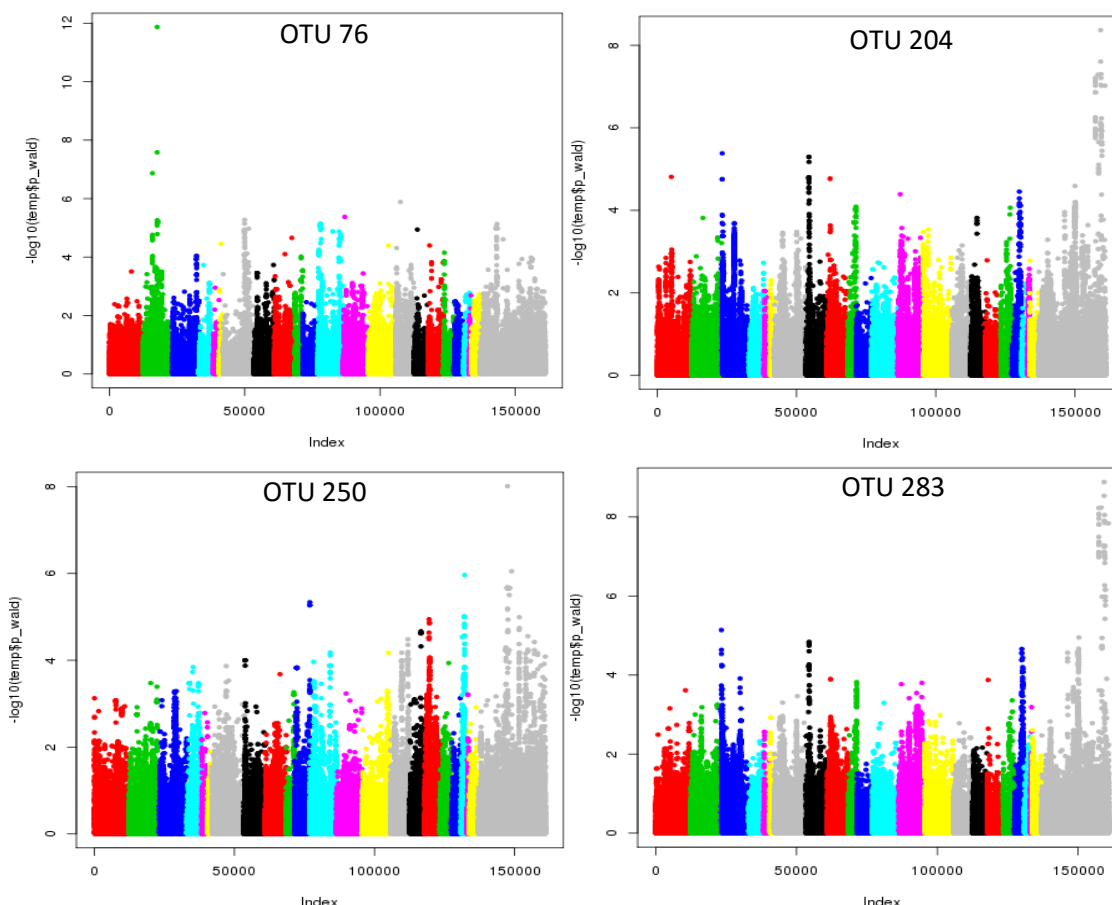
OTU>OTU name; domain	Phylum	Class	Order	Family	Genus
65>542830; Bacteria (0.76)	Proteobacteria (0.42)	Deltaproteobacteria (0.16)	Bdellovibrionales (0.05)	Bdellovibrionaceae (0.02)	Vampirovibrio (0.005)
192>589277; Bacteria (1.00)	Bacteroidetes (1.00)	Bacteroidia (1.00)	Bacteroidales (1.00)	Bacteroidaceae (1.00)	Bacteroides (1.00)
345>New.ReferenceOTU6518; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Ruminococcaceae (1.00)	Flavonifractor (0.28)
357>New.ReferenceOTU1958; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Lachnospiraceae (1.00)	Ruminococcus2 (0.73)
370>New.ReferenceOTU228; Bacteria (1.00)	Firmicutes (0.87)	Clostridia (0.66)	Clostridiales (0.50)	Ruminococcaceae (0.12)	Clostridium_III (0.02)
379>New.ReferenceOTU2381; Bacteria (1.00)	Actinobacteria (0.27)	Actinobacteria (0.07)	Actinomycetales (0.02)	Streptomyetaceae (0.002)	Streptomyces (0.0002)
412>New.ReferenceOTU7822; Bacteria (1.00)	Tenericutes (0.53)	Mollicutes (0.28)	Ntomoplasmatales (0.12)	Spiroplasmataceae (0.04)	Spiroplasma (0.02)
667>New.ReferenceOTU3225; Bacteria (0.6433)	Firmicutes (0.48)	Bacilli (0.17)	Bacillales (0.06)	Staphylococcaceae (0.01)	Salinicoccus (0.0005)
678>New.ReferenceOTU4395; Bacteria (0.8696)	Actinobacteria (0.25)	Actinobacteria (0.06)	Actinomycetales (0.02)	Streptomyetaceae (0.002)	Streptomyces (0.0003)
828>New.ReferenceOTU1858; Bacteria (1.00)	Firmicutes (0.99)	Clostridia (0.98)	Clostridiale (0.97)	Lachnospiraceae (0.96)	Clostridium_XIVa (0.32)
844>New.ReferenceOTU1049; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Ruminococcaceae (0.80)	Oscillibacter (0.14)

Highly significant QTL regions associated with OTUs abundancies

Nine OTUs had SNPs with P-values  $< 1.15 \times 10^{-9}$ , including three comprised in the previous category (OTU 345, 379, and 828), and one contributing to the QTL region on chromosome 3 mentioned earlier (OTU 379) (Figure 24). The highest signal was obtained for OTU 76 (from the *Firmicutes* phylum) on chromosome 2 ( $-\log_{10}(P\text{-value}) = 11.87$ , position 86.3 Mb). The maximum  $-\log_{10}(P\text{-value})$  for the remaining OTUs ranged from 7.94 to 9.34, and were located on chromosomes 2, 3, 7, 17, 20, or not positioned on any chromosome for four of these maxima. The heritabilities estimated for these OTUs ranged from 0.10 to 0.25. Six of these OTUs corresponded to the *Firmicutes* phylum, whereas three correspond to the *Bacteroidetes* phylum (Table 8).

Three OTUs belonged to the *Porphyromonadaceae* family (most probable genus *Odoribacter*), two to the *Lachnospiraceae* family (most probable genus *Roseburia*, which is a butyrate producing type of bacteria), three belonged to the *Ruminococcaceae* family, and one to the *Eubacteriaceae* family.

The OTUs 204 and 283 were assigned to the same genus *Odoribacter*, and given the similarity of their GWAS profiles it can be suspected that they represent, at least to some extent, the same bacteria.





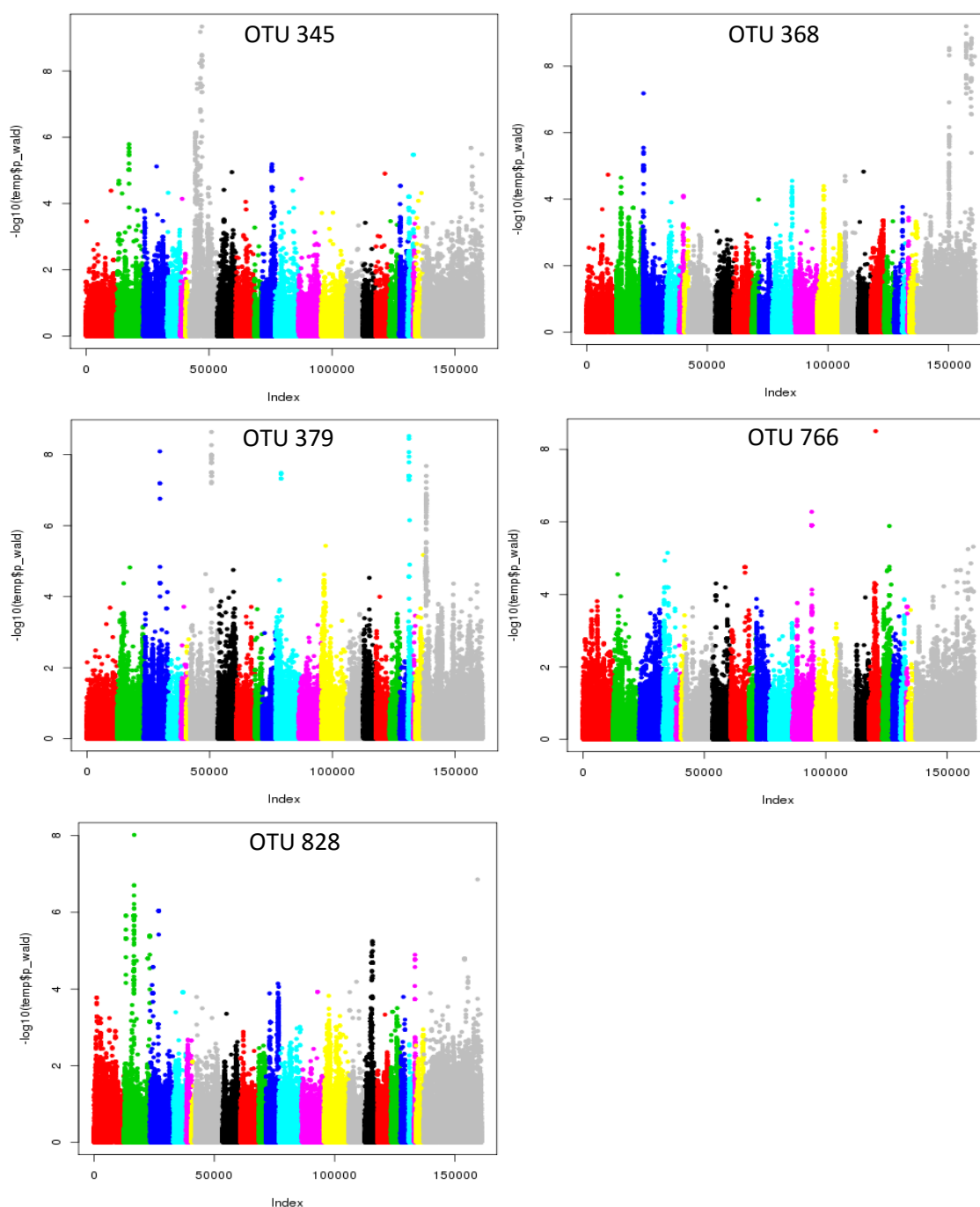


Figure 24. Manhattan plots ( $-\log_{10}(P\text{-values})$ ) for the nine OTUs showing the lowest  $P$ -values on the genome (a least one  $-\log_{10}(P\text{-value}) < 7.94$ ). Different colours indicate SNP from different chromosomes.

*Table 8. Taxonomy assignments of the nine OTUs with most significant signals, and associated probabilities*

OTU>OTU name; domain	Phylum	Class	Order	Family	Genus
76>291380; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Lachnospiraceae (0.99)	Roseburia (0.65)
204>73753; Bacteria (1.00)	Bacteroidetes (1.00)	Bacteroidia (1.00)	Bacteroidales (1.00)	Porphyromonadaceae (1.00)	Odoribacter (1.00)
250>1110037; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Ruminococcaceae (1.00)	Ruminococcus (0.99)
283>3579707; Bacteria (1.00)	Bacteroidetes (1.00)	Bacteroidia (1.00)	Bacteroidales (1.00)	Porphyromonadaceae (1.00)	Odoribacter (1.00)
345>New.ReferenceOT U6518; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Ruminococcaceae (1.00)	Flavonifractor (0.28)
368>New.ReferenceOT U2842; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Eubacteriaceae (0.99)	Eubacterium (0.981)
379>New.ReferenceOT U2381; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Lachnospiraceae (0.99)	Roseburia (0.65)
766>New.ReferenceOT U7190; Bacteria (1.00)	Bacteroidetes (1.00)	Bacteroidia (1.00)	Bacteroidales (1.00)	Porphyromonadaceae (1.00)	Odoribacter (1.00)
828>New.ReferenceOT U1858; Bacteria (1.00)	Firmicutes (1.00)	Clostridia (1.00)	Clostridiales (1.00)	Ruminococcaceae (1.00)	Ruminococcus (0.99)

### 3.3 Prediction of feed efficiency from microbiota data

#### INRA RABBITS

The link between the microbes and zootechnical performance was assessed by a partial least square regression to predict the performance from the microbiota. Indeed, the microbial data could explain feed conversion ratio, feed intake, and residual feed intake (RFI) with significant correlations ( $0.465 \pm 0.03$ ,  $0.43 \pm 0.04$ , and  $0.48 \pm 0.04$ , respectively) (Figure 25).



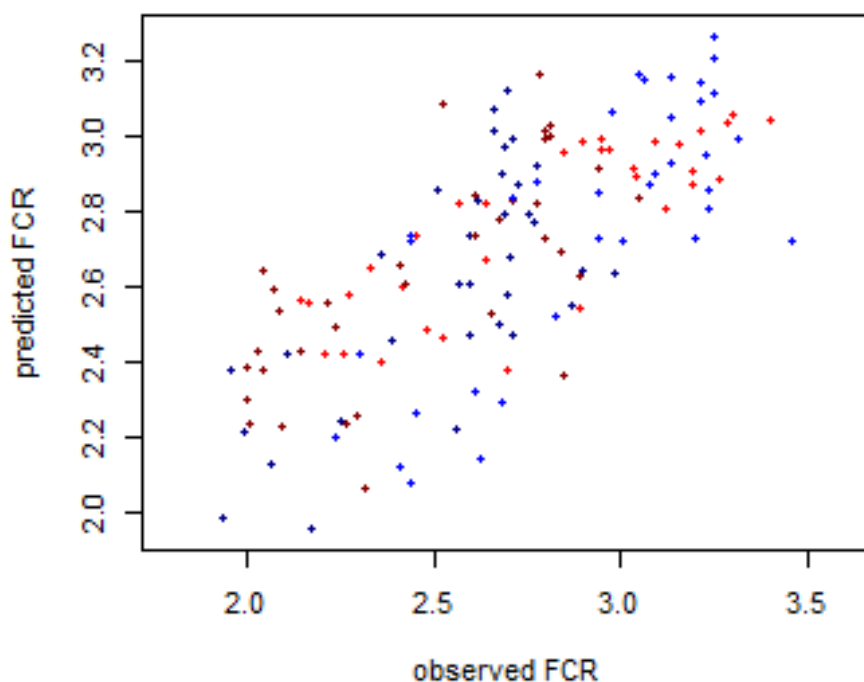


Figure 25. Prediction of the feed conversion ratio (FCR) from OTU abundances. The X-axis represents the observed value and the Y-axis is the predicted value. The  $R^2$  of this relationship is 0.53. The first batch is represented in brown, the second batch is in red, and the third batch is in blue.

As expected, the weights of the OTUs in the prediction of each trait were highly correlated, as were the parameters themselves (Figure 26). Interestingly, some microbes controlled either by the foster dam environment provided to the kit, or by kit genetics, could explain the performances, albeit with low correlations ( $0.33 \pm 0.05$ ,  $0.29 \pm 0.05$ , and  $0.359 \pm 0.07$  for feed conversion ratio, feed intake, and residual feed intake, respectively).

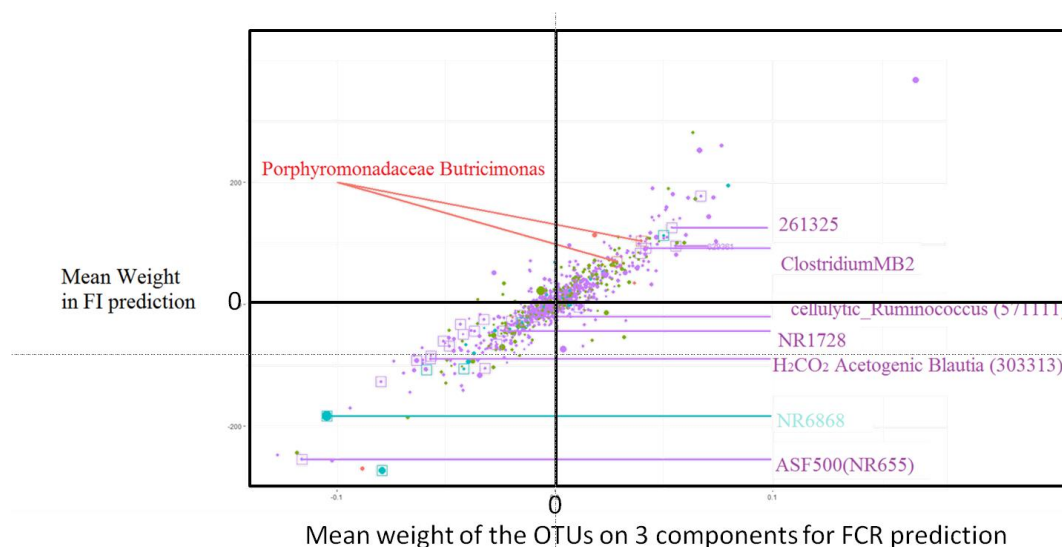


Figure 26. Contribution of the OTUs to the PLS regression for feed conversion ratio (FCR) and feed intake (FI). The axis values are the OTU weights in the regression for each trait, the dot size is proportional to the mean abundance of the OTUs across the dataset. The color indicates if the OTUs were impacted by the kit genetic background (blue), by the foster dam environment (green), by both (red), or not impacted by any of these factors (purple). The squares indicate the OTUs that are directly related to a least one of the zootechnical parameters across the three batches.

Furthermore, several OTUs were significantly linked to at least one of the zootechnical parameters (Figure 27). For instance, the genera *Butyrivibrio* counted two OTUs linked to residual feed intake, but only one of them was also linked to feed conversion ratio. Interestingly both OTUs were affected by the foster dam environment and by the kit genetics, which suggests that several driving forces interplayed.

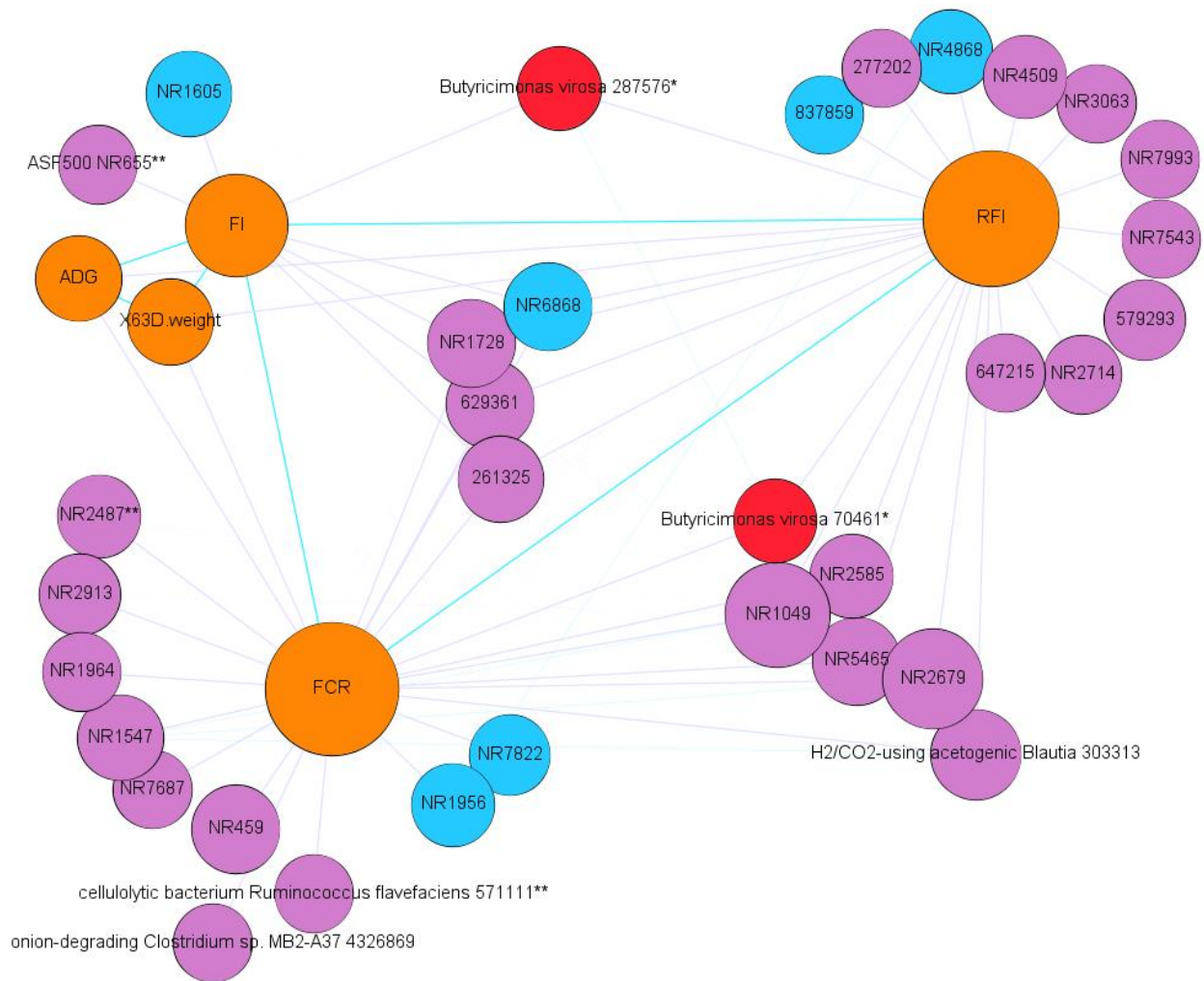


Figure 27. Significant linear (blue) and other (gray) associations between OTUs and the performances across the three batches; FCR (feed conversion rate), RFI (residual feed intake), FI (feed Intake), ADG (average daily gain), and weight of the rabbits at 63 days (X63D.weight). The numbers refer to the OTU ID. The OTUs that are significantly impacted by the kit genetics are in blue circles. The OTUs impacted by the kit genetics and the foster dam environment are in red circles. The unimpacted OTUs are in purple circles. The \* and \*\* refer Ruminococcaceae and Porphyromonadaceae families, respectively.

## INRA PIGS

The prediction of feed efficiency defined as the ratio of weight gain to feed intake was evaluated in 150 castrated male and female Piétrain x (Large White x Landrace) pigs.

Two methods to predict a performance trait using microbiota information were explored: sparse partial least square regression (sPLS) and random forest regression (RF). We will present the results of the prediction of feed efficiency. However, the results were very similar for the other production traits. The basic dataset contained a microbiota abundance table with 13,321 OTUs in 150 samples, and the feed efficiency associated to each sample.

For sPLS regression, the following pipeline was followed:

- From the basic dataset, 70% of the samples were randomly chosen to constitute the learning dataset. The remaining 30% of the samples constituted the validation dataset.
- A sPLS regression was applied on the learning dataset. The first step of this analysis was to apply a lasso penalization to select the OTUs that contributed most to a good prediction of feed efficiency. In our case, we used a minimum of five OTU. Using the selected OTUs, a prediction model was created. Linear regression was applied to compare the predicted feed efficiency to the real data and the resulting  $R^2$  was extracted (called  $R^2$  learning).
- The prediction model was used to predict feed efficiency from the microbiota information in the validation dataset. Linear regression was applied to compare the predicted feed efficiency to the real data and the resulting  $R^2$  was extracted (called  $R^2$  validation).
- The three previous steps were repeated 100 times and the  $R^2$  learning and  $R^2$  validation from the 100 iterations were averaged.

A sPLS regression was not able to improve the prediction compared to PLS regression (with no OTU selection), meaning that no OTU was significant. The  $R^2$  validation was close to 0 and revealed an important overfitting (Table 9, Figure 28).

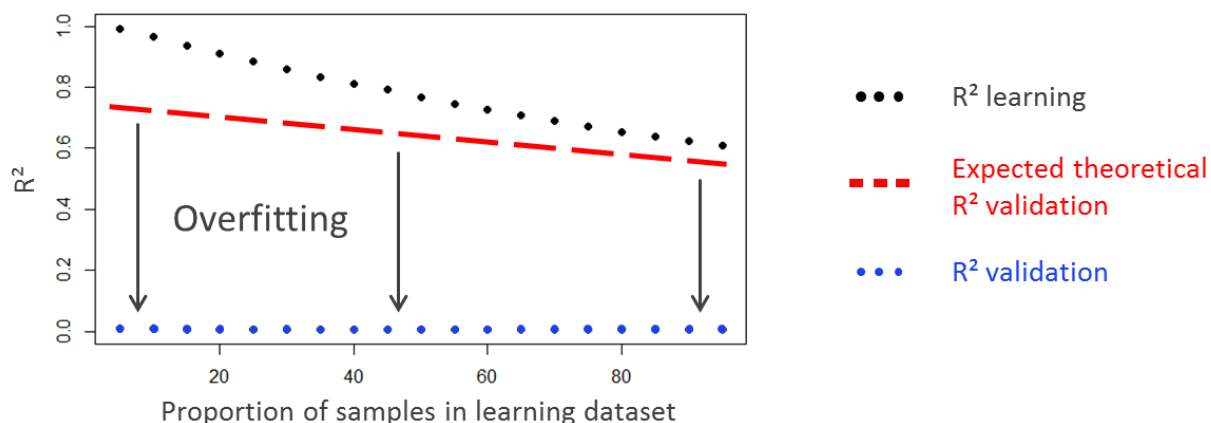


Figure 28.  $R^2$  from linear models comparing the observed and fitted feed efficiency from PLS regression models. PLS regression models were based on the OTU table. The X-axis represents the proportion of samples randomly chosen to constitute the learning dataset. The remaining samples constitute the validation dataset.

Table 9. Average  $R^2$  resulting from performance trait predictions using PLS regression in learning and validation datasets

Trait	$R^2$ learning	$R^2$ validation
Average daily gain	0.66	0.08
Average daily feed intake	0.70	0.02
Feed efficiency	0.67	0.01

Changing the number of samples in the learning dataset, it seemed that for one sample, a “perfect” model could be built but it was not possible to generalize this model. In any case, the  $R^2$  validation remained close to zero.

To test if the sPLS or the RF could extract OTU information to predict a phenotype from interesting relationship between some OTUs and the studied phenotype, we simulated several OTUs data correlated with feed efficiency. First, we used an already existing OTU from the basic dataset, which followed a negative binomial distribution. We reorganized the abundance of this OTU across samples to fit a specific correlation with feed efficiency. Doing so, we created 10 OTUs with Pearson correlations with feed efficiency ranging from 0 to 0.94 (Figure 29). These artificial OTUs were added to the basic dataset. The same pipeline as previously described was then applied.

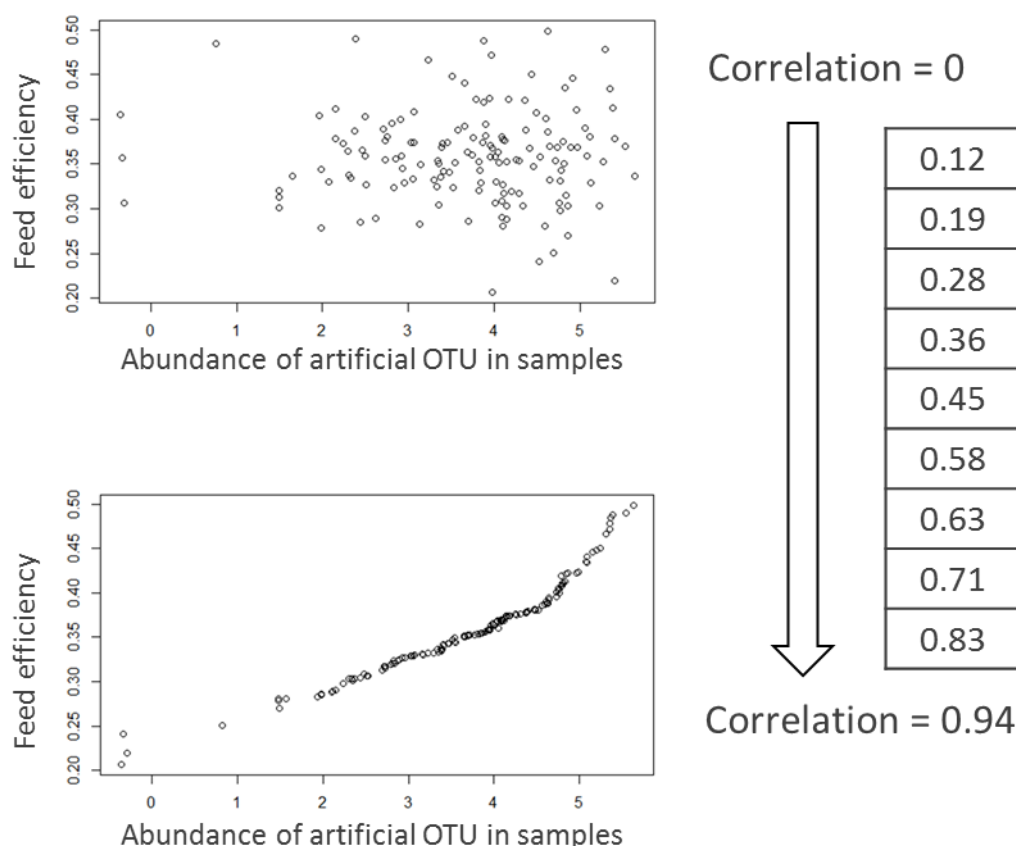


Figure 29. Abundance of the artificial OTUs reorganized to fit a specific correlation with feed efficiency. The correlations ranged from 0 to 0.94.

The  $R^2$  validation almost reached the same value as the  $R^2$  learning, as expected in case of a good prediction (Figure 30). The selected OTU was the one with a correlation value above 0.2, corresponding to the maximum Pearson correlation found between OTU and feed efficiency in the basic dataset.

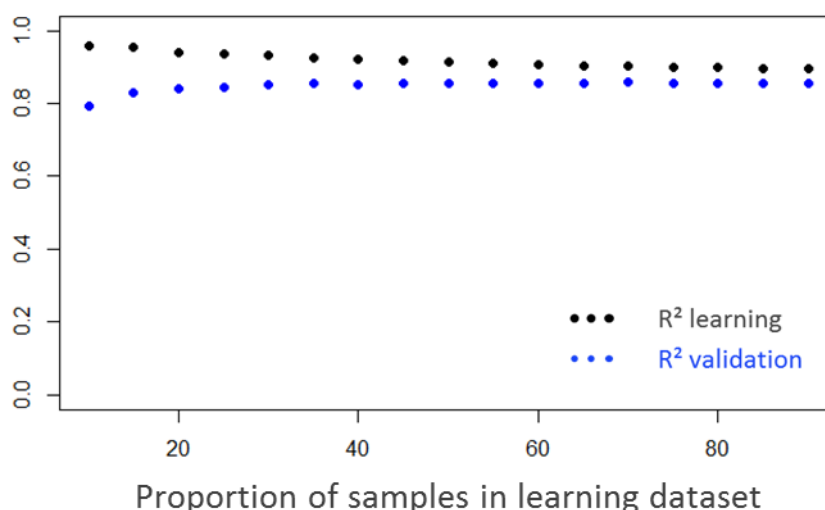


Figure 30:  $R^2$  from linear models comparing the observed and fitted feed efficiency from sPLS regression models. sPLS regression models were based on the OTU table including the artificial OTU. The X-axis represents the proportion of samples randomly chosen to constitute the learning dataset. The remaining samples constitute the validation dataset.

### 3.4 Mixed linear model models to estimate jointly host genetic effects and microbiota effect on growth and feed efficiency traits

The IRTA rabbit data set was used to predict phenotypic traits involved in the definition of feed efficiency. We conducted our assessment using two methodologies: classical linear mixed models and sPLS.

#### LINEAR MIXED MODELS.

Linear mixed models were used to assess predictive ability of models fitting additive genetic (heritability) and gut microbial composition effects on growth, feed intake, and feed conversion ratio (FCR). Growth was recorded individually under restricted and under *ad libitum* feeding, feed intake and feed conversion ratio refer to cage averages. For traits recorded at the cage level, mixed models were used assuming that all animals within the cage equally contributed to the cage average (Piles and Sanchez, 2019, under revision).

Mixed models fitting microbial composition considered the beta-diversity information to define a covariance or correlation matrix between animals. This allowed to extract the variance of the trait of interest explained by the microbial communities, by comparing the resemblance between animals with regard to their microbial composition and their performance. In our case, we used the Weighted Unifrac distance matrix to define the covariance between animals. In the experimental design, 2-3 animals per cage were sampled for gut microbial composition. The covariance matrices were expanded for animals not having microbial composition by including ones to the matrix diagonal and zeros outside the diagonal. It is then possible to explain entirely a cage performance, considering predictions for animals with and without microbial information.

To evaluate the improvement in predictive ability by fitting the gut microbial composition in the linear mixed models, results from two models are presented, one fitting with gut microbial composition and another one without this effect. The quality of the prediction was evaluated based on the parameters (intercept, slopes, and  $R^2$ ) of the regression of the observed traits on their predictions in the validation set, obtained from mixed model parameters obtained from the training set. The analyses of growth traits were conducted first by including all the data



available (i.e., from animals with and without gut microbial composition information) and then by considering only the data from animal with microbial composition.

For the cross validation assessment, the data was split into training and validation sets in two different ways depending on it concerned individual or cage records. In the first case, data for one animal was left out in 50% of the cages in each validation replicate. Approximately 100 records were considered for validation for both growth under feed restriction and under *ad libitum* feeding. In the case of cage records, data for 20% of the cages within the batch were left out in each validation replicate, thus approximately 20 records were included in the validation sets. Twenty replicates were run and results were summarized as means and standard deviations across replicates. In addition to prediction of performance (Tables 10 and 11) averages across replicates of variance components estimates in the training sets are also given (Table 11).

*Table 10. Parameters of the regression of the observed traits on their predictions in the validation sets. Mean (standard deviation) across 20 replicates. All available data were used, i.e., from animals with and without gut microbial composition.*

	ADG (ad libitum)	ADG (restricted)	Feed intake* (ad libitum)	FCR* (ad libitum)
<b>Model with fitting gut microbial composition</b>				
Intercept	9.42 (14.09)	3.67 (5.66)	152.48 (2.82)	0.40 (0.46)
Slope	0.83 (0.26)	0.9 (0.15)	1.14 (1.46)	0.86 (0.16)
R <sup>2</sup>	0.17 (0.06)	0.20 (0.07)	0.08 (0.09)	0.49 (0.15)
<b>Model without fitting gut microbial composition</b>				
Intercept	9.97 (14.34)	3.28 (6.74)	152.38 (2.7)	0.62 (0.57)
Slope	0.82 (0.26)	0.91 (0.18)	0.32 (1.22)	0.78 (0.2)
R <sup>2</sup>	0.19 (0.08)	0.20 (0.07)	0.05 (0.05)	0.41 (0.19)

\*Cage average predictions.

*Table 11. Parameters of the regression of the observed traits on their predictions in the validation sets. Mean (standard deviation) across 20 replicates. Only data from animals with gut microbial composition were used.*

	ADG (ad libitum)	ADG (restricted)
<b>Model with fitting gut microbial composition</b>		
Intercept	26.38 (16.65)	9.26 (9.6)
Slope	0.52 (0.31)	0.75 (0.27)
R <sup>2</sup>	0.07 (0.05)	0.16 (0.1)
<b>Model without fitting gut microbial composition</b>		
Intercept	24.56 (16.27)	9.64 (9.56)
Slope	0.55 (0.29)	0.74 (0.27)
R <sup>2</sup>	0.06 (0.04)	0.15 (0.1)

Given the uncertainty across replicates, including the gut microbial composition did not clearly improve the predictive ability of the models, even though the gut microbiota explained a large percentage of the phenotypic variation of the traits (Tables 12 and 13). The traits with the greatest improvement in the prediction ability considering bacterial composition were those recorded at the cage level. The R<sup>2</sup> increased from 0.05 to 0.08 for *ad libitum* feed intake and from 0.41 to 0.49 for the feed conversion ratio. Using all available data, no improvement in the prediction of ADG was observed by using the gut microbial composition. When only records

from animals with gut microbial composition were used, a very slight improvement in the predictive ability was observed.

*Table 12. Estimated variance components across 20 training replicates – mean (standard deviation)-. All the available data were used (i.e., from animals with and without gut microbial composition).*

	ADG (ad libitum)	ADG (restricted)	Feed intake (ad libitum)	FCR (ad libitum)
<b>Model with fitting gut microbial composition</b>				
Cage	2.78 (1.29)	0.02 (0)	--	--
Litter	4.38 (3.01)	9.17 (1.92)	15.27 (14.37)	0.02 (0.02)
Additive	10.23 (2.77)	3.02 (0.92)	81.63(16.04)	0.05 (0.02)
Bacteria	55.11(5.85)	38.2 (2.94)	101.26 (34.4)	0.12 (0.03)
Residual	16.36(4.21)	12.56 (2.46)	0.24 (0.16)	0 (0)
<b>Model without fitting gut microbial composition</b>				
Cage	3.34 (1.11)	0.01 (0)	--	--
Litter	7.29 (3.17)	7.69(1.59)	31.12 (28.61)	0.04 (0.04)
Additive	9.7 (2.34)	1.9 (0.83)	98.48( 27.08)	0.06 (0.04)
Bacteria	--	--	--	--
Residual	58.74 (2.93)	45.68 (2.1)	8 (5.66)	0.01 (0.01)

*Table 13; Estimated variance components across 20 training replicates – mean (standard deviation)-. Only data from animals with gut microbial composition were used.*

	ADG (ad libitum)	ADG (restricted)
<b>Model with fitting gut microbial composition</b>		
Cage	0.91 (1.62)	2.06 (1.57)
Litter	0.83 (1.66)	8.45 (4.28)
Additive	6.41 (3.62)	4.1 (3.79)
Bacterias	30.97 (11.41)	1.72 (1.37)
Residual	20.65 (5.32)	14.13 (3.29)
<b>Model without fitting gut microbial composition</b>		
Cage	1.58 (3.02)	2.17 (1.55)
Litter	1.08 (2)	8.13 (4.12)
Additive	6.75 (3.86)	4.21 (3.78)
Bacterias	--	--
Residual	28.86 (6.08)	14.66 (3.15)

The following conclusions and implications can be drawn from these results:

1. The overall role of gut microbiota in predicting performance using mixed models is limited, but it explains a large proportion of the phenotypic variance. The estimated bacterial variance is an artefact, most likely associated to the way the resemblance between individuals due to gut microbial composition is defined.
2. Despite that data on the gut microbiota was not available for all animals in a cage, the consideration of this effect for cage records seems to improve the prediction quality to a larger extent than when individual growth records are considered, particularly for FCR.

3. Further research is needed for exploring alternative ways for fitting the covariance between animals with regard to the composition of the gut microbiota. For animals not having such information, average data of cage mates can be used.

### **SPARSE PARTIAL LEAST SQUARES REGRESSION**

This analysis was only applied to traits recorded individually, i.e., ADG in *ad libitum* and restricted situations, and considering animals having data on the composition of the gut microbiota. The sPLS was applied to the residuals from a linear model fitting the experimental treatment to which the animals were submitted. The experimental treatment was defined by the combination of batch and farm (five levels), presence or absence of antibiotics in the diet, and size of cage in which the animals were raised (i.e., large or small). The predictors used in the sPLS regression were all available ASVs, after normalization and removing ASVs with low percentage of presence in our samples (see section 3.1)

The cross validation assessment was done using a 10-fold cross validation design: the data set was randomly divided in 10 subsets, leaving out one subset for validation in each replicate. Table 14 presents means across the 10 replicates for the regression parameters (i.e., intercept, slope, and  $R^2$ ) of the observed records in the validation data set on their prediction, obtained by applying sPLS parameters obtained with the training set. Mean squared error and correlation coefficient between observed and predicted records are also given.

*Table 14. Regression parameters, mean squared error (MSE), and correlation coefficient (rho) between observed and sPLS predicted records. Means across 10 cross validation replicates.*

Trait	Intercept	Slope	$R^2$	MSE	rho
ADG (ad libitum)	-0.074	-0.008	0.031	35.33	-0.003
ADG (restricted)	0.077	0.083	0.036	35.46	0.03

From these results, it is concluded that ASVs from the gut microbial composition cannot be used to predict the individual growth under *ad libitum* or restricted feeding. This result is in line with the low value attributed to the weighted Unifrac distance matrix to improve the predictive ability of mixed models in the previous section for predicting growth and feed efficiency traits. As in the study conducted with pigs in INRA, a problem of overfitting might happen. Alternative prediction tools based on multivariate methods and using ASVs as direct predictors should be explored.

## **4. Conclusions**

The deliverable D5.1 gives a number of methods and results to answer the question “How to use the gut microbiota to improve feed efficiency?”:

1. The microbial composition, diversity and richness of gut microbiota were characterized by means of Illumina sequencing of 16S rRNA gene amplicons (V4-V5 hypervariable regions). Filtered sequences were assembled into contigs and then clustered into OTUs (Operational Taxonomic Units).
2. Several statistical methods were used to analyse the microbiota data (OTUs abundance table):
  - Principal Component Analysis
  - sparse Partial Least Squares - Discriminant Analysis (sPLS-DA)
  - Linear mixed models
3. Kruskal-Wallis tests, glm methodologies, or generalized Friedman rank sum tests with replicated blocked were used with success to point out OTUs with significant abundance



differences between conditions (i.e., sex, temperature, diet, maternal effect, genetic line effect)

4. Prediction of growth and feed efficiency traits from microbiota data were evaluated using the Partial Least Square Regression method. The microbial data could explain the feed conversion ratio, feed intake, and the residual feed intake with significant correlations in rabbits, but the prediction of phenotype was not so good in pigs.
5. Genetic determinism of microbiota composition has been assessed in rabbits using animal linear mixed models and QTL analyses. The genetic parameters and a number of significant signals detected for these OTU validated a host control of fractions of the gut microbiota in the rabbit, suggesting a possible selection of the abundance of some OTUs. The association studies showed some significant signals, confirmed across different OTU or with very low *P*-values. However, the sequence draft for rabbits is still ongoing, and 23,900 SNP (15%) retained for the analyses did not have a location on a chromosome yet. Similarly, the annotation of the rabbit sequence is relatively poor compared to other species, and in most detected regions no gene could be identified as putative candidate for the genetic control of the gut microbiota.

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## 5. Annexes

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## Annex 1. ASVs differentially represented between IRTA rabbits raised in two different farms.

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
003d72ccee9466e7e26f64c621af78a1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	1.77	0.18	0.00
016d51b738ee5237bab773cc5fe72412	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-2.32	0.37	0.00
01e9fe66416dc5432c63790cf02f38f6	Bacteria	Tenericutes	RF3	ML615J-28	#N/A	#N/A	#N/A	1.42	0.26	0.00
02b6e652f5e9730671be77c9cd3d57b2	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.86	0.18	0.00
0311b959548e90b28d720b302f3aed8b	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.65	0.17	0.00
0475aa7f2f1c57b921140c71aec02590	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.30	0.17	0.00
049fb8b9352fc4d009a025d1321d80ea	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.93	0.22	0.00
04ba14daf75ec53f30a0ac080517042d	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.37	0.14	0.02
082b159b855614efcb0a8db5b2d6ba4b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.58	0.22	0.02
0a01f7ecb5617788cd2a97fa3275063	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-3.85	0.40	0.00
0a6e302c0cadd43290416c19ba1452f8	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.52	0.27	0.00
0b62fa48425f3f630e10bbacd956830d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.88	0.31	0.00
0b9c3393cffece2ab2de88da17c196e	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.43	0.16	0.01
0bba0a010fd937112e8023c5e2c3ccaf	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.73	0.17	0.00
0c1debf864bf67772875c2f639cd2f68	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.53	0.12	0.00
0c64ff0c04694bd3441f1b8e5ee3f953	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-0.38	0.12	0.01
0cfff5a5924c01c11d393f3f21f61a247	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.18	0.28	0.00
0d9a738985cd40dddde9b7249fb49a97	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.50	0.14	0.00
0de773e9d077346bf5b3d348e31f673c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.76	0.13	0.00
0e375a6cbdc00451e926e07a9c7d7472	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.50	0.19	0.00
0ecddb2c30cf00313615308b9f72eb42	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-1.18	0.32	0.00
0f0ce833b8c3049fc0ae4251ed4b339	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	0.63	0.12	0.00
0fccbf53dc7fe57aaf7078ebc82fe27	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.38	0.15	0.02
10f839faa1d022e9feb7d8c899fe8b36	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.49	0.17	0.02
1105984	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	1.23	0.15	0.00
1106281	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	3.06	0.20	0.00
1108377	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	0.53	0.20	0.02
1110218	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.65	0.16	0.00
112931	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.38	0.34	0.00
113430	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	#N/A	0.42	0.15	0.02
116a4249678cb341f95d688c6280fef6	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.78	0.18	0.00
123165	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	3.93	0.29	0.00
124470	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Butyrivibrio	#N/A	2.14	0.17	0.00
1266bc5f057ae1859c44d62d3971f605	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.59	0.16	0.00
1277410e6ed74713099e6ab15026472b	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	flavifaciens	0.63	0.21	0.01
12a8ebd6fa4461b1202bf8a2eae841e1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.74	0.14	0.00
1317a9ff3431d5f1aed67061bd826c60	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	-1.03	0.21	0.00
14978fff3725e6c91043cd5d38eac085	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.93	0.28	0.01
14a240918f268328aabc4d711ed4169e	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenella	#N/A	-1.86	0.37	0.00
152014	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.32	0.19	0.00
155e4fec1151794fab6ad4ddc2e03504	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	Allobaculum	#N/A	1.65	0.36	0.00
166515	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	-1.16	0.24	0.00
166758	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.12	0.23	0.00
1679e596a40f1e12ffb70b9bebecea1f	Bacteria	Proteobacteria	Alphaproteobacteria	#N/A	#N/A	#N/A	#N/A	-1.05	0.24	0.00
177697	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.81	0.12	0.00
185420	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes	#N/A	-0.45	0.18	0.03



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ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
1877cc7bf5884b2c317a12131cc195d6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.30	0.10	0.01
188348	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.44	0.16	0.02
189f08563b118f8c05337aea124847cd	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenella	#N/A	-1.74	0.36	0.00
198403	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	2.39	0.22	0.00
19912527246badfe490329d00348136f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	1.49	0.30	0.00
19b84a007e31c1e23bb6a34847e782f1	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.64	0.28	0.05
1a24d314db828f75738d5ace26a8181d	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	#N/A	#N/A	-1.65	0.32	0.00
1a601a15ec969198ba86fba775e37518	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.84	0.25	0.00
1c45d88f6d167268e3efe687cfc58de9	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.15	0.32	0.00
1cd9b4d74e0f4190870f668c4f5b7a1c	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	rc4-4	#N/A	0.93	0.21	0.00
1d1bf8c50b6e61ccf78d8fc7be586056	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.40	0.19	0.00
1d2e10232746907562e636e6767816db	Bacteria	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	Anaeroplasma	#N/A	-1.73	0.37	0.00
1d92f1c3e7d69ec0a7d78aff6d9689f4	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-0.60	0.19	0.01
1f28478b96cf91f24f1cb490ea628519	Bacteria	Proteobacteria	Alphaproteobacteria	RF32	#N/A	#N/A	#N/A	-0.28	0.11	0.04
1f28d31fb04f7c61eb54421c63ded634	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenella	#N/A	1.57	0.15	0.00
200ea7a9859b3b03db95d20e01e29ca9	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.50	0.08	0.00
203594	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.87	0.23	0.00
204155	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.87	0.21	0.00
205179	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	flavefaciens	3.65	0.22	0.00
2055681	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Odoribacter	#N/A	2.52	0.30	0.00
205659	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-3.06	0.37	0.00
205846	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.68	0.33	0.00
205940	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.47	0.15	0.00
207532	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-0.61	0.23	0.02
207770	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-1.74	0.36	0.00
208042	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.99	0.35	0.00
208769	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.00	0.20	0.00
209492	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.82	0.37	0.00
209524	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	1.75	0.36	0.00
20d045864910735387e04d13e3a81afd	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.82	0.18	0.00
210361	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.85	0.13	0.00
210945	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	2.13	0.23	0.00
211066	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.63	0.38	0.00
211388	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.68	0.12	0.00
213084	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.08	0.34	0.00
214315	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	0.99	0.36	0.01
214519	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.77	0.33	0.04
216140	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.77	0.31	0.00
216557	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.09	0.32	0.00
2168b6a2e36ccd30437ed3a300e5e6d9	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.61	0.27	0.03
216941	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-1.00	0.28	0.00
21b8a05bbcad645a7961f4b361603a2b	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-0.55	0.17	0.01
234488	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-0.46	0.15	0.01
241805526e79f46563052cbf47ec0c85	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.34	0.11	0.01
24cc0d65e267ce8b572d0ee049abed37	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.77	0.26	0.00
269360	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.48	0.19	0.02
2716517c86dc8303e296dd7e8411646d	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.55	0.19	0.01
279579	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-0.48	0.18	0.01



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ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
2807528	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis	0.82	0.19	0.00
284123	Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacteriales	Campylobacteraceae	Campylobacter	#N/A	-0.43	0.14	0.02
286d5872c51e09b64f91398716101b2e	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.51	0.24	0.00
288312	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.53	0.34	0.00
288588	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.68	0.29	0.03
288843	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	#N/A	#N/A	-5.72	0.36	0.00
289001	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-2.16	0.43	0.00
289306	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.36	0.21	0.00
28988df903864c8724d52de9c3a305b9	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.23	0.09	0.03
290079	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.39	0.27	0.00
291348	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	2.69	0.34	0.00
292377	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	flavefaciens	-1.36	0.35	0.00
293101	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.95	0.28	0.00
296062	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.40	0.16	0.00
297503	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.00	0.22	0.00
299422	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-1.35	0.29	0.00
299902	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.82	0.25	0.00
29d0ec9dfbfa4bf0c01cc6c4e5f14521	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.92	0.30	0.01
29f3702f5a607f1b576c6d8c3d5d3acb	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	#N/A	#N/A	-2.46	0.34	0.00
2b283f3a84856e080209ede19927da83	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	#N/A	#N/A	0.41	0.15	0.01
2b4e18795750cff0347a4c511eed8412	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	-0.63	0.23	0.00
2d92f82b06962217ec1874862450ba0b	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.88	0.21	0.00
2ddc66968a23b8b4b1b5a440a21096e3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.64	0.13	0.00
2de1f0c6db5504a089f8652950453e90	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.56	0.14	0.00
2e6c4e8a91800f9be22b89b87b637ab6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	[Ruminococcus]	gnavus	2.89	0.23	0.00
2efe1cf8476e17eb1daf01741f72ce3b	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.67	0.29	0.03
2ff369e928d2b4116475775d9037d25d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.46	0.16	0.02
30d40171d0fe83669491429c7e2de36f	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Phascolarctobacterium	#N/A	-0.65	0.22	0.01
314542	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.55	0.12	0.00
316539	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.69	0.17	0.00
316761	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	eggerthii	-0.64	0.21	0.01
3168538	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	#N/A	-1.91	0.34	0.00
319501	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	muciniphila	1.61	0.27	0.00
319983	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	fragilis	2.64	0.20	0.00
3211e121c4202e461c0cc75f23c4158c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.97	0.35	0.02
326209e4a4a460ec2bfdbabf346a1132	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	#N/A	#N/A	1.79	0.35	0.00
332242b8bf154b5b531438e80e663479	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	#N/A	#N/A	1.14	0.13	0.00
332490	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.77	0.32	0.03
332732	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-0.69	0.21	0.00
336012	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis	1.19	0.26	0.00
338091	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis	-2.38	0.34	0.00
345591	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.45	0.19	0.03
347791	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.28	0.12	0.03
349019	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.47	0.17	0.02
350438	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.61	0.39	0.00
351253	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.67	0.26	0.02
351272	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-4.15	0.40	0.00
353782	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-1.84	0.32	0.00





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ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
3540202b17a98bf508fcb2e628626f60	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	3.34	0.34	0.00
355ba91627ebf3aa2f5fe6cd0abcd7f2	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.72	0.25	0.01
361927	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	#N/A	#N/A	0.88	0.27	0.00
3653528a04f8b557d870429fa7815665	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.60	0.30	0.00
38b035c95e46923237b6a317cbce9d6b	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.43	0.21	0.00
38ef267340142e6f2e12889beb2e87d5	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.41	0.11	0.00
393026	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-0.66	0.26	0.02
39608795e9813d65d281896881a1e6cc	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.46	0.15	0.00
39c47e25e1b361216accb794a0461afe	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	0.90	0.12	0.00
39cf35f83e8f7c9107db7891d0ec1a4d	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Olsenella	#N/A	1.39	0.28	0.00
3a1755b31d7d164b7a5ff8d9e61e0d4f	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.04	0.29	0.00
3adcaf18972a0a7863a6a29e87201e0c	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	0.77	0.22	0.01
3b24accfa2f506d0211379bdb35d9a72	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.73	0.11	0.00
3d1954592e8e5ad84dc38f5b1424a877	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.81	0.25	0.00
3d2ec70b7f63321e94bfde5747cab90e	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.98	0.21	0.00
3d67540b6ad1442f877109c73a53815d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.59	0.21	0.01
3ea53f6a1603d26a0cb7c51231163b08	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.38	0.08	0.00
3eecd6669fc72dc703079b1b8c8346b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.76	0.30	0.03
3facd4fb20ec1f1f76c37ee5248d1382	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.68	0.15	0.00
3fcc72e0ba4cfa7e03fe92449527240	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	3.14	0.34	0.00
414600	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.42	0.11	0.00
41af26e77e10d9d22b146d196b3ea629	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.82	0.14	0.00
425567dcb2c4bc081d3113fc79ab17e1	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	3.32	0.33	0.00
42be02a3f634c30003c46aa6483f25da	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.31	0.16	0.00
4312024	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-1.12	0.26	0.00
4326741	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	#N/A	#N/A	0.49	0.17	0.01
4363611	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.96	0.29	0.00
4367058	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	ovatus	-0.42	0.17	0.01
43dbdc9be7ad64560f01abfe58fc10ed	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-1.11	0.27	0.00
4433835	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes	finegoldii	0.91	0.28	0.00
44f74ec7622e77a91cd95ce225f4e961	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.20	0.27	0.00
45228224054458b73c236dccac82a8a0	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.38	0.31	0.00
459119	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.36	0.16	0.04
45f5e9507f1c2f85ce106aa2354caf65	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	-2.29	0.38	0.00
46ada1d0938f8511a10654721c5aee17	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.70	0.37	0.00
46c87e62f21c5aef16b821510fb173b3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium	colinum	0.54	0.20	0.02
470759	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Oxalobacter	formigenes	1.31	0.21	0.00
47a9e7ef576bd937053741bd77f7cb1b	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-0.36	0.12	0.00
47adb790951ac354b61cf4e4f7849317	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.93	0.13	0.00
485b88e5a30f16dbb209d6bbbfa4b96f	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.57	0.24	0.03
486d975a7886ae8e571e6d38e9016ce3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	2.04	0.31	0.00
48ec5578b74586a9f55a7adf9c99b461	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.87	0.32	0.02
4987510b691c55d53e3eb55c02edb593	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.47	0.12	0.00
4abe627e926dc5d052f1b69eae2a054c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.48	0.17	0.02
4b95bac7f4f4d483a4308801baa83bb9	Bacteria	Cyanobacteria	4C0d-2	YS2	#N/A	#N/A	#N/A	0.71	0.25	0.01
4c07dc3ed041a6ca52dca8e971d5cc67	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.82	0.17	0.00
4d1a92f0f7a097880d4b651cba436d82	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	#N/A	#N/A	1.53	0.20	0.00
4d454457a0107eb2125de7b530a85c3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.39	0.10	0.00



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ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
4eab629d7abca92319c5b100cec6ff	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-3.22	0.39	0.00
4f6a40f24d9e0c4303d7e3d92aac1426	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.29	0.34	0.00
4f703f3311911ff98dbc75d36fed337d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.05	0.18	0.00
4f72dc076d7559c4348cf13c8b93b53b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.23	0.28	0.00
503fa9178942c43113da6dd301b8419e	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.60	0.15	0.00
5499855d7be896610cb96d114ab7bc88	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.81	0.25	0.00
54c8e621f67be196da5650167ce0b5c2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.18	0.22	0.00
55d3217d966d55fcd2d00f61ec3a123b	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	#N/A	#N/A	0.83	0.28	0.01
55f25c838cbc8ae7bf77c0a6e89405e9	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	#N/A	-1.16	0.27	0.00
5648fa0559480ce3d6dbe0507c41c607	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.68	0.20	0.00
56db1df2bb07346db4ecaa8d735cd11c	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	0.23	0.09	0.03
577377	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-1.02	0.29	0.00
57851b41499921c5e98cfe48e934b8b5	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.35	0.12	0.01
589b530cbce0c1a06114517a44e57eff	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.00	0.29	0.01
58ed357e8356d6669c5f2cd20f2bee25	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.67	0.25	0.02
58f8b67aa1532da283ec0121d36545c7	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.75	0.19	0.00
5a6a45192e168c1e5d912f809edee0bc	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	0.33	0.14	0.03
5ad48b8a3ab12b95b147112d2d7a0068	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.99	0.10	0.00
5b774b7989796b302aee4a59964475f6	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.77	0.32	0.00
5c85ac5cb7260872579259a70e2d4977	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes	#N/A	0.31	0.11	0.02
5ca212b05cbe7ece0258768461fcd8b8	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.31	0.07	0.00
5d56a4aed325f2bd59fc53301087e707	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.98	0.19	0.00
5d67a5ad2a7ef4a2974fc6d135eebac7	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.07	0.34	0.01
5d73adc9bed1d0c0c7614ddc39c9a7ac	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.44	0.13	0.00
5d9e82657c453d7a717686f76088e5b9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.36	0.14	0.02
5edb14ba5c7f64f3108d4706a4e02961	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.70	0.20	0.00
603a631aba956ea96ca45b548144b73f	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.81	0.14	0.00
6042e7545fe73e275dd65f5fe9e7c63d	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	#N/A	#N/A	-1.93	0.31	0.00
6165e3ecaf7015e731e571e40931bc6b	Bacteria	Tenericutes	RF3	ML615J-28	#N/A	#N/A	#N/A	2.14	0.26	0.00
625ad8a3c63003137e565498eb4143c0	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.80	0.31	0.02
629c66a950b5426b15a55f01a7469a70	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	#N/A	-1.80	0.32	0.00
62aba018bf6a40ec8371b3e40d192d2e	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.36	0.16	0.04
630247b36298541addb4c53bccdf5e6f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.38	0.17	0.04
630bcf9e33770d7cb690063bf8bf46b9	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	-0.99	0.30	0.00
63ac6fad66f0e8f96f45387999702f5	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	#N/A	-2.08	0.34	0.00
63cb437dbcbae05bef94ef0130c26738	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.40	0.29	0.00
6598c5e1aad22c07b30ac207cfe8a337	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.74	0.26	0.01
6658a8116aee26c190cf39f693e66c76	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.07	0.35	0.01
6660599f80a52bca7d22bc09faef740c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.25	0.29	0.00
66c6ed6d8dc722ff6448f363b9b2500f	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.54	0.17	0.01
67006f927b3e8c62d8634b2c239c3e3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.63	0.16	0.00
67790098d958208fd35038b1692aa8a5	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.63	0.12	0.00
68532b6a6cbbf1f28467efa280f71d2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	1.41	0.27	0.00
69033f5c84d4790f5eb992f639b92bc6	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.33	0.25	0.00
69b20e6fbba506a7244da805a315661	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.11	0.16	0.00
6a47937f1a5d4fc5350f199dd1b1a267	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.89	0.16	0.00
6bc3986027185dba9ed398b0383034	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.53	0.15	0.00
6c98f4ed8734b5486b06c75dddab7a37	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-1.56	0.31	0.00



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ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
6d5a1c02cbc558dc39368de6e2ada7f3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Epulopiscium	#N/A	-1.80	0.24	0.00
6e76bbcf16e68f093fd66693c64afc	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.33	0.12	0.02
6f909158dd6836dce91a118787937999	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	#N/A	#N/A	-0.23	0.09	0.02
6fd44623fc004d0a58312ecb7a787eb7	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-0.32	0.14	0.03
705b9cd95aefd0e56d7d82569de4c92b	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	#N/A	#N/A	#N/A	2.42	0.37	0.00
723ee11afb5a2f467d2a44e0473e589b	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-0.98	0.24	0.00
729e2aa43be34f3c94fdbbe8ed1d904f6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	0.56	0.16	0.00
72d723d6b5ee9912910d8f52d8b60937	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.87	0.25	0.00
7319c52ba072b339e9d79c845edce85a	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.32	0.11	0.01
76c4217512b296dd44cacb0fc596bf8f	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.33	0.36	0.00
775d50162d645cabb41195d0b0c1767a	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.41	0.10	0.00
78229d778767ae446f70342a95beca34	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.89	0.14	0.00
782367e5eb1f28f3af4bcb4299002b73	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.46	0.11	0.00
78e48559f94152923a2366eb159f2c3d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.48	0.11	0.00
7998bf806cad9bfa40eb40df7f2a7d65	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.69	0.14	0.00
79fda4085857688dda11f0887d1583a9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.55	0.21	0.02
7aad2a3ebdb24d25d204a53b4f117678	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.13	0.19	0.00
7aad8737d547e2b8fa89aebc725d74d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.68	0.11	0.00
7db7e7242b194d1de87e013cff637c7b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.33	0.14	0.04
7de7d3737a9fde98f1ba02a7e074f300	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.28	0.11	0.02
7e5fa0e711068fbef113c3aef3061853	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	#N/A	#N/A	-0.42	0.16	0.02
7ef61e66ab37cbe16abca1f7ca866d50	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.02	0.18	0.00
7ef7236763779da18ae99afa255bb742	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.21	0.06	0.00
7f7ccb576990ba2d0e4d1848131bcb4f	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	0.70	0.28	0.03
7fc0dbd5aefde956b3cd2f882ca14f39	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.71	0.38	0.00
7fe5031a7e0f0d8308cb38ce3f2cd31	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.07	0.25	0.00
803a1277a8033516a6904c0cb61f1b92	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	eutactus	-0.64	0.16	0.00
80db2c34688b90e5d60a77f072264441	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.30	0.13	0.04
82217e9b84479e7700f23731634ffc97	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.95	0.22	0.00
8239e098214fb2f0fd47eda3273d1b9f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.82	0.39	0.00
825939	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.36	0.14	0.02
82882322124d5e4a9d44be664ef5d2db	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.33	0.12	0.01
830095	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	flavefaciens	0.84	0.28	0.02
834ab329e414a875075cb44e0c16b8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	3.30	0.24	0.00
839714	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteriaceae]	Butyricimonas	#N/A	-0.43	0.18	0.02
84a38b949b31fceb532bf177d0e56e9b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.55	0.10	0.00
851323	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	#N/A	-1.12	0.27	0.00
8569d48e8c338f867ac84564741bf1ae	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.68	0.22	0.00
86261bd146905aa7c456de8d9ad52cd1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	-0.64	0.30	0.05
86f454ed8f071ea49a72572e9bd05857	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.46	0.18	0.00
874486e318277dbaeb83cb46dfb52c214	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.14	0.15	0.00
8786c4844d9015f8677c54cebe2fa827	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-0.61	0.18	0.00
8792e1f740d6bfb21a13b4d9ed456b4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.01	0.33	0.01
88602bff4c92ff31b36070af0141e77d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.78	0.20	0.00
886a3eb722d0a2f7cada3cd26f18385f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.49	0.12	0.00
886b80a6f1dda4bab907037eec03849e	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.00	0.10	0.00
88bb397cf72ef4b99e83b3a1d15e339	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	0.83	0.12	0.00
8af63aabbcca2f26f14af2555d689ae9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	2.77	0.44	0.00



# Feed-a-Gene – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
8b5f63d51b582e59ee23aa6fd9dbbfe	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.42	0.23	0.00
8bda1c93c5784284d381e9d4d9a52b96	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.80	0.14	0.00
8bec33f490e4bd5dea7a0e4f7623b67	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.49	0.15	0.00
8c476d729399d10d22a335c27094b6bb	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.23	0.14	0.00
8d79f0b06cd21406dec287ae909ca705	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.66	0.19	0.00
8e484fb9317fe9d54c9d80bb4a35f18e	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	#N/A	#N/A	-2.64	0.36	0.00
8e6c460e57c17d3ecbaf68db49cd877	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.51	0.16	0.00
8f6542fdb17730430b756314702d3f6d	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	0.26	0.10	0.03
8fe8eae00dfa556af3cd9e021c4ab2a3	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.48	0.19	0.00
9048e110e1bd72c6ef5cae66ee50b17a	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-1.43	0.37	0.00
90bef4f9a364c85c5297670aa8d4454f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.29	0.12	0.02
9298c20d5f5e39895c6ec8e63ea7d25f	Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Treponema	#N/A	-1.39	0.29	0.00
93132f2e14ae61bf73807cede91cea9b	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.59	0.26	0.00
931af3387edd5940184c02c72e4dc70c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.31	0.12	0.02
935d6e475097cf5381160f0c1b2e1f42	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.46	0.16	0.01
94f4401e9e4e653a33604df88c8a3db4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.87	0.32	0.01
9501ee854d39af8c937ad7747400ef12	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	#N/A	#N/A	-1.05	0.39	0.01
95479da3b5b6312c50e0b3a3b06c41b4	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.53	0.14	0.00
9678bf3c1d9a6a5e5355cabdb80ee1e	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.60	0.17	0.01
96d3f36f9ba11c509e0a2243794844eb	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.74	0.07	0.00
97fea4c9a75320679d5c1c121f41b965	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.13	0.19	0.00
981db9bada3bd5ae1a9818acf964a7c	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.49	0.17	0.00
983b82d11be5861dfbd8e3b0afa30d13	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-1.80	0.34	0.00
98bd98fa73affdb761fa0fe9fbd4bba	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.95	0.30	0.00
99cdb262295f53d04beef39f1342c900	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.75	0.20	0.00
9b3e5009f42ee2f2e3bc85a5b5ec1c6	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.36	0.35	0.00
9cf347e6ea35c0a76c57b6f7114d30f1	Bacteria	Tenericutes	RF3	ML615J-28	#N/A	#N/A	#N/A	1.96	0.24	0.00
9d4472ee0435227d69129ac6ca16755	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-5.45	0.37	0.00
9d64c0465809ff3e788ec138b15d1b61	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	4.00	0.19	0.00
9d7a54a493169084e4fd3bd577d17a4e	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.36	0.14	0.02
9e1d559fe7110a36ad29342c44f6c8f6	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.85	0.29	0.01
9e5ca071e831771e0374d643ab782022	Bacteria	Tenericutes	RF3	ML615J-28	#N/A	#N/A	#N/A	2.40	0.23	0.00
a1aa1c3f908f366ebf4f35c09f6686d0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	-1.12	0.27	0.00
a1dfda4d13c5344cf37a0d7b3f988d72	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.28	0.21	0.00
a2b053bea7137250d7d08c3bd2ad0536	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.36	0.14	0.02
a2fe19c86995cdc987b16b90390e0790	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.12	0.15	0.00
a63efa4dae934e67db98e98df62435f2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-0.57	0.22	0.02
a6e950733b59c867e52758df0e5c24d8	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	6.30	0.13	0.00
a87989189a3cf294e18a93c1a191d895	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.97	0.32	0.01
a8a4d698c5336c23c1f8896cdb8de19a	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.58	0.18	0.00
aa57b28eea7276af23616de0dfb25b94	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.20	0.08	0.03
aba56d55f8ccfaf9ecb354e6d4046697	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-0.78	0.21	0.00
ac0e35816e704f4f5094424b365763a6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	2.53	0.20	0.00
ac166c306a3f0ecd2a2d59c924cfd531	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.40	0.13	0.01
ad0821c79b0dd0bf61e6285ad8f2efd	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.70	0.26	0.01
ae49c777b36274f88051cc925b25e7b4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.71	0.11	0.00
ae4cae9a2714ed2bf98e6118cbda374b	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	2.75	0.28	0.00
af0cb7547bc6c818a18a20386dcbe5ba	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.62	0.14	0.00



# Feed-a-Gene – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
afec3e2cb9903918b816d80a1c4afb7	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	#N/A	#N/A	0.31	0.10	0.01
b0449bb97f1bd1ace6be503535bc7b0a	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	#N/A	#N/A	-0.77	0.18	0.00
b0f64a5e566d655dde65f0b9f5e8bf3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.35	0.10	0.01
b261977f5d01112021bd92e5fd52cda8	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.80	0.23	0.00
b309376c3d8d1c584d31cd3105d79c2c	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.43	0.15	0.01
b4578b2c8630d8794dfcbb7679285e8e	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	#N/A	#N/A	2.29	0.25	0.00
b474738c4d1dae36bab5a46be329ae02	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.75	0.12	0.00
b685825ca72e45ac545c505a236d2209	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	-0.24	0.09	0.04
b688e23af71caac86e4c9c979253ed6d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.38	0.16	0.03
b8037bb0a1f245a35bd7ac2498a9fed6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.48	0.21	0.00
b856e55c90bad6ec7c65f9579e83affe	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	0.56	0.11	0.00
b982c069d4b4109b6b29e830d14347b0	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.29	0.28	0.00
baa877a0f333560ade8f490b2a5f4bb9	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.31	0.12	0.02
bc6e719cf3b5b05f5829cebe8788f25d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.74	0.18	0.00
bcd20ebd9bfb1655755df6a7441d7b0e	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.48	0.19	0.02
bd905ec1f51d614a5a338102a5c4fbc	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.72	0.25	0.00
be5215fbd4721bfca5bac755b0c6eecd	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.52	0.21	0.03
bf40b5271c819a82fc856cda3988725e	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.98	0.27	0.00
bfd66c21aff9f5bfeaad234afc54cb90	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.50	0.19	0.02
bff73b94c7400104b28251efc43cff00	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.62	0.19	0.00
c1512b3c126ed8d5e08dd2fc6fbce5e0	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	#N/A	#N/A	0.48	0.10	0.00
c17e1096d1b9584c042740c961401b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.43	0.18	0.03
c1da07db83053cdf6029f4c2724b461	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.42	0.14	0.01
c3a6a71ed6065d3282123c1d956c478f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	1.24	0.22	0.00
c3c25cd3ec36c147ec6f89b081784b6c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.53	0.32	0.00
c52afc564f14189de25ee74bb73cadfd	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.56	0.14	0.01
c56c4900e586e7d4edac670b32f0d53f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.58	0.23	0.00
c5c63d11ea82f6c6a807c0c31012222b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.83	0.19	0.00
c5d744fe7789a092862da54db0a44687	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.55	0.25	0.00
c6204514aff8c70b184f5354793ee1	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	1.70	0.20	0.00
c6dbbf63d05241312aa50b7a5be6fe7c	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.82	0.10	0.00
c80018f3d573963b9727e69ca17f9164	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.34	0.06	0.00
c838493a8603213a86019c9b6eddd39a	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.40	0.26	0.00
c8eb15b8c729cb2b7447d6332e836166	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	3.27	0.38	0.00
c9f8b270df45769b1ca314af41562308	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.57	0.19	0.01
ca8174f6b29c09866bf47fac97deaad7	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.31	0.22	0.00
caa809316159c0fc334f209534848ee1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-0.44	0.19	0.03
ccbc787914705382e55f47d192ec3465	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.08	0.16	0.00
cc88b39f81913c8192cad426f8b74fa9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.82	0.16	0.00
cd066d8f308915024176645aa4072636	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.67	0.23	0.01
cd258e21df588502d582ac166c98d02b	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.11	0.24	0.00
cd7cb5308cf6db996de0f1d25a62b9bc	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	0.61	0.10	0.00
cdc2d6a54108a20d96a804cc99b94d9	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.98	0.28	0.00
ce076e02a0784bdef362b5a356756cc1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.45	0.35	0.00
ce474e05756e73e7c39b6d0f78d2f852	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenella	#N/A	-1.43	0.31	0.00
ce8849f9dcf230f8c8f1a75bda18affc	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	2.95	0.26	0.00
ce895848a2e75aef13ecb3b1b1508060	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyrivibrio	pullicaeorum	1.05	0.18	0.00
cf52c4f48fa5d0f78ab8ff9c4556f4cb	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.44	0.16	0.00





# Feed-a-Genes – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
d01c41febdbff113c934d1fbb8c77f35	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.25	0.10	0.03
d08e72343f9e1ba791da49578837584a	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.88	0.22	0.00
d10ea4cbd153b94a3cefe239795bda5	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.57	0.22	0.02
d1b974b3578c1fc95f8956a40b9258d6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	2.16	0.17	0.00
d213f33c61bcd3ac9db8a736652271a7	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.61	0.24	0.01
d331a816912685e6b04a22e97103dd97	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.14	0.20	0.00
d3338fc58cccf471d4dc3c3e595942b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.60	0.21	0.01
d38d6d73292c1e90e35857d2eadd93ff	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	2.08	0.33	0.00
d46ff826fe49003f6ef7ea40a62536ad	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.64	0.15	0.00
d537e4622dbb11fb5eb6402c4bb3e9f5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.56	0.12	0.00
d60ba08903466ccd228d9605fcd554c2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-1.51	0.25	0.00
d66f2de45c110ff4154169eb05e63846	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.30	0.15	0.00
d78cca3255fc415db787cd61ee3f277	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	1.30	0.27	0.00
d8118490b6e240781db584192bbd6f3d	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	#N/A	#N/A	-0.26	0.10	0.01
d858342dfd07394a03e8fdd10f110931	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	#N/A	#N/A	1.62	0.37	0.00
da6ccc14876f29ef5c2b0c22e2991882	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.95	0.11	0.00
dfdaf1e82ad4f92cac2ae52a7e33e85a	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.29	0.29	0.00
e0240bfb8fcbcae66824868dcebbba55	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.45	0.33	0.00
e08d92283f3581e963c8660e9721c360	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-1.17	0.29	0.00
e27c0d511b4a5f9aa122bd280fbcccc3	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.82	0.13	0.00
e2c70155c43b4cb8eefbba3b0be94385	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.34	0.11	0.00
e373ebfd2e394338bc6d255196f026a0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	2.68	0.42	0.00
e3a5f4d7976823ea7b93bb077da6ce25	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.68	0.35	0.00
e3bf030ad280a190f2d36d8b33a2d0a3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	-0.44	0.18	0.02
e4b1b6380a4bc007df8a6d47d6133bfe	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.38	0.12	0.00
e4c14f3fa127b79bbcb7ca7e6d40ba74	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.23	0.10	0.04
e4ced446cfd338e3f70d012c1fe7d25	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.39	0.14	0.01
e4f0eb2ce68349ccb5a57f55019ee7b	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-4.10	0.39	0.00
e56b1f62d28a77b52fc6686678b3d04c	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.08	0.18	0.00
e572227c0ab65ff291500957f3e33548	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.84	0.17	0.00
e6d690342a524b51547df7bd8d04fb7d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	1.81	0.27	0.00
e7793539918cf2113d734e6002a383b3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.02	0.20	0.00
e835437d820f8869618eb747c14f8d5b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.39	0.45	0.01
e8cc8131ef4453337c5e2dcb1f69db8b	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-1.42	0.37	0.00
e911c38e602ca8440211098da8c6507b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.72	0.13	0.00
e93ff5b570371549555fea0a8841219d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum	variabile	1.21	0.34	0.00
eb4db02872f97305ee155b071ceb065c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.29	0.12	0.04
eb909c4fa2b067b93b31eb99dd9879ab	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.44	0.16	0.01
ebeeda312904011b871ae1859c9cd90	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.51	0.18	0.01
ecd1bfc90bd4c48336a3709e763d735c	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	1.07	0.27	0.00
ece4aab55d5caa4b2dcb3c336d48a288	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	1.20	0.20	0.00
ef8385a0fc2a11435810f00535a515e5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	#N/A	0.41	0.12	0.01
ef9fe4cc994fbb3a446af09e8f2ba0a9	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.34	0.11	0.01
efc02e3e084f38981af2e95a83786ad9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.57	0.22	0.02
efeadc2312a2502895294b8f30117395	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	-0.39	0.16	0.02
efebf3c76869c96d205b7707bb018b0a	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.46	0.19	0.03
f00aa090eafe0172d99105c5a8b0e8ed	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.31	0.11	0.02
f05a810c44eebe4aeebf118fe08c093e	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	-0.99	0.22	0.00





# Feed-a-Gene – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between farms	SE	P <sub>FDR</sub>
f05bffad8158f82b6903fbaf3cc21aed	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.15	0.06	0.03
f11c4ef778c9fb4086c11184edca1323	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.51	0.19	0.03
f253883144ad0c74c78c2a827327964e	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.43	0.16	0.02
f2e9ef2cae77545f3ce4590b7998a5c0	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-1.01	0.26	0.00
f3c7e5f071d16ab72443988fe93c1309	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.26	0.06	0.00
f3de7bd7925ff97a424d85b84c8dd078	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.22	0.13	0.00
f3f1f6ccff45e5ba4ea279df29be2d24	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.74	0.16	0.00
f565bd755aea15dd113f252ed683f01f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.97	0.26	0.00
f6957c4d46386078a4ee23330263d061	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.67	0.24	0.01
f6fd7be78c44a07ff29714f45e61c299	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.28	0.18	0.00
f70240a423d1c6e7087cab1970e7f078	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.74	0.16	0.00
f896e9c660d79a2ff308dffd12ac650	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.79	0.32	0.02
f89b8937486e67bebb14acd9edcb2c6d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.98	0.22	0.00
f9c00d3f81ca0e31c8ac369b624b03c6	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-0.59	0.22	0.02
fa0bbf7b57575251bace8a71dea1da2e	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.59	0.15	0.00
fbcd25636b97631b8b30118b7fafb808	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.55	0.21	0.02
fcf7211f46ec512773d05ef599b67a4	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.47	0.17	0.01
fdedf0b9b578ade7fb27041df09a7bba	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.15	0.14	0.00
fe3755d2764c1bd115db51cd88942be2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.26	0.06	0.00
ff9c628312f5e92d04a9945e688e9220	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	3.55	0.24	0.00

*Annex 2. ASVs differentially represented between IRTA rabbits fed under restriction and ad libitum.*

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between feeding regimes	SE	P <sub>FDR</sub>
013dfca5cd2ff4c37e211d03fe5803fd	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-0.54	0.16	0.00
02b6e652f5e9730671be77c9cd3d57b2	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	-0.54	0.15	0.00
4d1a92f0f7a097880d4b651cba436d82	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	#N/A	#N/A	-0.66	0.16	0.00
67790098d958208fd35038b1692aa8a5	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.45	0.10	0.00
88602bff4c92ff31b36070af0141e77d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.54	0.16	0.00
970248e7fc4cb317d3ac51e71f33ec6c	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-1.38	0.36	0.00
981db9bada3bd5ae1a9818afcf964a7c	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	-0.74	0.14	0.00
ce895848a2e75aef13ecb3b1b1508060	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyrivibrio	pullicaecorum	0.73	0.15	0.00
fcf7211f46ec512773d05ef599b67a4	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-0.70	0.14	0.00

## Annex 3. ASVs differentially represented between IRTA rabbits fed diet with or without antibiotics.

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between diets	SE	P <sub>FDR</sub>
003d72cce9466e7e26f64c621af78a1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	2.18	0.29	0.00
016d51b738ee5237bab773cc5fe72412	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-1.86	0.59	0.01
02b6e652f5e9730671be77c9cd3d57b2	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	2.26	0.29	0.00
0475aa7f2f1c57b921140c71aec02590	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.93	0.28	0.00
049fb8b9352fc4d009a025d1321d80ea	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.06	0.35	0.01
0a01f7ecb5617788cd2a97fea3275063	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-3.08	0.63	0.00
0e375a6cbdc00451e926e07a9c7d7472	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.01	0.31	0.00
0ecddb2c30cf00313615308b9f72eb42	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-1.27	0.51	0.05
1106281	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	2.18	0.32	0.00
123165	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	3.66	0.47	0.00
124470	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Butyrlicimonas	#N/A	1.65	0.27	0.00
12a8ebd6fa4461b1202bf8a2eae841e1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.10	0.22	0.00
152014	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.14	0.30	0.00
177697	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.92	0.20	0.00
198403	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	2.35	0.36	0.00
1d1bf8c50b6e61ccf78d8fc7be586056	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.12	0.31	0.00
203594	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.15	0.36	0.03
205179	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	flavesciens	2.57	0.35	0.00
2055681	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Odoribacter	#N/A	1.70	0.49	0.01
205659	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-2.45	0.60	0.00
205940	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.37	0.24	0.00
208042	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.87	0.57	0.00
208769	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.65	0.32	0.00
209492	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.90	0.59	0.02
20d045864910735387e04d13e3a81afd	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.12	0.29	0.00
210361	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.75	0.21	0.01
211066	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.11	0.61	0.00
211388	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.92	0.19	0.00
213084	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.81	0.54	0.00
269360	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	-0.72	0.30	0.05
288312	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.49	0.55	0.03
288843	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	#N/A	#N/A	-4.58	0.57	0.00
289001	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	-2.13	0.70	0.00
289306	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.05	0.34	0.02
291348	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	2.50	0.55	0.00
296062	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.11	0.25	0.00
297503	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.92	0.35	0.00
29f3702f5a607f1b576c6d8c3d5d3acb	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobivibrionales	Desulfobivibrionaceae	#N/A	#N/A	-1.97	0.54	0.00
2e6c4e8a91800f9be22b89b87b637ab6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	[Ruminococcus]	gnavus	2.08	0.37	0.00
2e869305b8851ca95016b83a673ceec0	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	1.48	0.40	0.00
2ff369e928d2b4116475775d9037d25d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.74	0.26	0.05
3168538	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	#N/A	-1.53	0.54	0.03
319501	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	muciniphila	1.43	0.44	0.02
319983	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	fragilis	2.16	0.32	0.00
332242b8bf154b5b531438e80e663479	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	#N/A	#N/A	1.07	0.21	0.00
338091	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis	-1.90	0.55	0.00



# Feed-a-Genes – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between diets	SE	P <sub>FDR</sub>
350438	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.91	0.63	0.02
351272	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-3.32	0.65	0.00
3540202b17a98bf508fcb2e628626f60	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	#N/A	2.87	0.54	0.00
3653528a04f8b557d870429fa7815665	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.92	0.48	0.00
38b035c95e46923237b6a317cbce9d6b	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.05	0.34	0.00
39608795e9813d65d281896881a1e6cc	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.08	0.25	0.00
39c47e25e1b361216accb794a0461afe	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	0.93	0.20	0.00
3adcaf18972a0a7863a6a29e87201e0c	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	#N/A	1.13	0.36	0.04
3d1954592ebe5ad84dc38f5b142a877	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.24	0.40	0.01
3d2ec70b7f63321e94bfde5747cab90e	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.90	0.34	0.00
3fcc72e0ba4cfa76e03fe92449527240	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	3.07	0.55	0.00
41af26e77e10d9d22b146d196b3ea629	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.02	0.22	0.00
425567dcb2c4bc081d3113fc79ab17e1	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.52	0.54	0.00
42be02a3f634c30003c46aa6483f25da	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.97	0.25	0.01
45228224054458b73c236dccc82a8a0	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.40	0.50	0.03
45f5e907f1c2f85ce106aa2354caf65	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	-1.83	0.61	0.02
46ada1d0938f8511a10654721c5aee17	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.08	0.59	0.01
470759	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Oxalobacter	formigenes	1.27	0.34	0.00
47adb790951ac354b61cf4e4f7849317	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.79	0.21	0.01
485b88e5a30f16dbb209d6bbbf4a96f	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.38	0.39	0.00
486d975a7886ae8e571e6d38e9016ce3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.95	0.49	0.01
4b95bac7f4f4d483a430801baa83bb9	Bacteria	Cyanobacteria	4C0d-2	YS2	Cyanobacteria	#N/A	#N/A	1.20	0.40	0.00
4d1a92f0f7a097880d4b651cba436d82	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	#N/A	#N/A	1.43	0.32	0.00
4d4544574a0107eb2125de7b530a85c3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.59	0.17	0.01
4eab629d7abca92319ccc5b100ccc6ff	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	#N/A	-2.57	0.63	0.00
4f6a40f24d9e0c4303d73d92aac1426	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.78	0.55	0.01
4f72dc076d7559c4348cf13c8b93b53b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.32	0.45	0.01
51eab6d43588164f929ae4085c689240	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	1.04	0.32	0.01
5648fa0559480ce3d6dbe0507c41c607	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.14	0.31	0.00
5ad48b8a3ab12b95b147112d2d7a0068	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.52	0.16	0.00
5b774b7989796b302aee4a59964475f6	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.58	0.51	0.01
5d56a4aed325f2bd59fc53301087e707	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	1.00	0.30	0.02
603a631aba956ea96ca45b548144b73f	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.25	0.22	0.00
6042e7545fe73e275dd65f5fe9e7c63d	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	#N/A	#N/A	-1.55	0.50	0.01
629c66a950b5426b15a55f01a7469a70	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobivibrionales	Desulfobivibrionaceae	Desulfobivibrio	#N/A	-1.44	0.51	0.01
63ac6fad66f0e8f96f45387999702f5	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobivibrionales	Desulfobivibrionaceae	Desulfobivibrio	#N/A	-1.66	0.54	0.02
6660599f80a52bca7d22b0c09faef740c	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.17	0.46	0.04
67006f927b3e8c62d86334b2c239c3e3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.25	0.26	0.00
68532b6a6cbbbf1f28467efa280f71d2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	1.61	0.43	0.00
6a47937f1a5d4fc5350f199dd1b1a267	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.71	0.26	0.03
6d5a1c02cbc558dc39368de6e2adaf73	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Epulopiscium	#N/A	-1.44	0.39	0.00
705b9cd95aefd0e56d7d82569de4c92b	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	#N/A	#N/A	#N/A	2.06	0.59	0.00
72d723d6b5ee9912910d8f52d8b60937	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.63	0.40	0.00
73df0cf02748724a10b9dd21035d20ef	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	-1.64	0.58	0.04
775d50162d645cabb41195d0b0c1767a	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.53	0.17	0.03
78229d778767ae446f70342a95beca34	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.69	0.23	0.01
7aadbb8737d547e2b8fa89aebc725d74d	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.60	0.18	0.03
7b3f67d5235a04d7283c4e7db11fc2e0	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.97	0.33	0.04



# Feed-a-Genes – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between diets	SE	P <sub>FDR</sub>
8239e098214fb2f0fd47eda3273d1b9f	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.98	0.63	0.01
834ab329e414a875075cb44ec0c16b8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	2.42	0.39	0.00
84a38b94b31fceb532bf1770e56e9b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.79	0.16	0.00
8569d48e8c338f867ac85464741bf1ae	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.60	0.36	0.00
86261bd146905aa7c456de8d9ad52cd1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	-1.25	0.48	0.02
874486e318277dbae83cb46dfb52c214	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.69	0.24	0.00
886b80a6f1dda4bab907037e0c03849e	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.86	0.15	0.00
88bb3979cf72ef4b99e83b3a1d15e339	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	#N/A	#N/A	0.65	0.19	0.03
8af63aabbcca2f26f14af2555d689ae9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	2.18	0.70	0.00
8bec33f490e4bd5dea7a00e4f7623b67	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.79	0.23	0.02
8c476d729399d10d22a335c27094b6bb	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.97	0.22	0.00
8e484fb9317fe9d54c9d80bb4a35f18e	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	#N/A	#N/A	-2.11	0.58	0.01
8fe8eae00dfa556af3cd9e021c4ab2a3	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.06	0.30	0.00
9048e110e1bd72c6ef5cae66ee50b17a	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	-1.92	0.59	0.00
93132f2e14ae61bf73807cede91cea9b	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.33	0.42	0.00
9501ee854d39af8c937ad7747400ef12	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	#N/A	#N/A	-2.16	0.62	0.01
96d3f36f9ba11c509e0a2243794844eb	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	0.81	0.11	0.00
97fea4c9a75320679d5c1c12f41b965	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.40	0.31	0.00
981db9bada3bd5ae1a9818afc964a7c	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.81	0.27	0.00
983b82d11be5861dfbd8e3b0afa30d13	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-1.44	0.55	0.04
98bd98fa73affdb761fa0f0e9fbd4bba	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.65	0.47	0.00
9d4472ee0435227dc69129ac6ca16755	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	#N/A	#N/A	#N/A	-4.36	0.59	0.00
9d64c0465809ff3e788ec138b15d1b61	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.87	0.31	0.00
9e5ca071e831771e0374d643ab782022	Bacteria	Tenericutes	RF3	ML615J-28	#N/A	#N/A	#N/A	2.50	0.37	0.00
a1aa1c3f908f366ebf4f35c09f6686d0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	-1.36	0.43	0.01
a1dfda4d1c3544cf37a0d7b3f988d72	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.37	0.34	0.00
a2fe19c86995cdc987b16b90390e0790	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.87	0.24	0.02
a6e950733b59c867e52758df0e5c24d8	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	5.02	0.21	0.00
a8a4d698c5336c23c1f8896cdb8de19a	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.00	0.29	0.00
ac0e35816e704f4f5094424b365763a6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	3.22	0.33	0.00
ae49c777b36274f88051cc925b25e7b4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.59	0.17	0.01
ae4cae9a2714ed2bf98e6118cbda374b	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	2.60	0.45	0.00
b4578b2c8630d8794dfcbb7679285e8e	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	#N/A	#N/A	1.48	0.41	0.00
b474738cd4d1dae36bab5a46be329ae02	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.74	0.20	0.00
b8037bb0a1f245a35bd7ac2498a9fed6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.48	0.34	0.00
bd905ec1f51d614a5a338102a5c4fbc	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.43	0.41	0.00
c5d744fe7789a092862da54db0a44687	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.25	0.40	0.01
c6204514faff8c70b184f5354793ee1	Bacteria	Tenericutes	Mollicutes	RF39	#N/A	#N/A	#N/A	1.56	0.32	0.00
c6dbbf63d05241312aa50b7a5b6fe7c	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	0.56	0.17	0.02
c838493a8603213a86019c9b6eddd39a	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.12	0.42	0.02
c8eb15b8c729cb2b7447d6332e836166	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	albus	2.94	0.60	0.00
cbcb787914705382e55f47d192ec3465	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.78	0.26	0.00
ce076e02a0784bdef362b5a3565cc1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	2.66	0.57	0.00
ce8849f9dcf230f8c8f1a75bda18affc	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	2.68	0.42	0.00
ce895848a2e75aef13ecb3b1b1508060	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyrivibrio	pullicaecorum	1.17	0.29	0.00
cf52c4f48fa5d0f78ab8ff9c4556f4cb	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.49	0.25	0.00
d1b974b378c1fc95f8956a40b9258d6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	#N/A	1.52	0.27	0.00
d213f33c61bcd3acd9b8a736652271a7	Bacteria	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.67	0.39	0.00



## Feed-a-Gene – H2020 n°633531

ASV ID	Kingdom	Phylum	Class	Order	Family	Genus	Species	Difference between diets	SE	P <sub>FDR</sub>
d60ba08903466ccd228d9605fcd554c2	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	-1.21	0.40	0.02
d66f2de45c110ff4154169eb05e63846	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.18	0.25	0.00
da6ccc14876f29ef5c2b0c22e2991882	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.93	0.18	0.00
dfdaf1e82ad4f92cac2ae52a7e33e85a	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.63	0.46	0.00
e27c0d511b4a5f9aa122bd280fbccc3	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	2.26	0.21	0.00
e373ebfd2e394338bc6d255196f026a0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	2.35	0.68	0.00
e4f0eb2ce68349ccb5a57f555019ee7b	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	#N/A	#N/A	-3.28	0.63	0.00
e6d690342a524b51547df7bd8d04fb7d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	#N/A	2.45	0.43	0.00
e7793539918cf2113d734e6002a383b3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.21	0.32	0.00
e911c38e602ca8440211098da8c6507b	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	1.11	0.21	0.00
f3de7bd7925ff97a424d85b84c8dd078	Bacteria	Firmicutes	Clostridia	Clostridiales	#N/A	#N/A	#N/A	0.87	0.21	0.00
f6fd7be78c44a07ff29714f45e61c299	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	0.90	0.28	0.02
f89b8937486e67bebb14acd9edcb2c6d	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	3.22	0.35	0.00
fdedf0b9b578ade7fb27041df09a7bba	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	#N/A	#N/A	1.28	0.23	0.00
ff9c628312f5e92d04a9945e688e9220	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	#N/A	#N/A	2.78	0.38	0.00