

Porcine feed efficiency (FE)-associated intestinal microbiota and physiological traits: Finding consistent cross-locational biomarkers for residual feed intake (RFI)

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Introduction



- **Feed efficiency (FE)**

- Feed accounts for ~70% of the cost of producing a pig (Teagasc, 2015)

- Improving FE: ↓ production costs ↓ environmental impact ↑ profitability

- **The porcine intestinal microbiome**

- Ecosystem of microbes located along the gastro-intestinal tract

- Metabolism & immune response (Ramayo-Caldas *et al.*, 2016)

- Growth rate (Mach *et al.*, 2015)

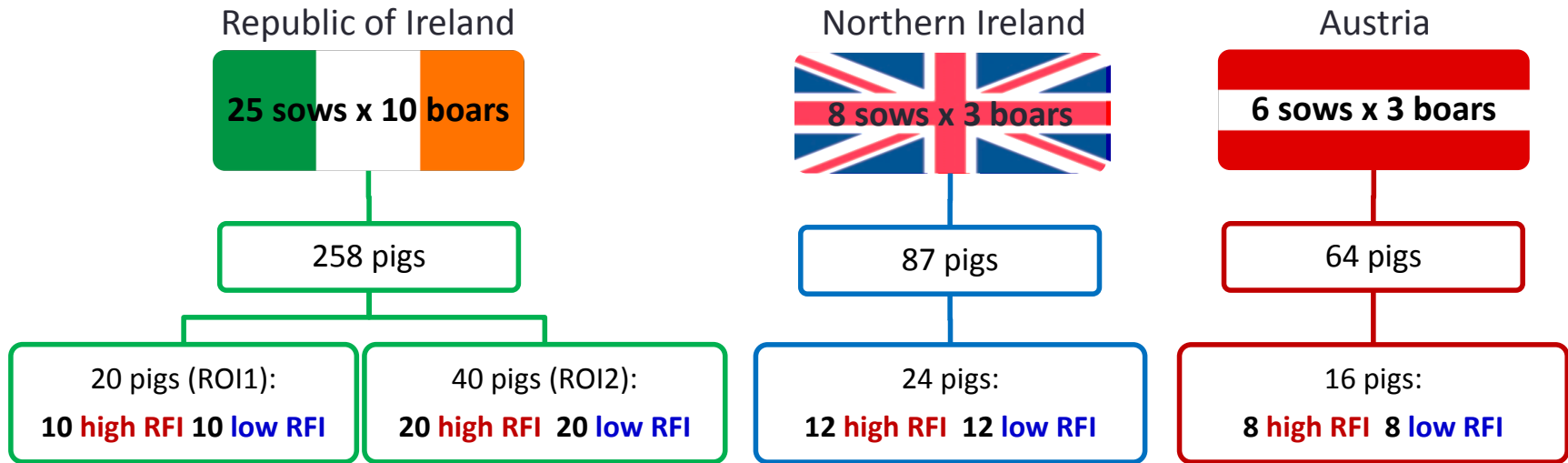


Objective

- Identify microbial biomarkers linked with residual feed intake (RFI)
- Investigate intestinal microbiota of pigs ranked on RFI across 3 European sites using common genetics and management practices



Study design



- ✓ Common boar
- ✓ Identical diet specifications
- ✓ Management protocols

- ✓ Day 42-91 pw, within litter
- ✓ Extremes of RFI
- ✓ Low RFI = better FE

Residual feed intake (RFI)

- Measure of feed efficiency

“Difference between observed feed intake & expected feed intake, the latter based on the animal’s rate of gain & body fat content”

Patience *et al.*, 2015

$$\text{ADFI} = \text{ADG} | \text{sex} + \text{M.wt} | \text{sex} + \text{backfat} + \text{muscle}$$



Microbiota analysis

- High throughput sequencing of 16S rRNA gene

- **α -diversity:**

Diversity among species within a sample/group

How many species are present in a sample

- **β -diversity:**

Diversity between samples/groups

How similar/different samples are

- **Phylogeny & taxonomy:**

Domain

Kingdom

Phylum

Class

Order

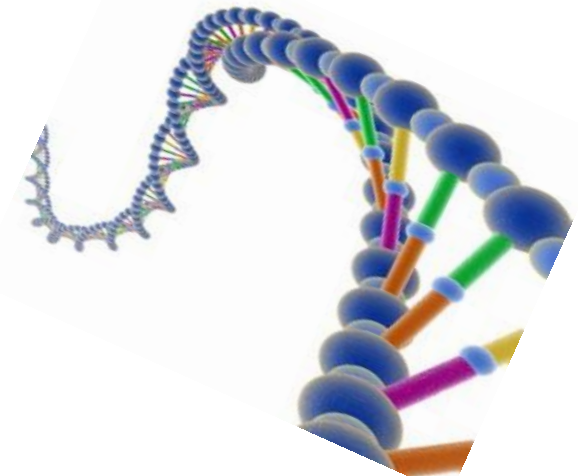
Family

Genus

Species

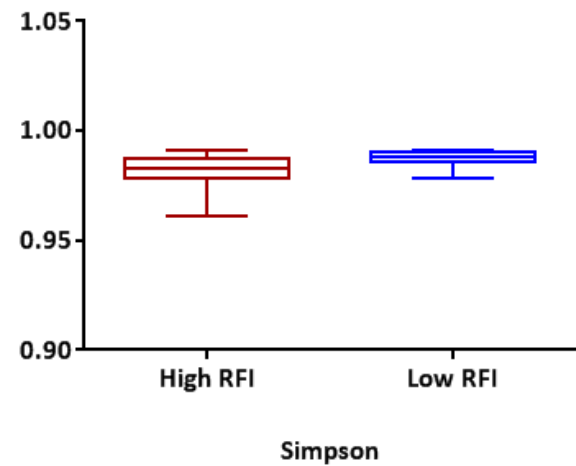
- **Functionality:**

Predicted function of the microbiota using KEGG annotations

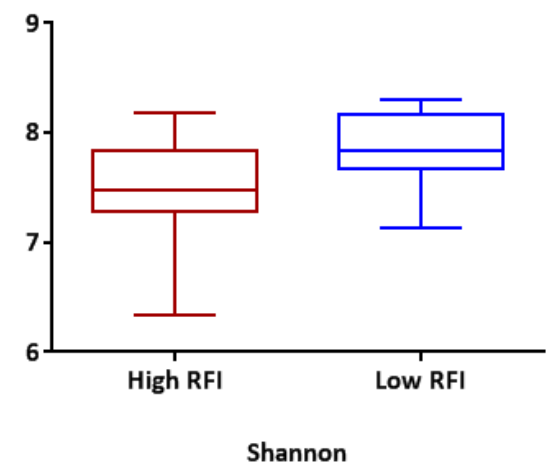
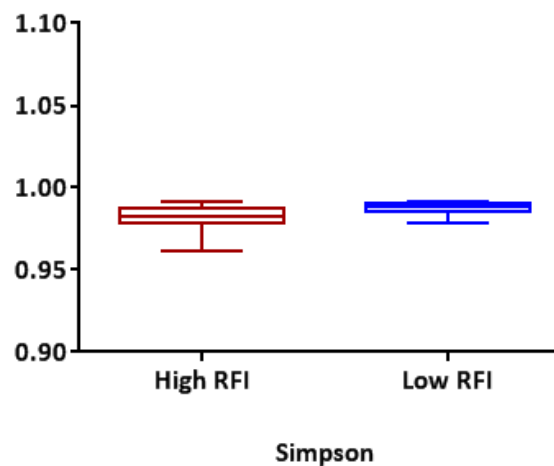


α -diversity: microbial diversity within a sample

Ileum

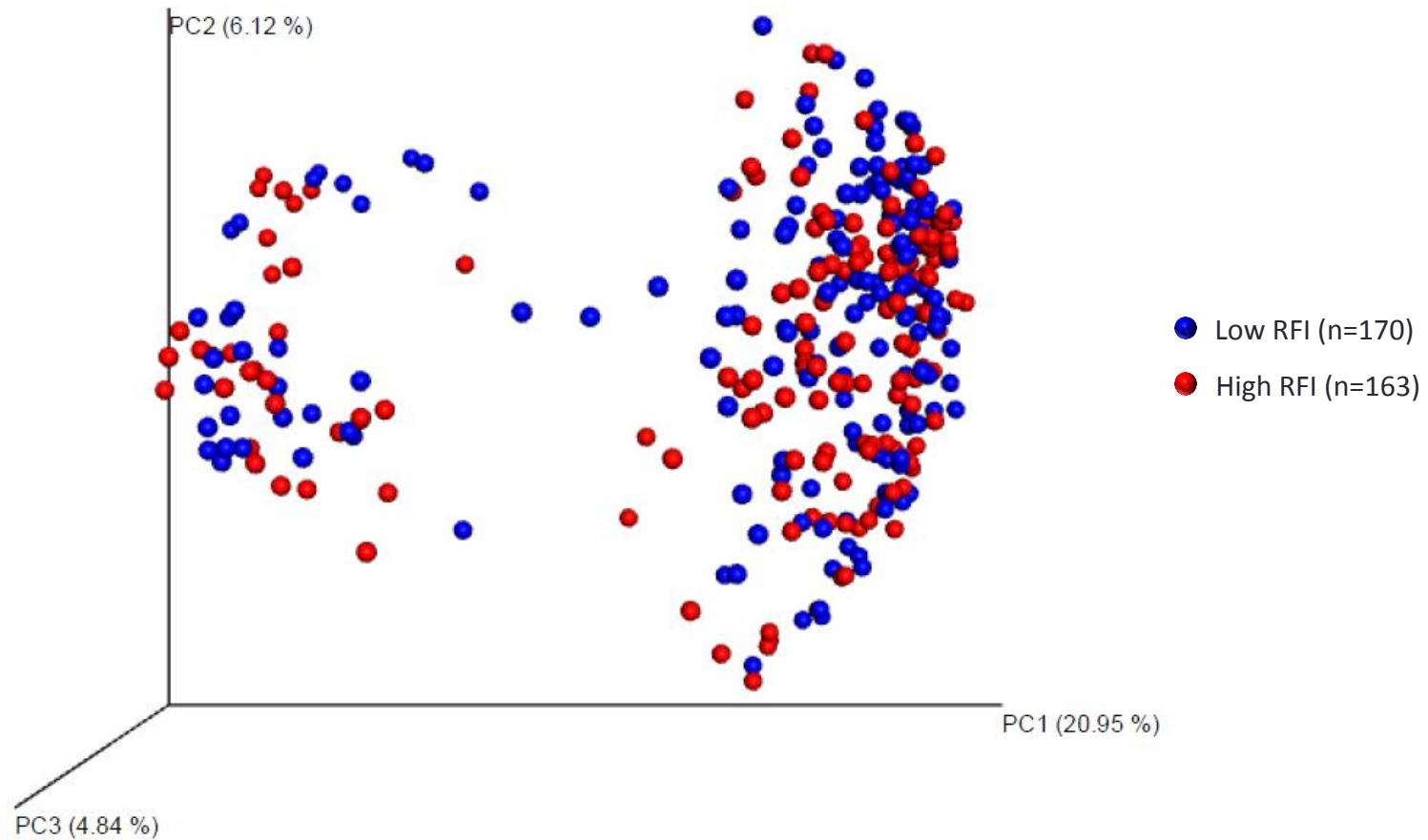


Caecum



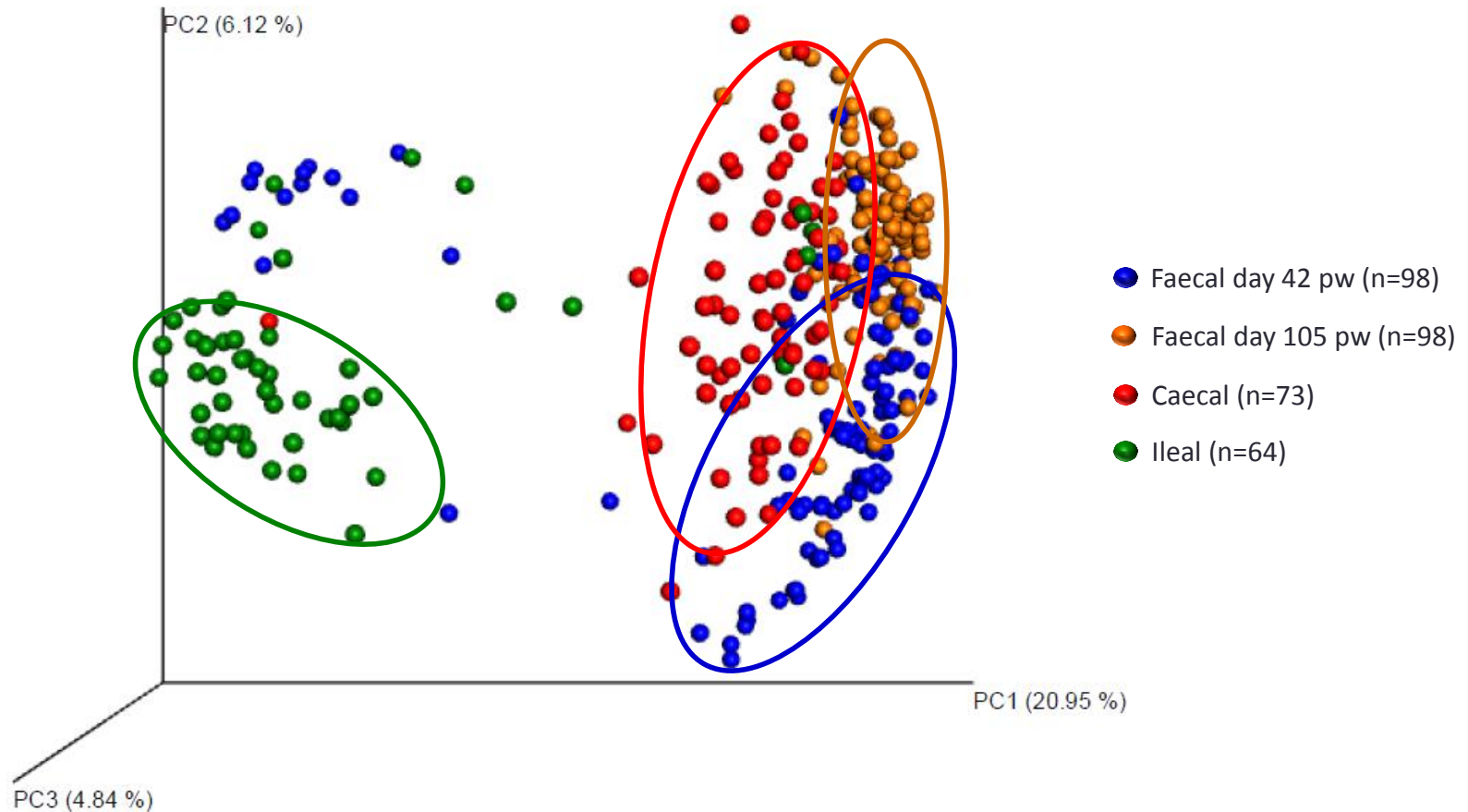
Diversity \uparrow in more feed efficient pigs (ROI2 pigs only)

β -diversity: microbial diversity between samples



No clustering by RFI rank

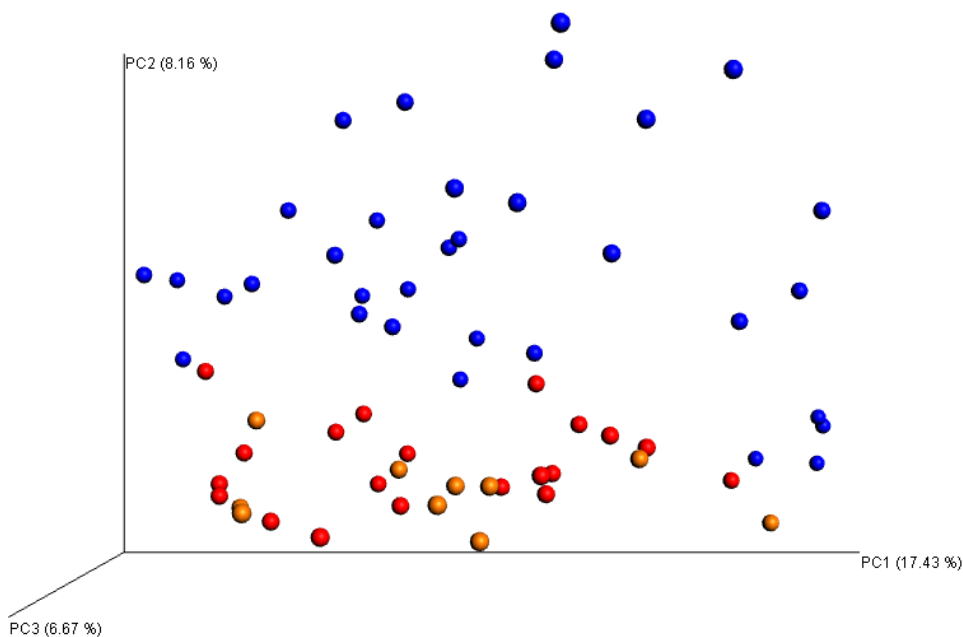
β -diversity: microbial diversity between samples



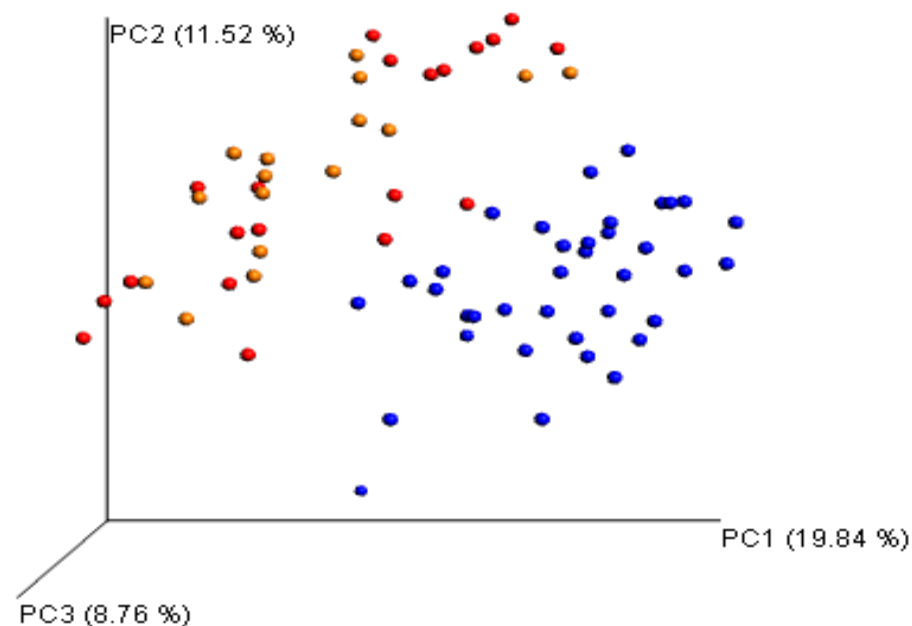
Clustering by sample type/intestinal site

β -diversity: microbial diversity between samples

Ileum



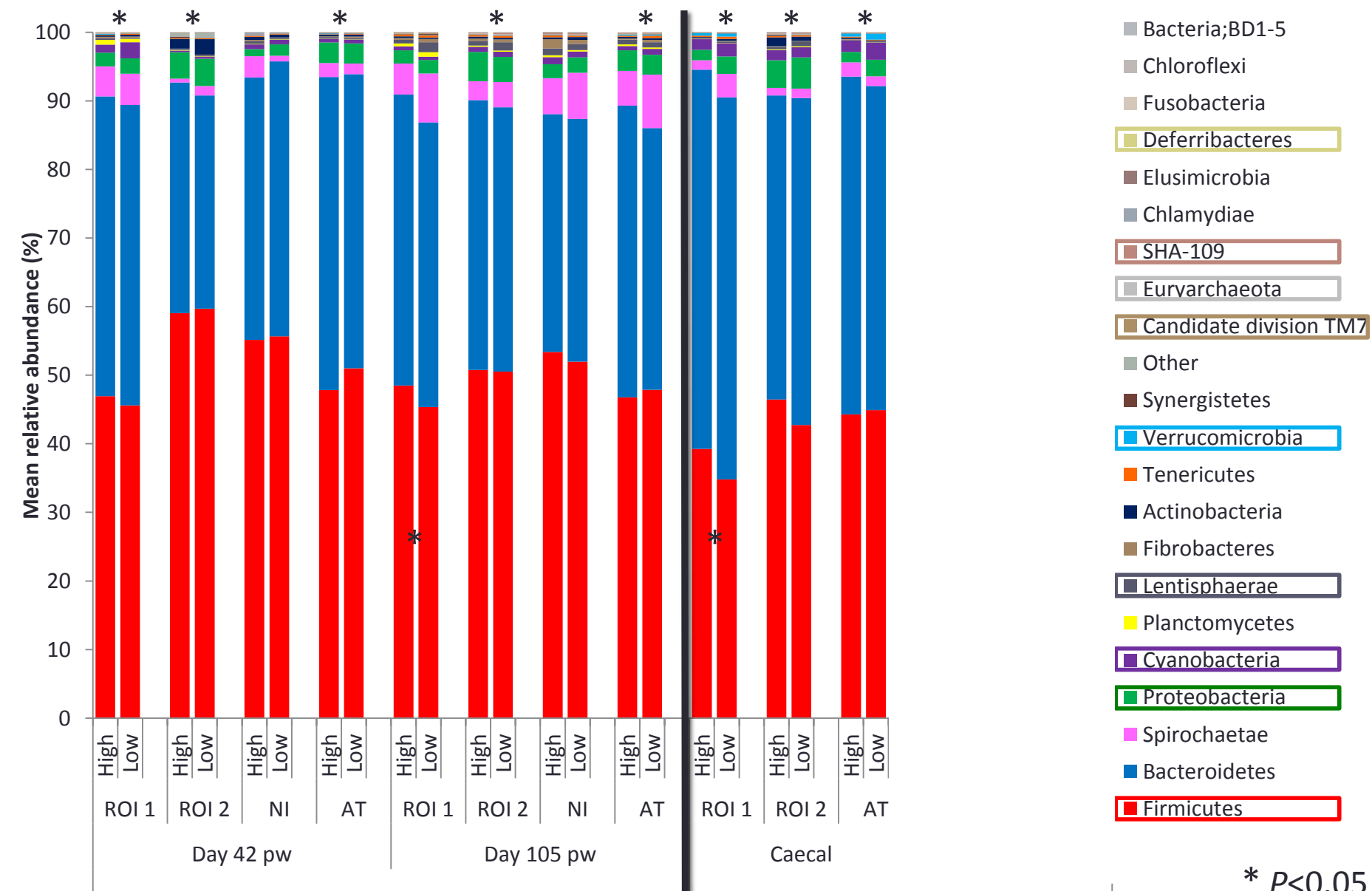
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● ROI1 ● ROI2 ● AT

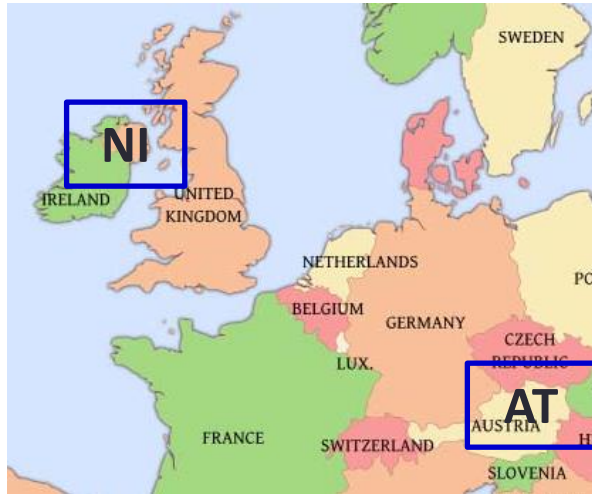
Clustering by European site/rearing environment

Microbial composition: phylum level



RFI-associated microbes across European sites

Faeces: 70 days of age



G_Mucispirillum 0.03 vs. 0.002%

Faeces: 133 days of age



P_Lentisphaerae 1.44 vs. 0.59%
G_Methanobrevibacter 0.01 vs. 0.003%

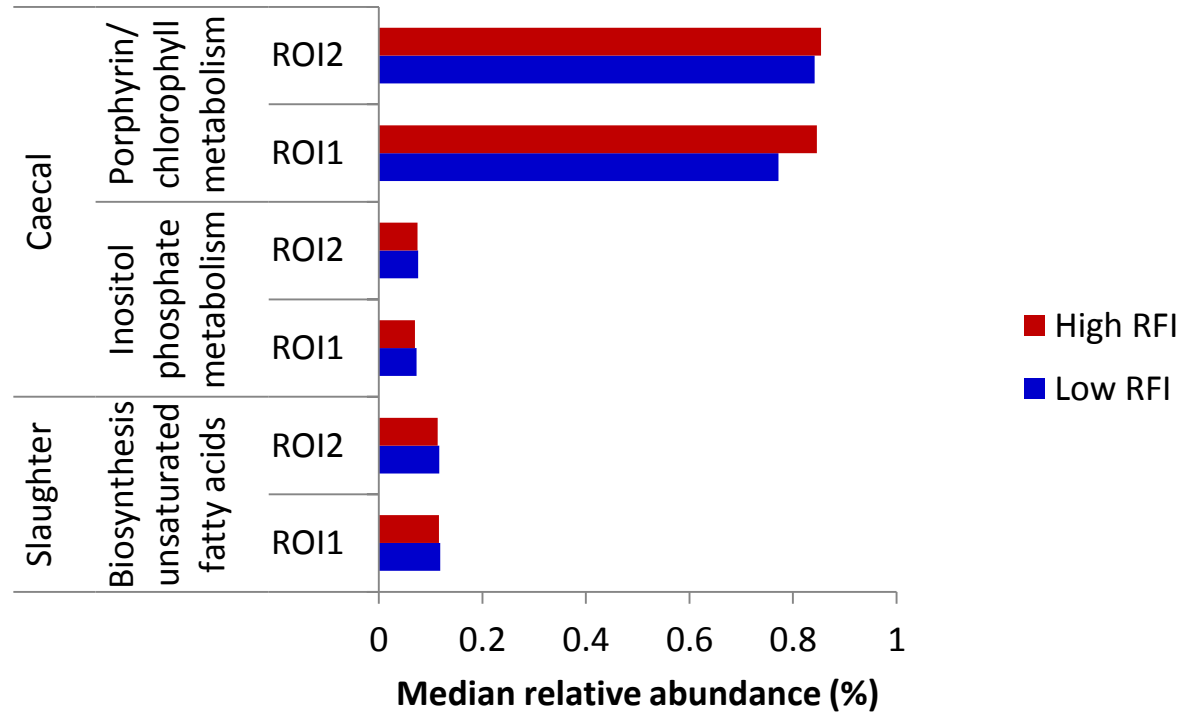
Caecal digesta: 133 days of age

F_RF16 1.13 vs. 0.05%



G_unc. bacterium 4C0d 11.01 vs. 9.5%
F_Ruminococcaceae 2.19 vs. 1.49%

RFI-associated pathways across European sites



Common pathways related with metabolism/cell information
Only between the 2 batches in ROI

$P < 0.05$
(102 pathways)

Conclusions



- **Intestinal microbiota in low RFI pigs**
 - Higher microbial diversity in ROI2 pigs= health benefits??
 - Rearing environment more influential than RFI rank
 - RFI-associated microbes common across different rearing environments
 - Biomarkers for FE?
 - Probiotics to improve FE?
 - Targets for nutritional strategies

Site specific FE-associated intestinal microbiota

Future work



- Cause-effect studies
- Manipulation of the microbiota to improve FE
- Biomarkers for FE
- Functionality of the entire microbiome

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Thank you