INTESTINAL MICROBIOTA DIFFERS IN PIGS RANKED ON RFI ON THREE EUROPEAN SITES

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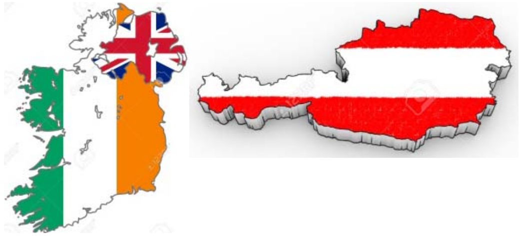
Intestinal microbiota and feed efficiency (FE) in pigs

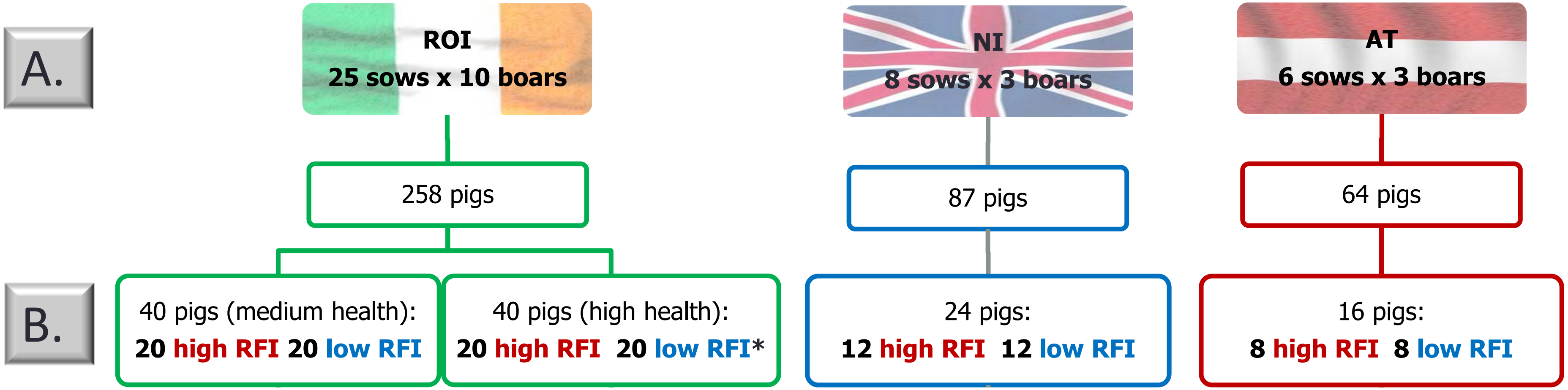
- **Improved FE = ↓ feed costs** and **environmental impact**
- The **intestinal microbiota** has a crucial role in aiding **nutrient digestion** and **energy harvest**
- Potential to enhance FE?
- Little known about **link between intestinal microbiota** and **FE in pigs**

- Will the FE-associated microbiota be consistent for pigs raised in different environments?



- Will the microbial functionality differ between high and low feed efficient pigs across geographic sites?

Study design



A.

ROI
25 sows x 10 boars

258 pigs

NI
8 sows x 3 boars

87 pigs

AT
6 sows x 3 boars

64 pigs

B.

40 pigs (medium health):
20 high RFI 20 low RFI

40 pigs (high health):
20 high RFI 20 low RFI*

24 pigs:
12 high RFI 12 low RFI

16 pigs:
8 high RFI 8 low RFI

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

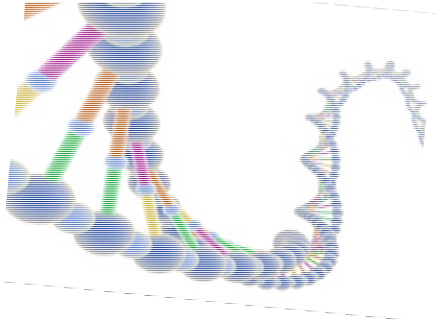
- ✓ Low RFI = better FE
- ✓ Day 42-91 pw, within litter
- ✓ Extremes of RFI

* Used in FMT study
(*abst. no. 24595*)

Methodology

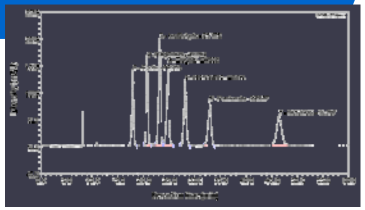
Microbial profiling

- DNA extraction from faeces and digesta
- 16S rRNA gene sequencing (Illumina)
- OTUs classification and taxonomic assignments (QIIME)
- α- and β- diversity
- Predicted microbial functionality (PICRUSt)



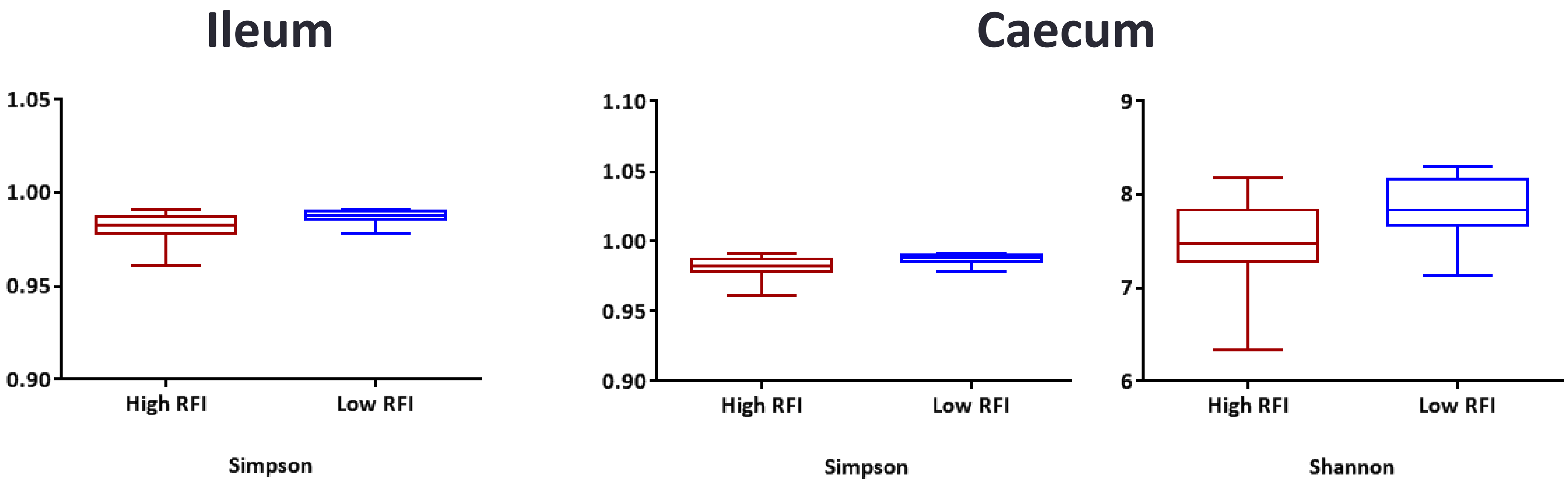
Volatile fatty acid concentration

Gas chromatography (acetic, propionic, butyric, valeric, iso-butyric and iso-valeric)



α-diversity: effect of RFI

ROI (high health)

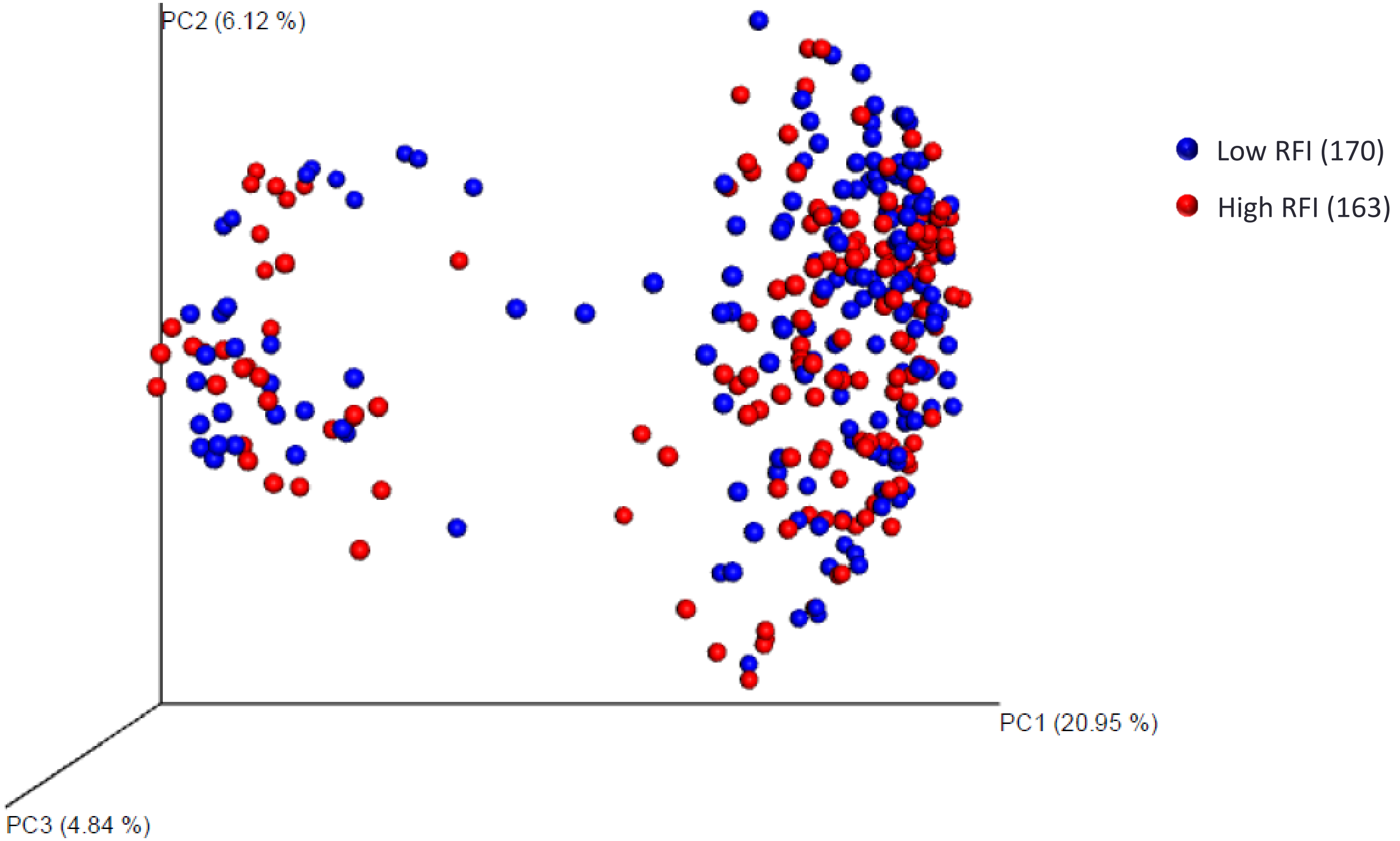


Low RFI: ↑ microbial species

P<0.05

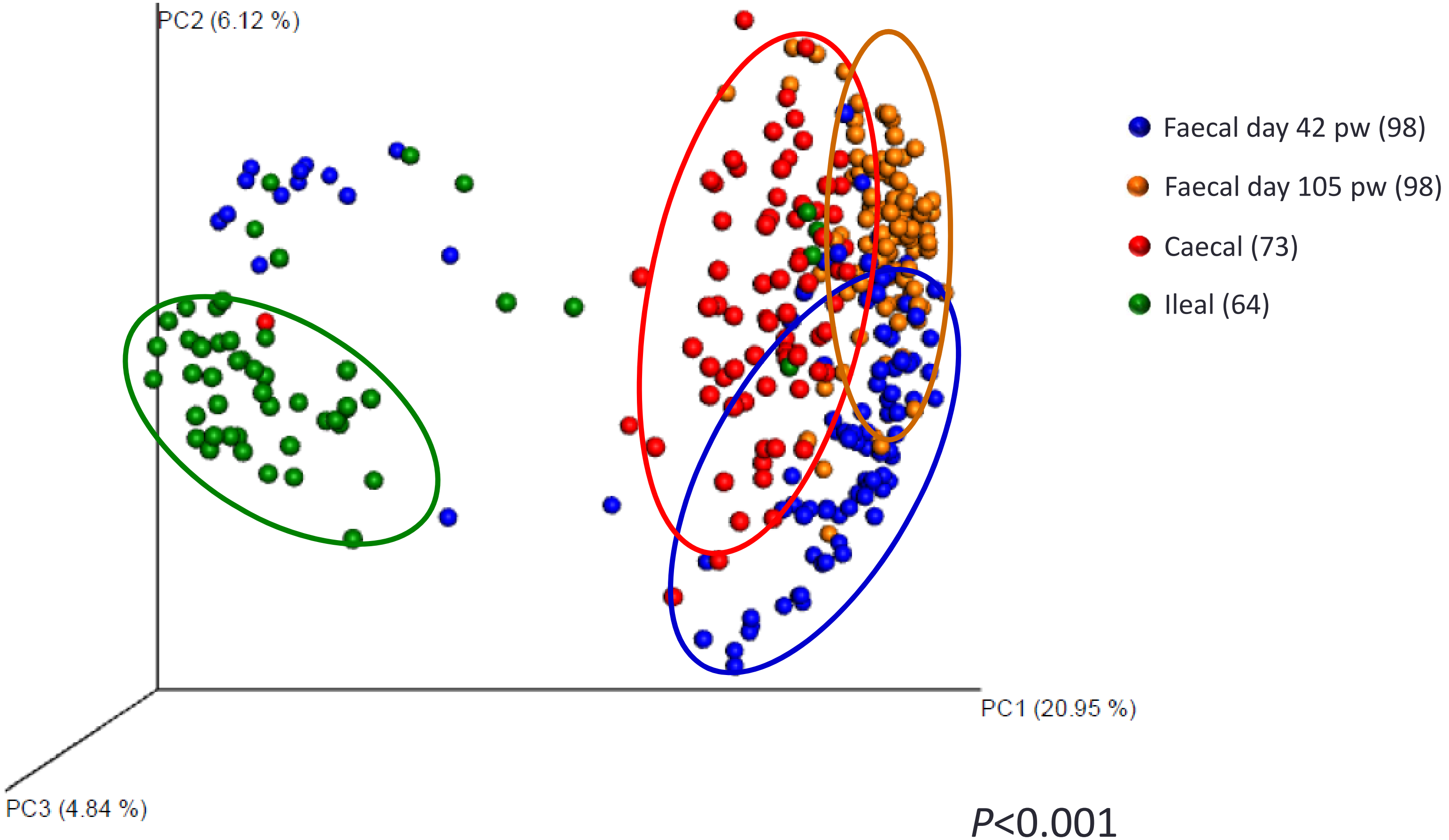
β-diversity: no RFI effect

Overall or by site



All faecal and digesta samples

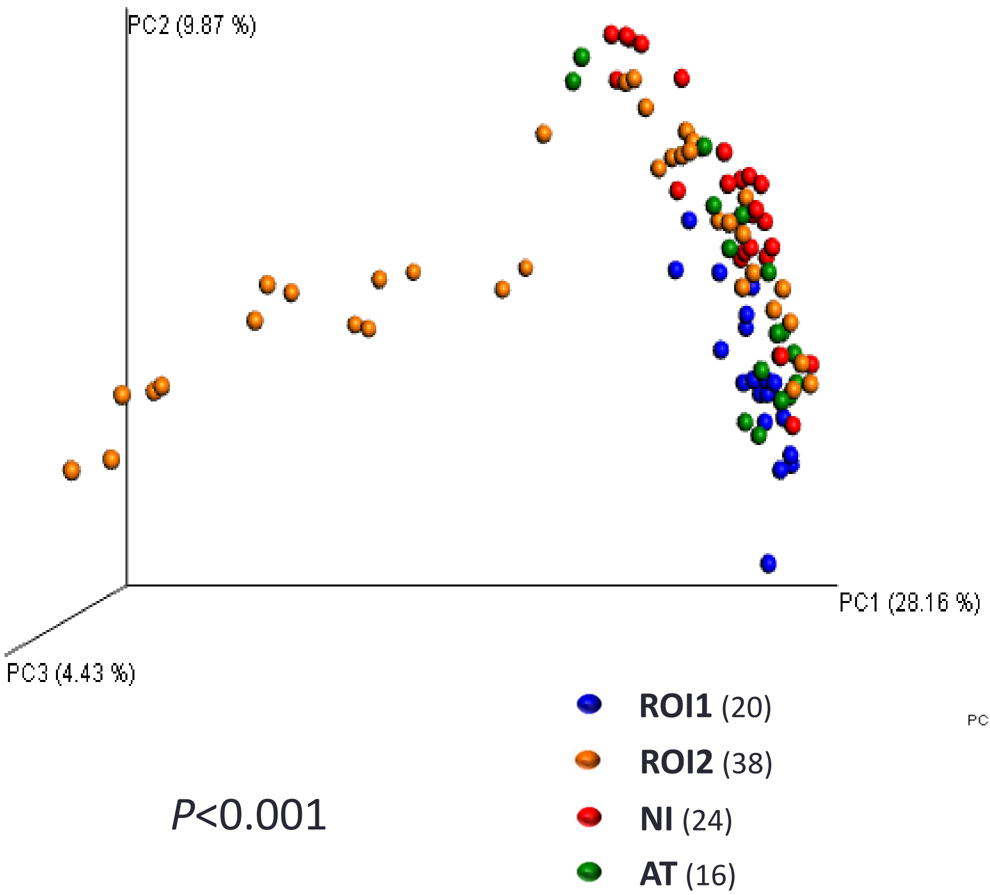
Sample-specific diversity



P<0.001

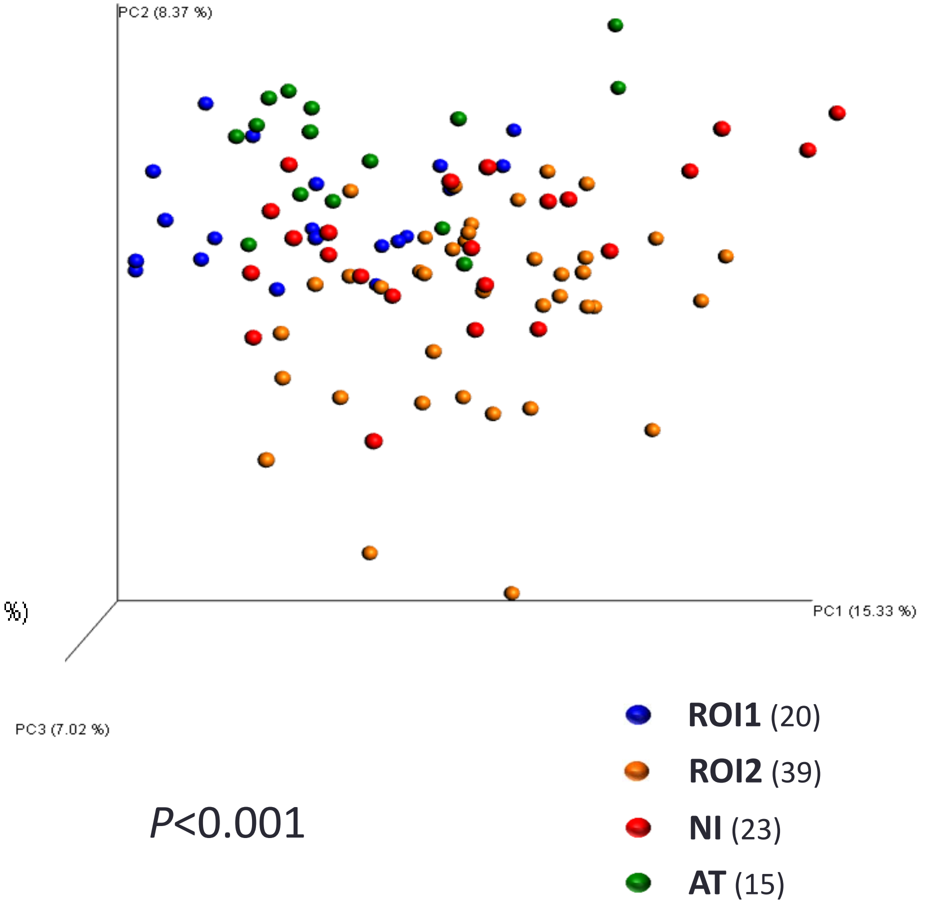
European site-specific diversity

Faecal day 42 pw



P<0.001

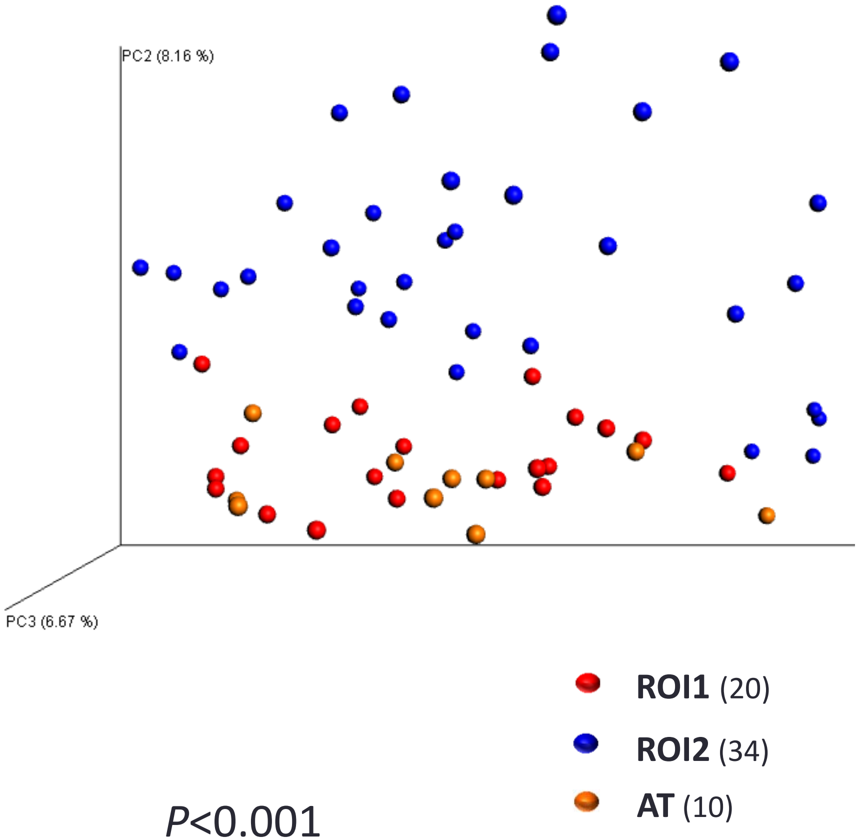
Faecal day 105 pw



P<0.001

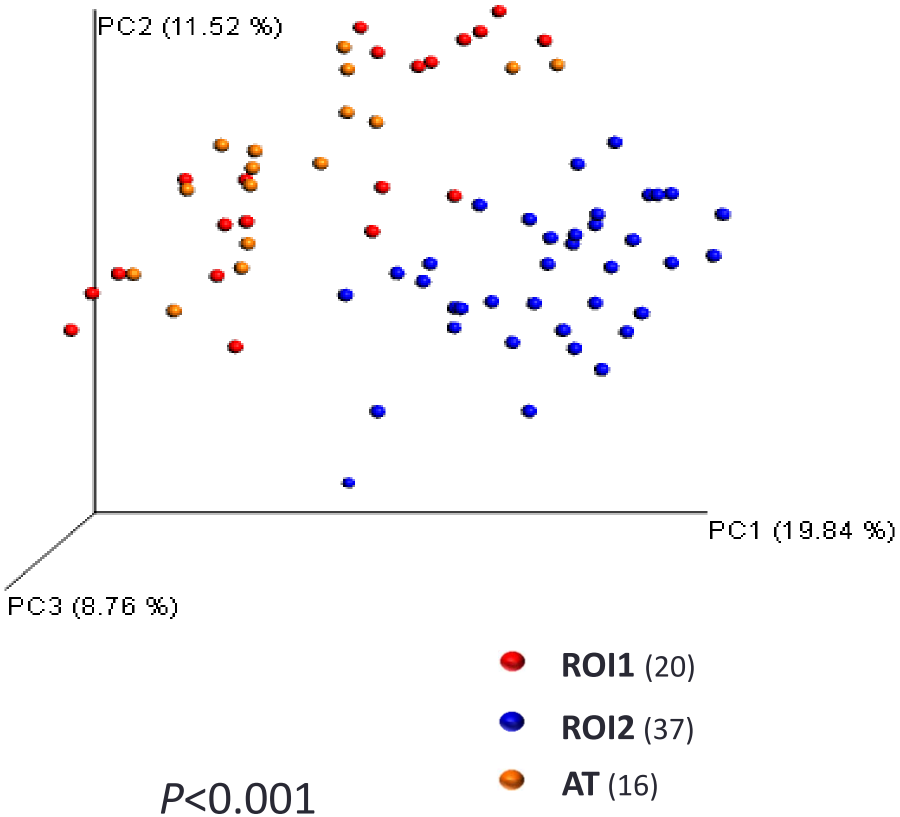
European site-specific diversity

Ileal digesta



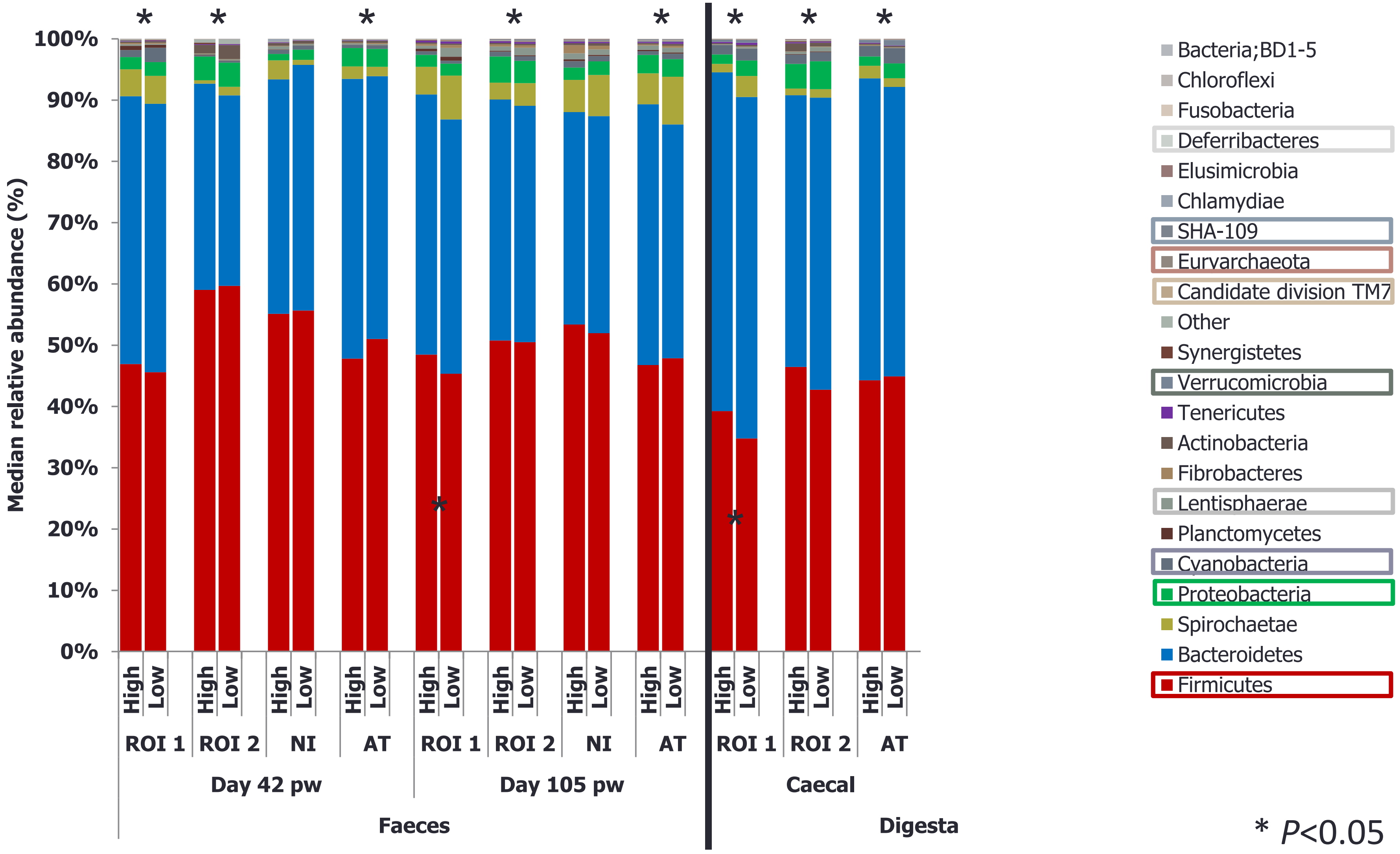
P<0.001

Caecal digesta



P<0.001

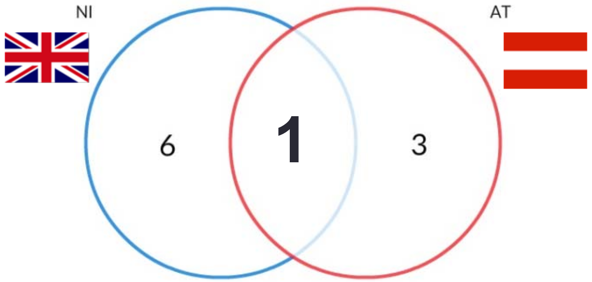
Compositional differences: phylum



* *P*<0.05

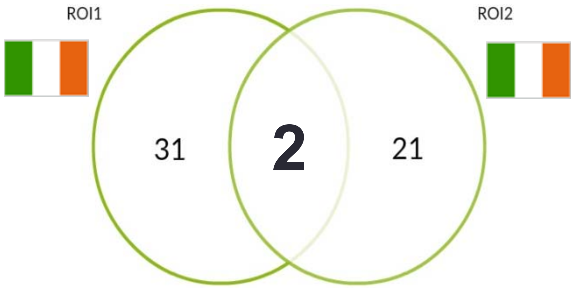
Common RFI-associated taxonomic differences in microbiota across sites

Faecal day 42 pw



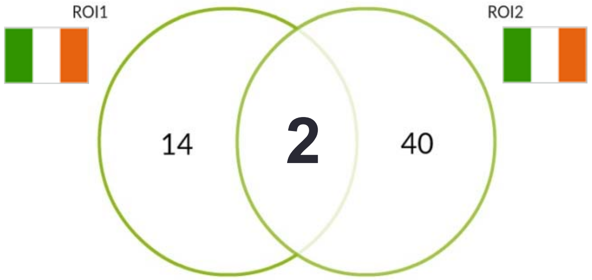
Mucispirillum ↑ 2-fold low RFI

Faecal day 105 pw

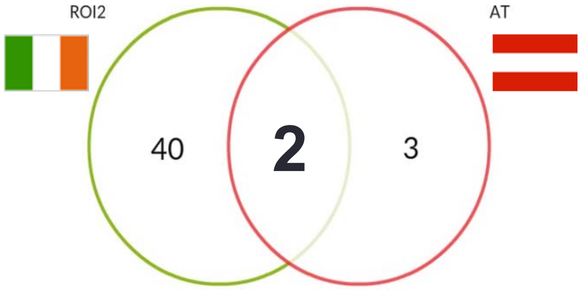


Lentisphaerae ↑ ≈2-fold low RFI
Methanobrevibacter ↑ ≈2-fold low RFI

Caecal



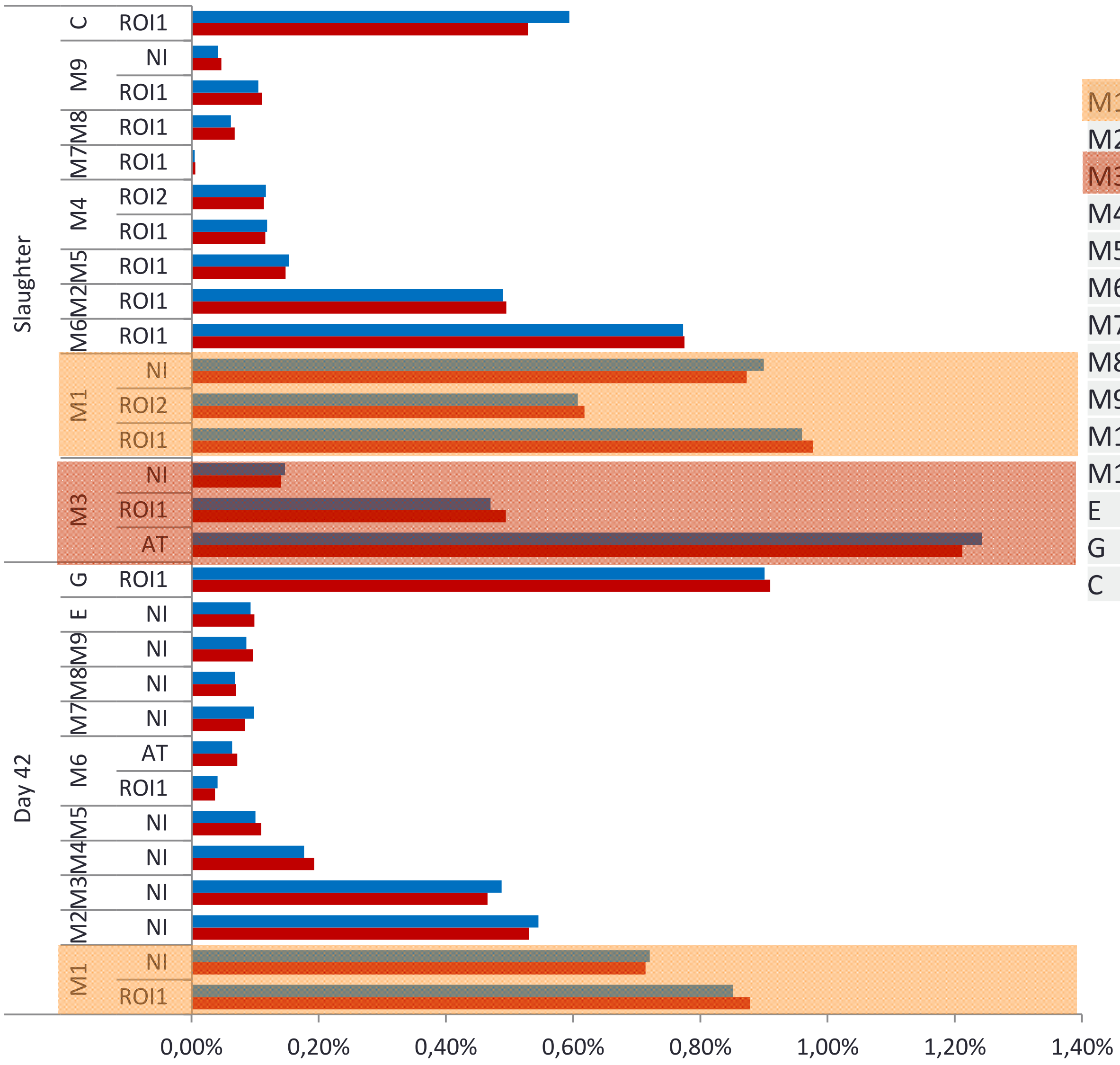
RF16 ↑ 20-fold low RFI
unc. bacterium (RF16) ↑ 20-fold low RFI



unc. bacterium 4C0d (Cyanobacteria) ↑ ≈1-fold low RFI
Ruminococcaceae ↑ ≈1-fold low RFI

$P<0.05$, Wilcoxon-Rank test for paired samples

Predicted functional metagenomes



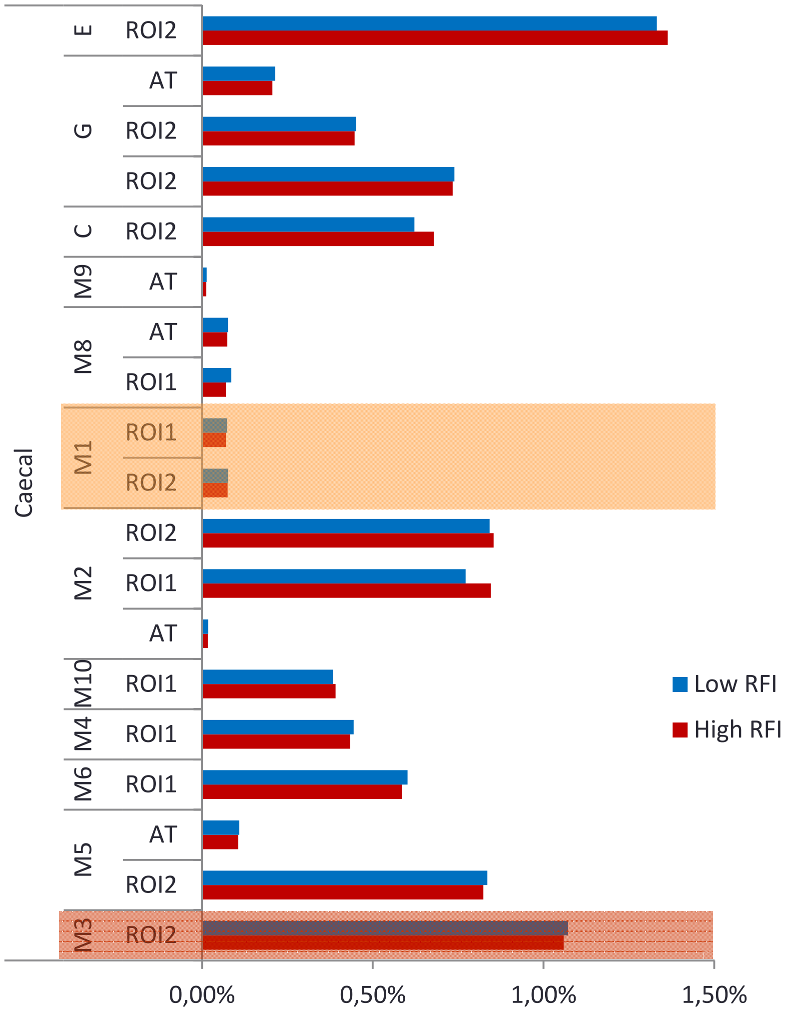
M1	Carbohydrate metabolism
M2	Metabolism of cofactors and vitamins
M3	Energy metabolism
M4	Lipid metabolism
M5	Amino acid metabolism
M6	Glycan biosynthesis and metabolism
M7	Biosynthesis of other secondary metabolites
M8	Metabolism of terpenoids and polyketides
M9	Xenobiotics biodegradation and metabolism
M10	Metabolism of other amino acids
M11	Nucleotide metabolism
E	Environmental Information Processing
G	Genetic information processing
C	Cell motility

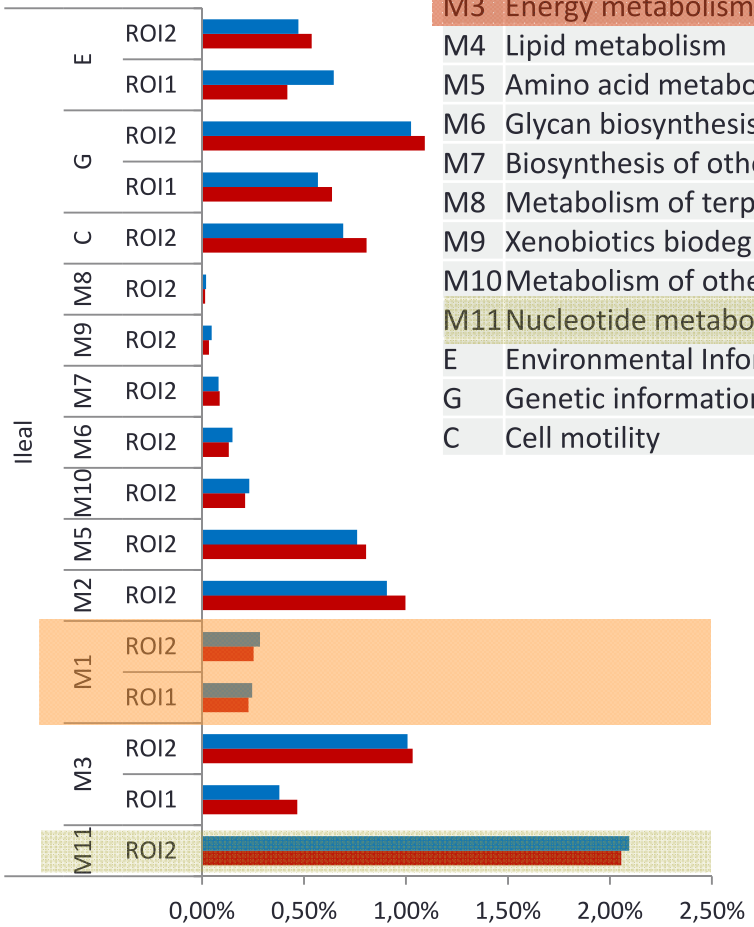
🟦 Low RFI

🟥 High RFI

$P<0.05$
(102 pathways)

Predicted functional metagenomes





M1	Carbohydrate metabolism
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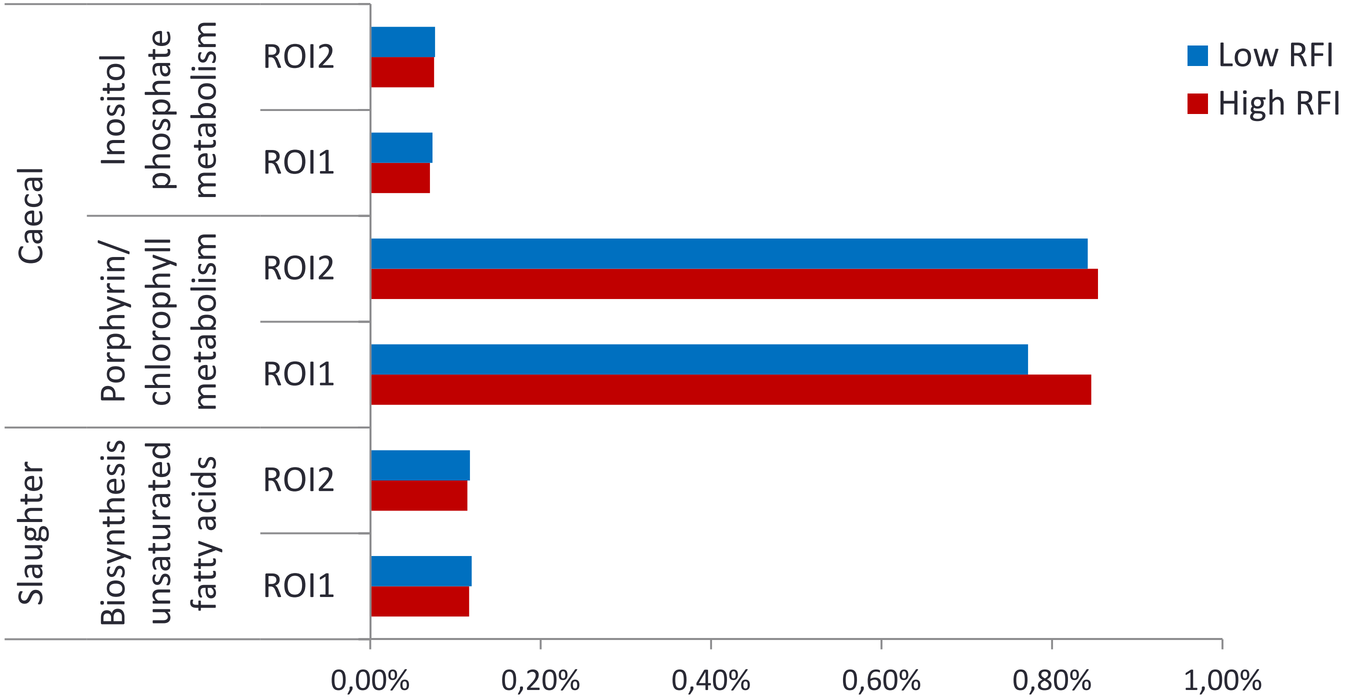
(102 pathways)

Common predicted microbial pathways

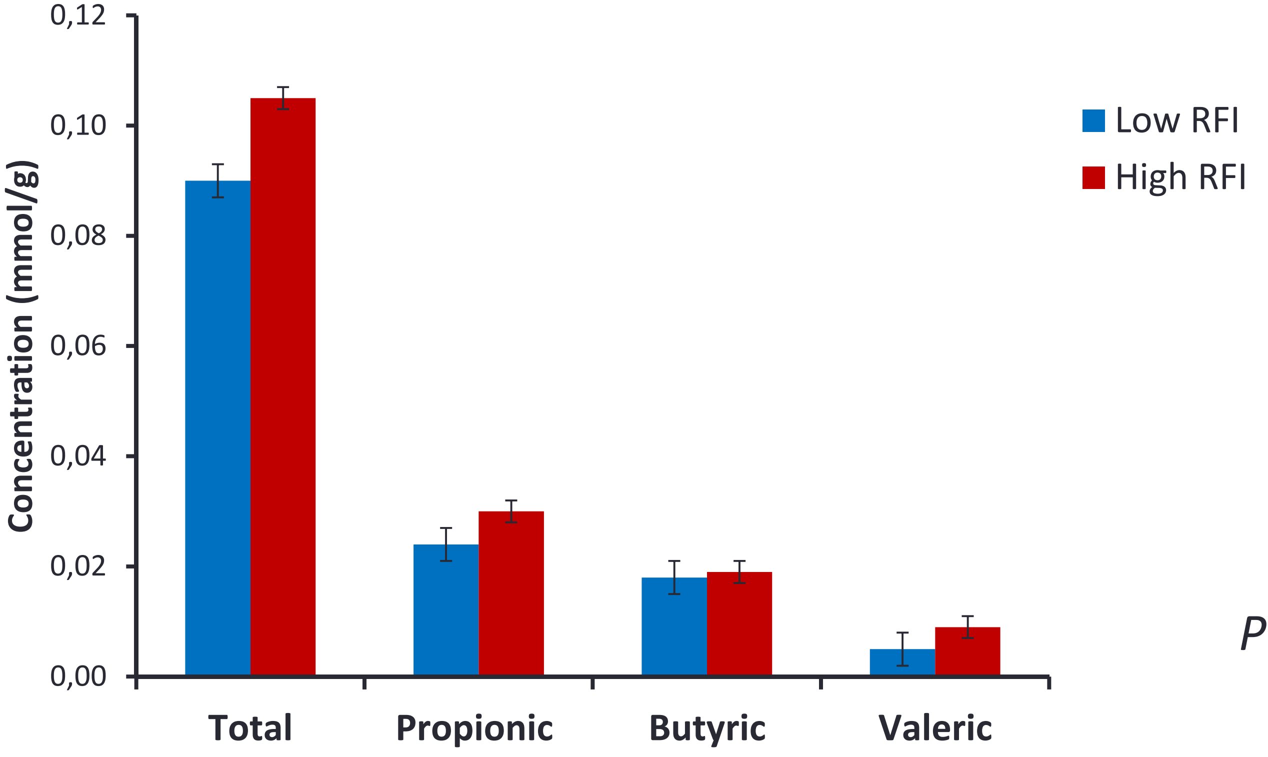


- Common pathways related with core metabolism
- Only between the 2 batches of ROI

P<0.05
(102 pathways)

Volatile fatty acid concentrations

Faeces (day 105 pw)
ROI medium health



P<0.05

No significant differences found in ileal or caecal digesta

Conclusions

- **Intestinal microbiota**
  - Higher diversity in ileal and caecal digesta of low RFI pigs (ROI high health)
  - No clustering by RFI, but clustering by age, sample type & geographic site

  - Compositional differences between high and low RFI across sites:

some **possible biomarkers** for improved FE

- ↑ *Mucispirillum* (carbohydrate-degrading activity)
- ↑ *Lentisphaerae* phylum, *Methanobrevibacter* (improved health and reduced obesity)
- ↑ *Ruminococcaceae* (cellulose degrading ability)
- ....

Conclusions

- **Predicted microbial functionality:**
  - Most abundant bacterial pathways (↑ low RFI, some sites) belonging to **CHO, energy** and **nucleotide metabolism**
  - 3 metabolic pathways common between ROI1 and ROI2

- **Volatile fatty acids (VFAs)**
  - ↓ VFAs concentrations in faeces from low RFI pigs: better colonic absorption?

❑ It may be possible to target certain bacterial taxa to improve FE, BUT on a site-specific basis?

Acknowledgements

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Thank you

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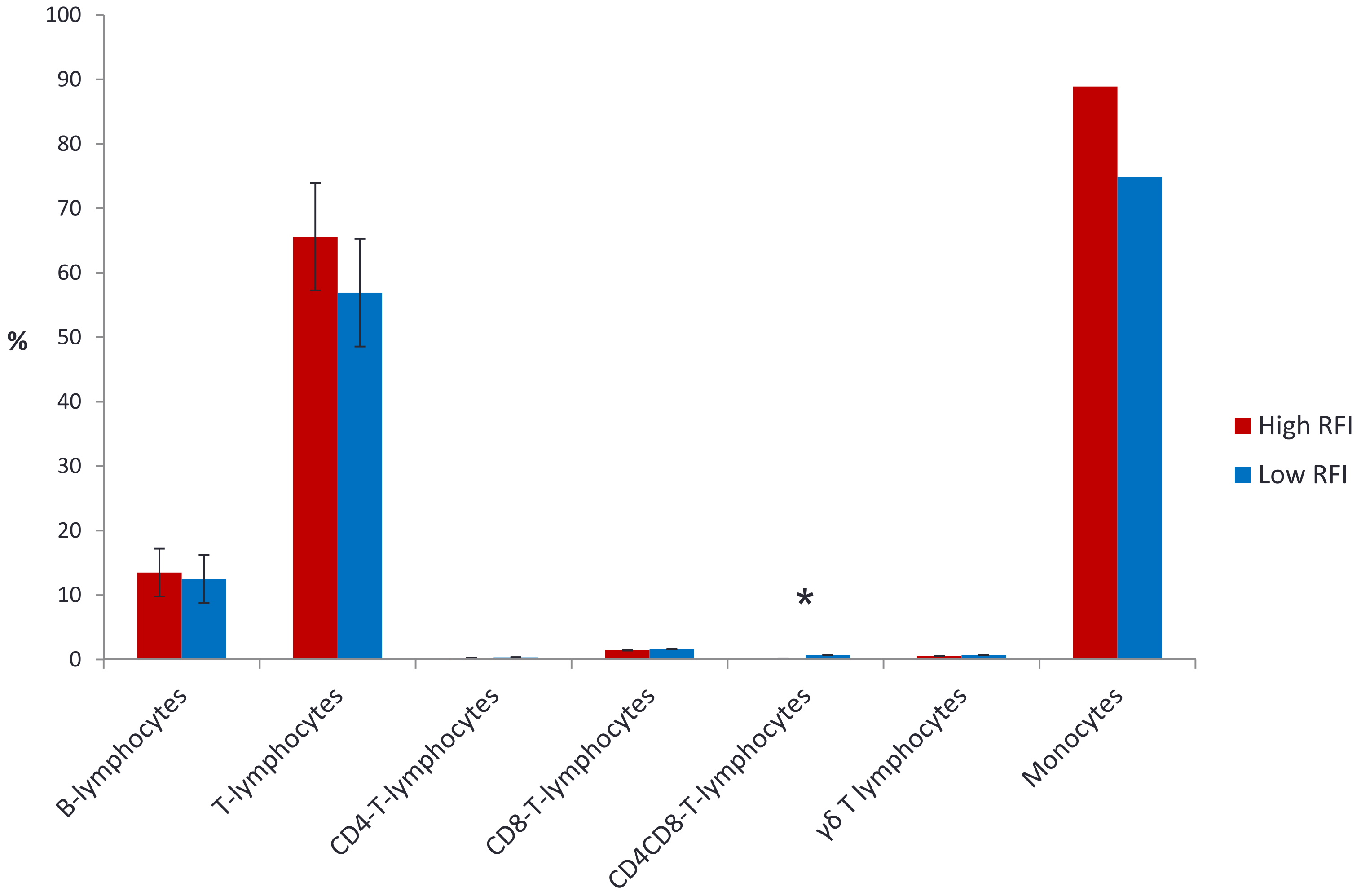
Lymphocytes



* P<0.05

Cytokines

PBS	**High RFI**	**Low RFI**	**S.E**	**P-value**
IL-4	3.28	4.94	0.260	0.69
IL-6	3.77	2.41	0.310	0.76
IL-8	7.76	5.61	0.403	0.61
TNFα	3.28	3.92	0.302	0.98
PMA	**High RFI**	**Low RFI**	**S.E**	**P-value**
IL-4	4.16	3.86	0.270	0.97
IL-6	4.36	4.08	0.320	0.99
IL-8	5.93	6.33	0.400	0.71
TNFα	2.58	3.73	0.300	0.83

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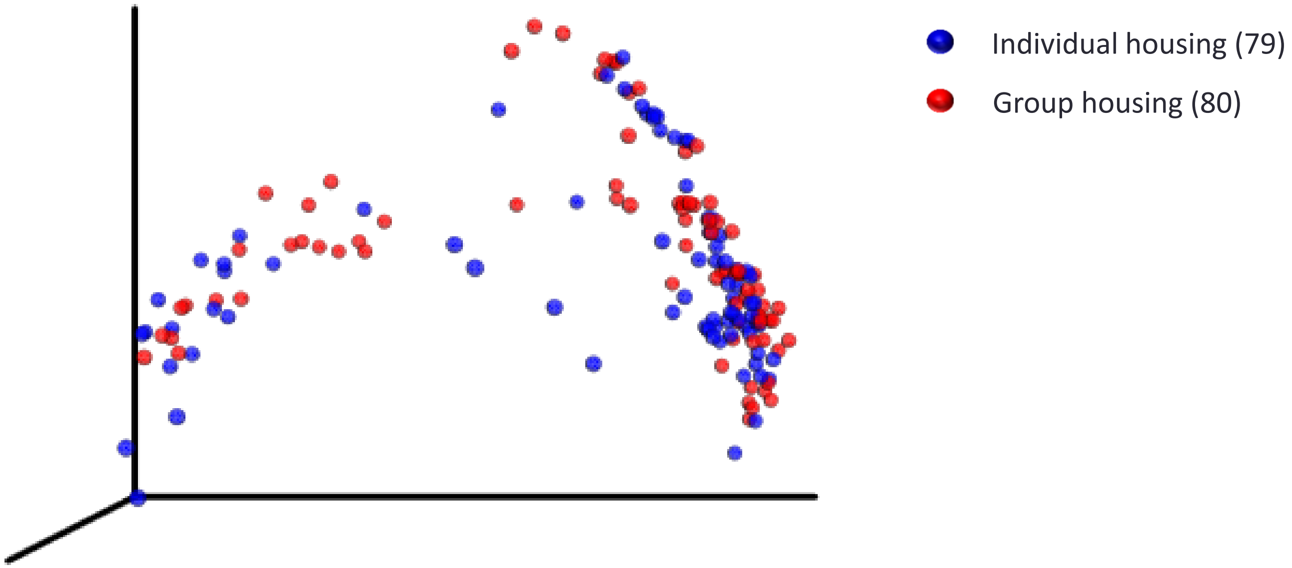
Effect of housing: medium health pigs (ROI)



P>0.01