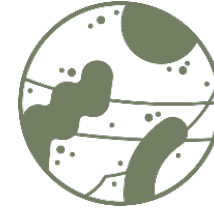




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Hohenheim Center for ———
Livestock Microbiome Research

Microbial architecture and enterotypes for improved nitrogen utilization efficiency in fattening pigs

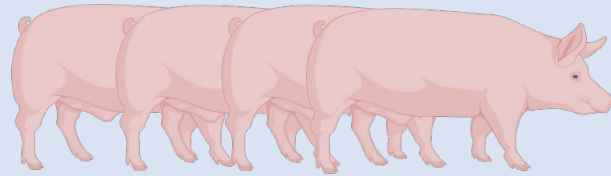
Naomi Sarpong, Jana Seifert, Jörn Bennewitz, Markus Rodehutschord,
Amélia Camarinha-Silva

Introduction

Pig production
with challenging
issues

Reduce negative environmental impact:

↑ Nitrogen utilization efficiency (NUE)



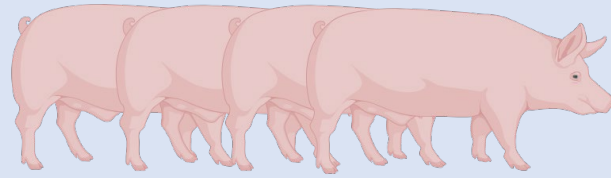
NUE = proportion of ingested N retained in the body

Introduction

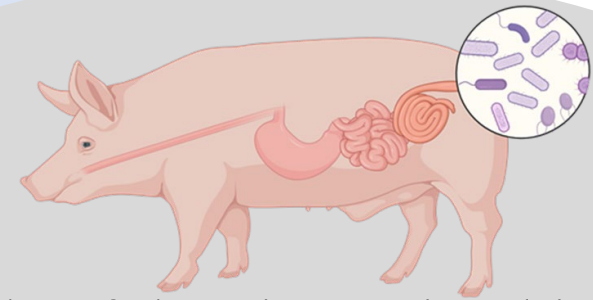
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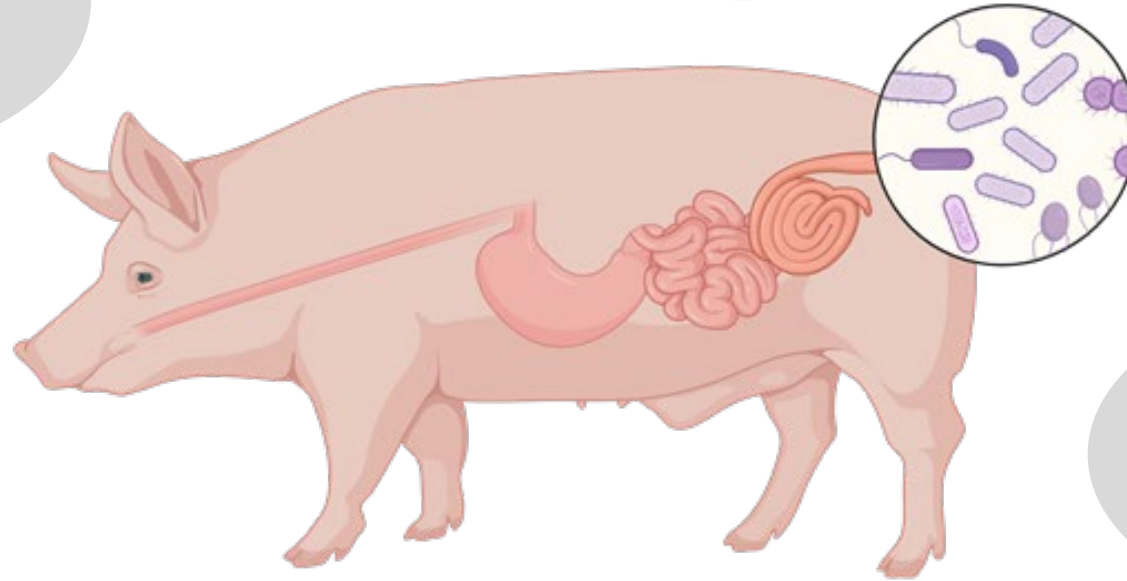


Role of the pig's microbiota?

Introduction

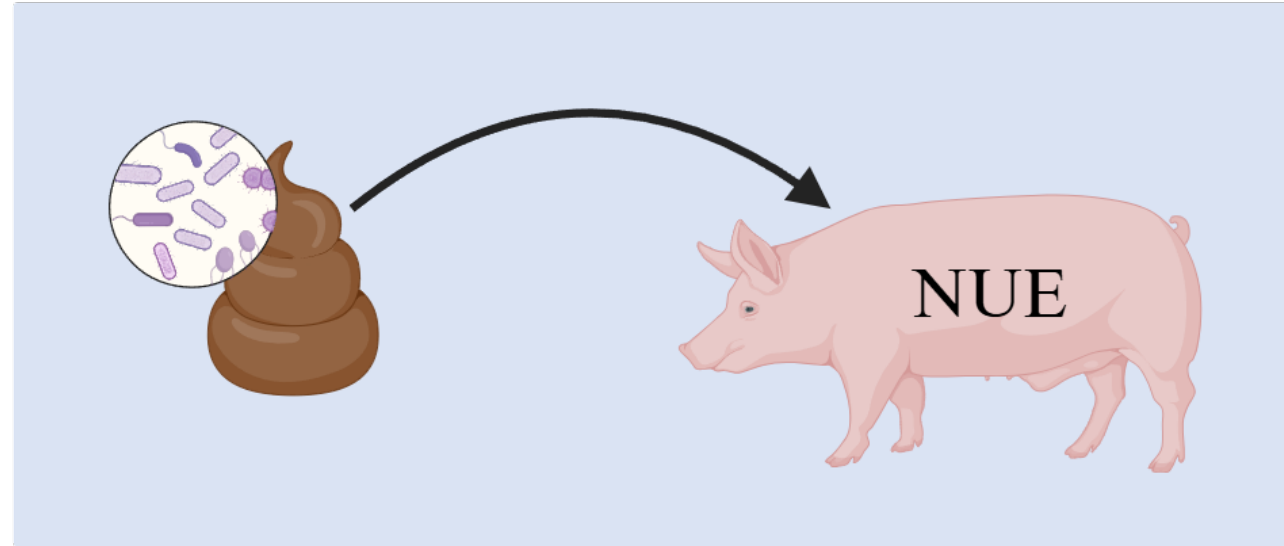
“Microbial
accessible
protein”

BCFAs serve
as marker



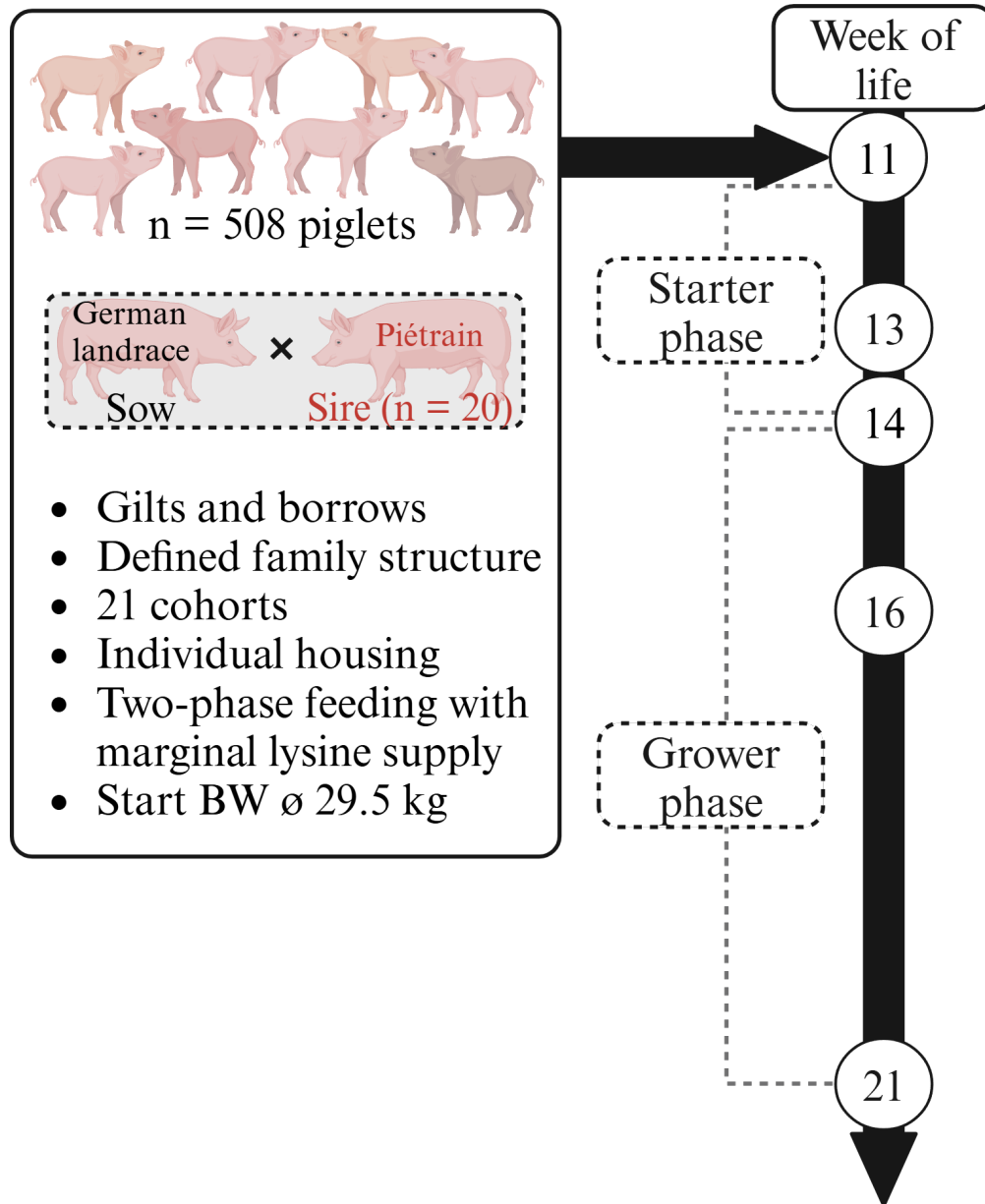
Bacteria with
proteolytic
abilities

Aim of the study

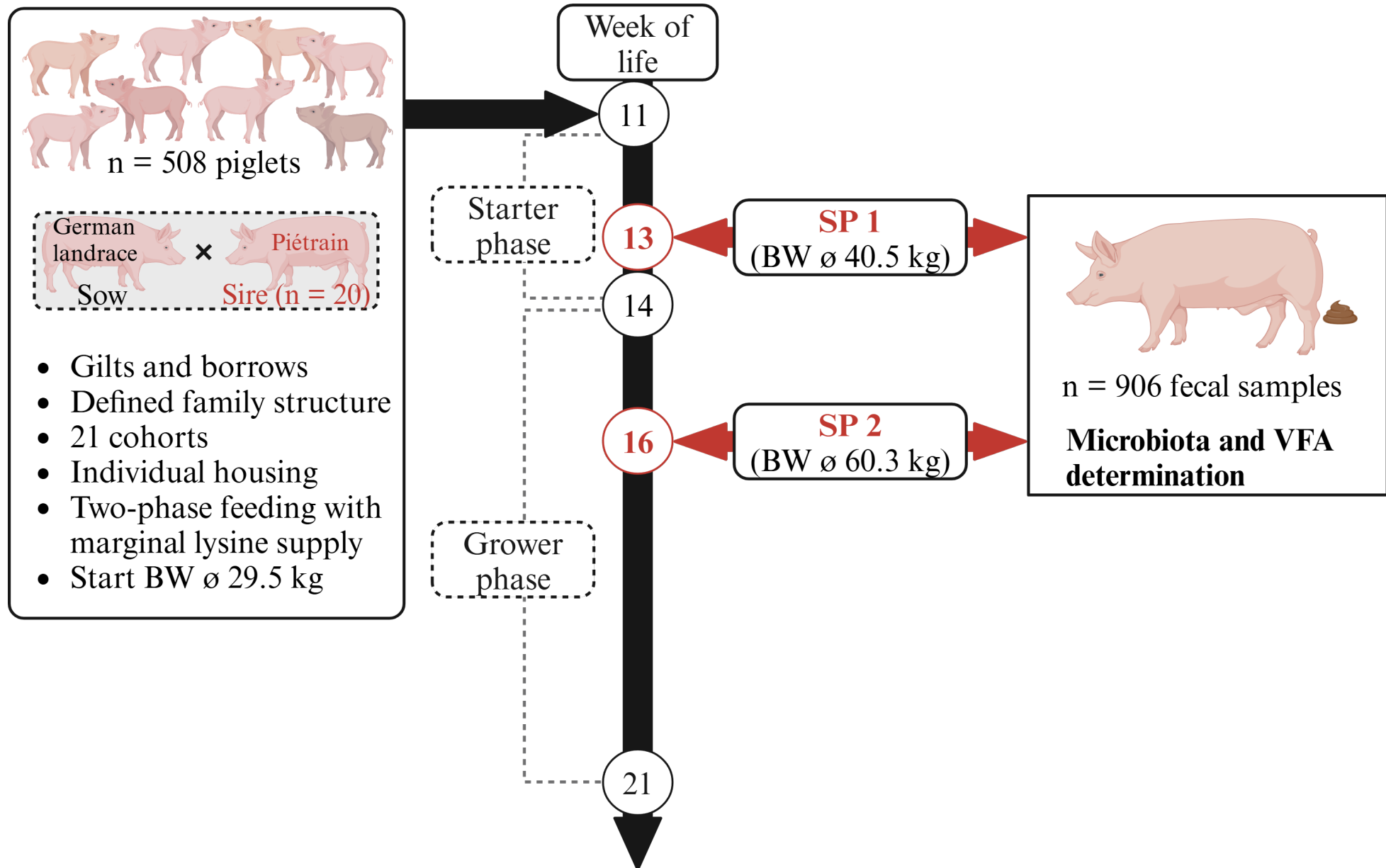


- to reveal the interrelationship between the **fecal microbiota** of fattening pigs with a defined family structure, their produced **metabolites**, and **NUE**.

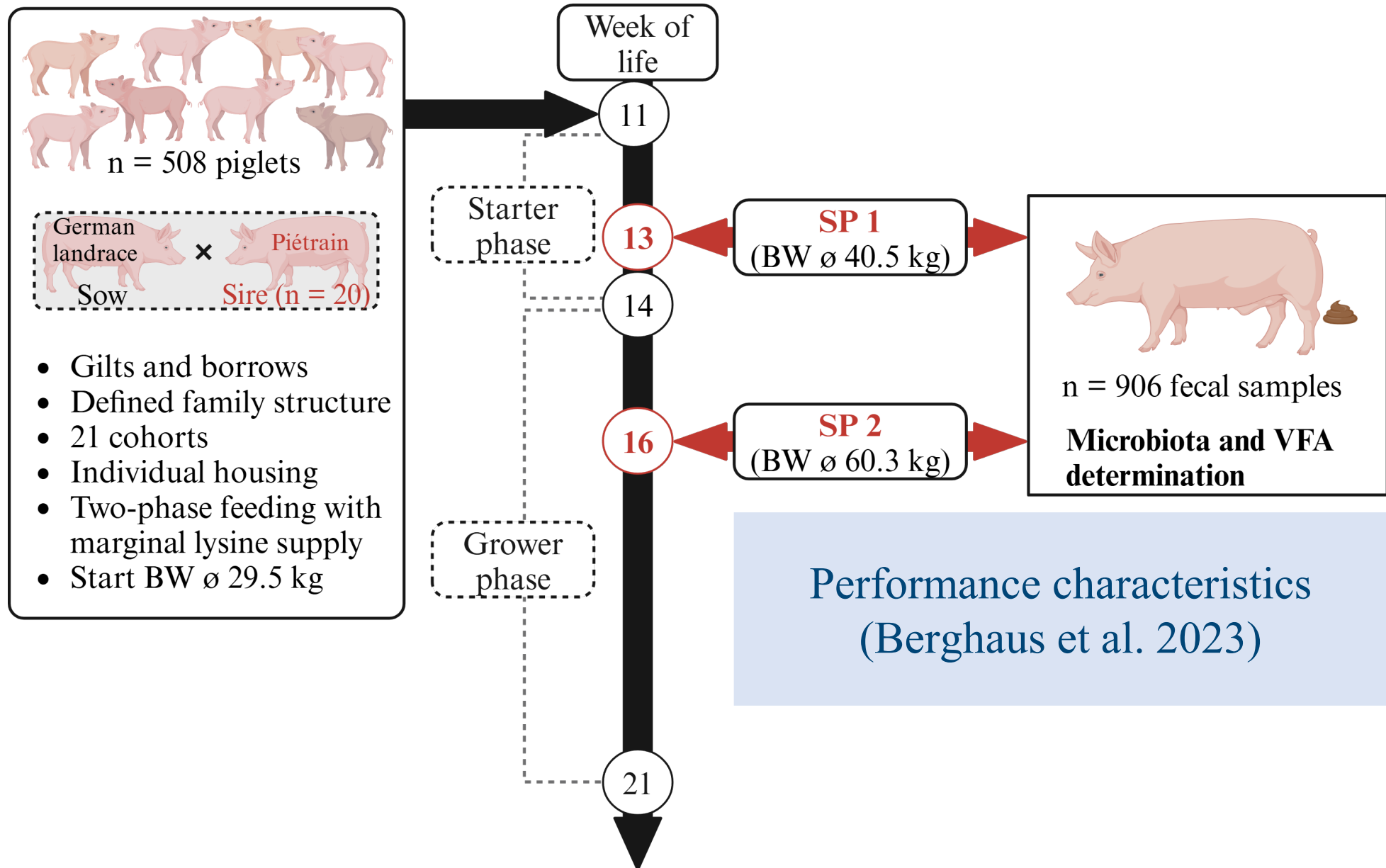
Material and methods



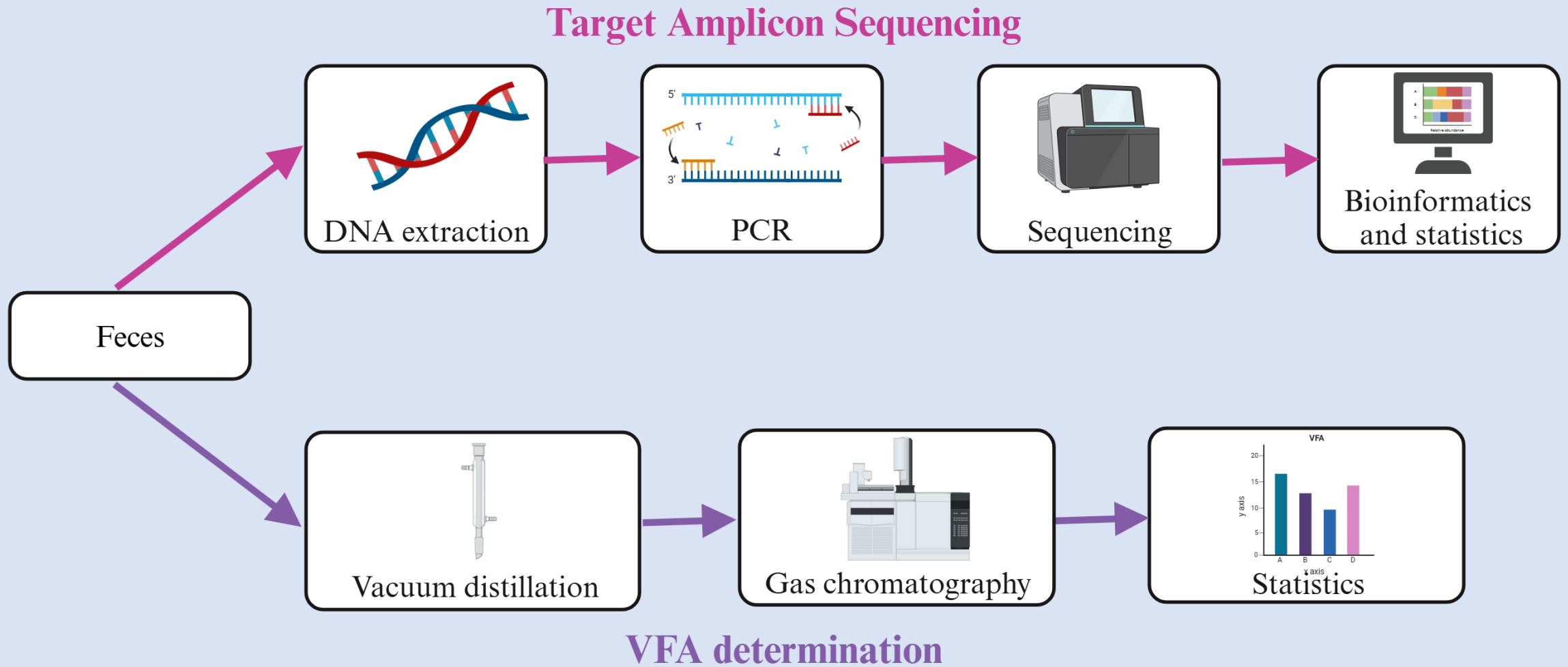
Material and methods



Material and methods



Material and methods



Results

Link between NUE and microbial composition? (**individual SPs**)

Comparison of NUE_{High} and NUE_{Low} group within each SP:

SP 1	NUE_{Low}	38-47% (n = 111)
	NUE_{High}	50-58% (n = 112)
SP 2	NUE_{Low}	35-43% (n = 109)
	NUE_{High}	46-52% (n = 110)

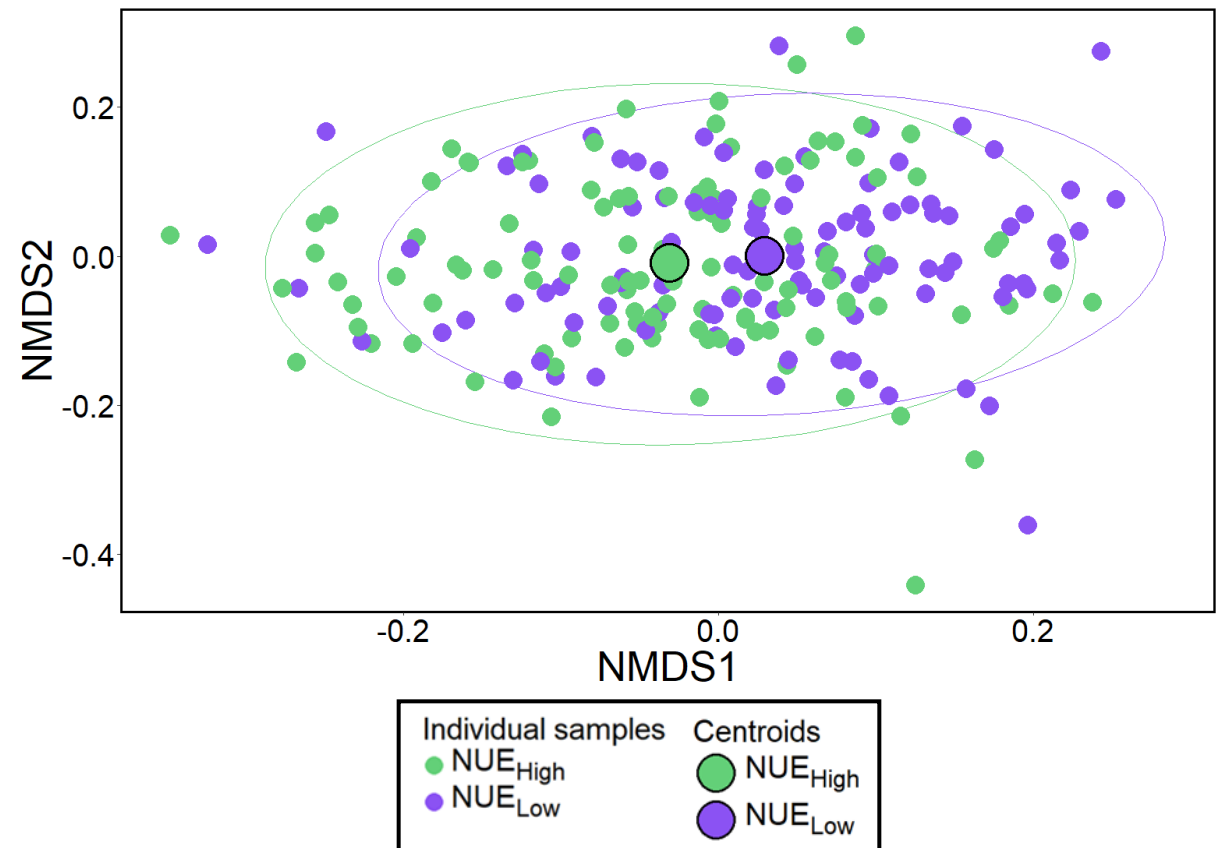
Results

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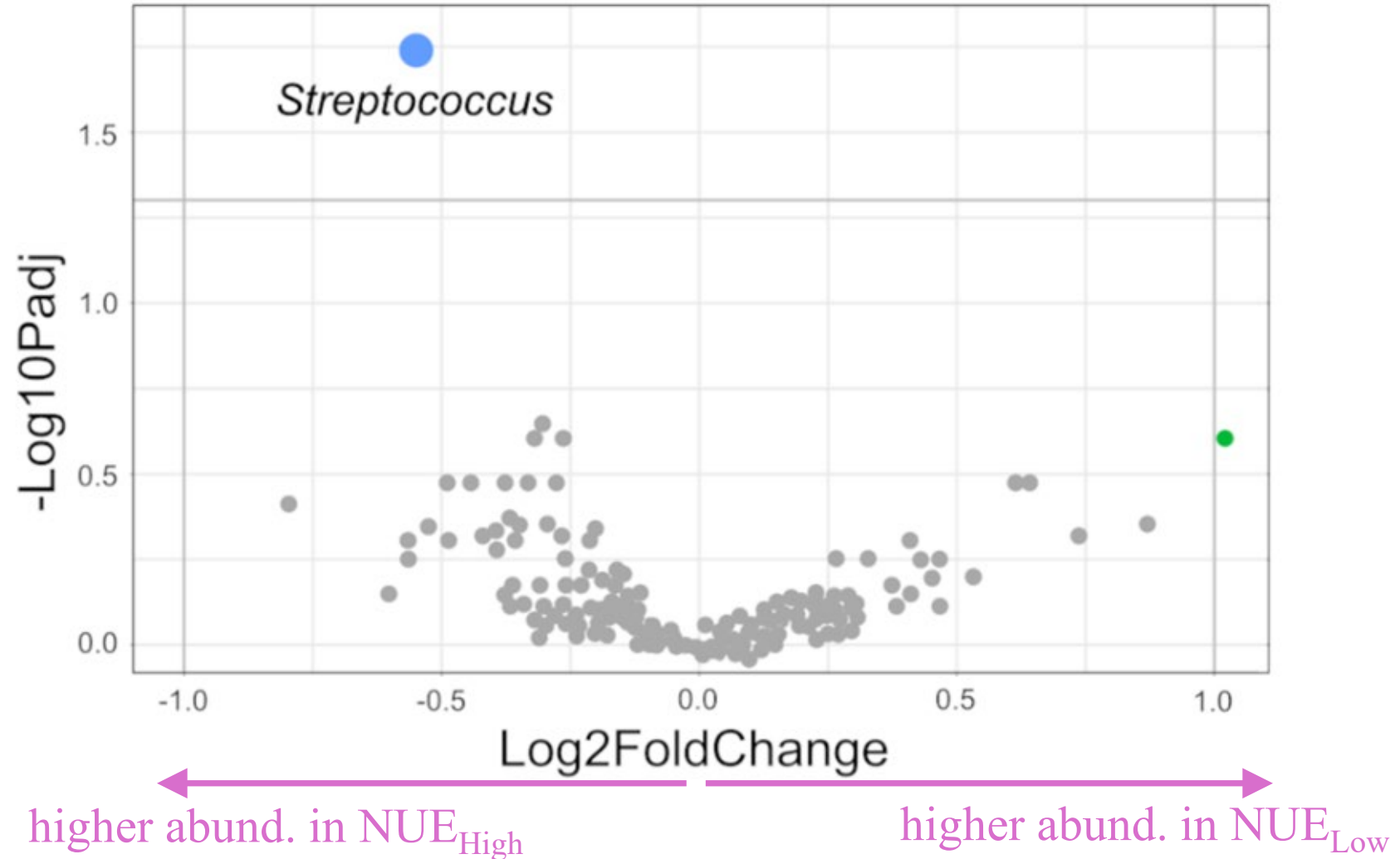
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	NUE_{High}	46-52% (n = 110)

NUE_{High} vs. NUE_{Low}
SP 1: $P < 0.001$; SP 2: $P = 0.06$



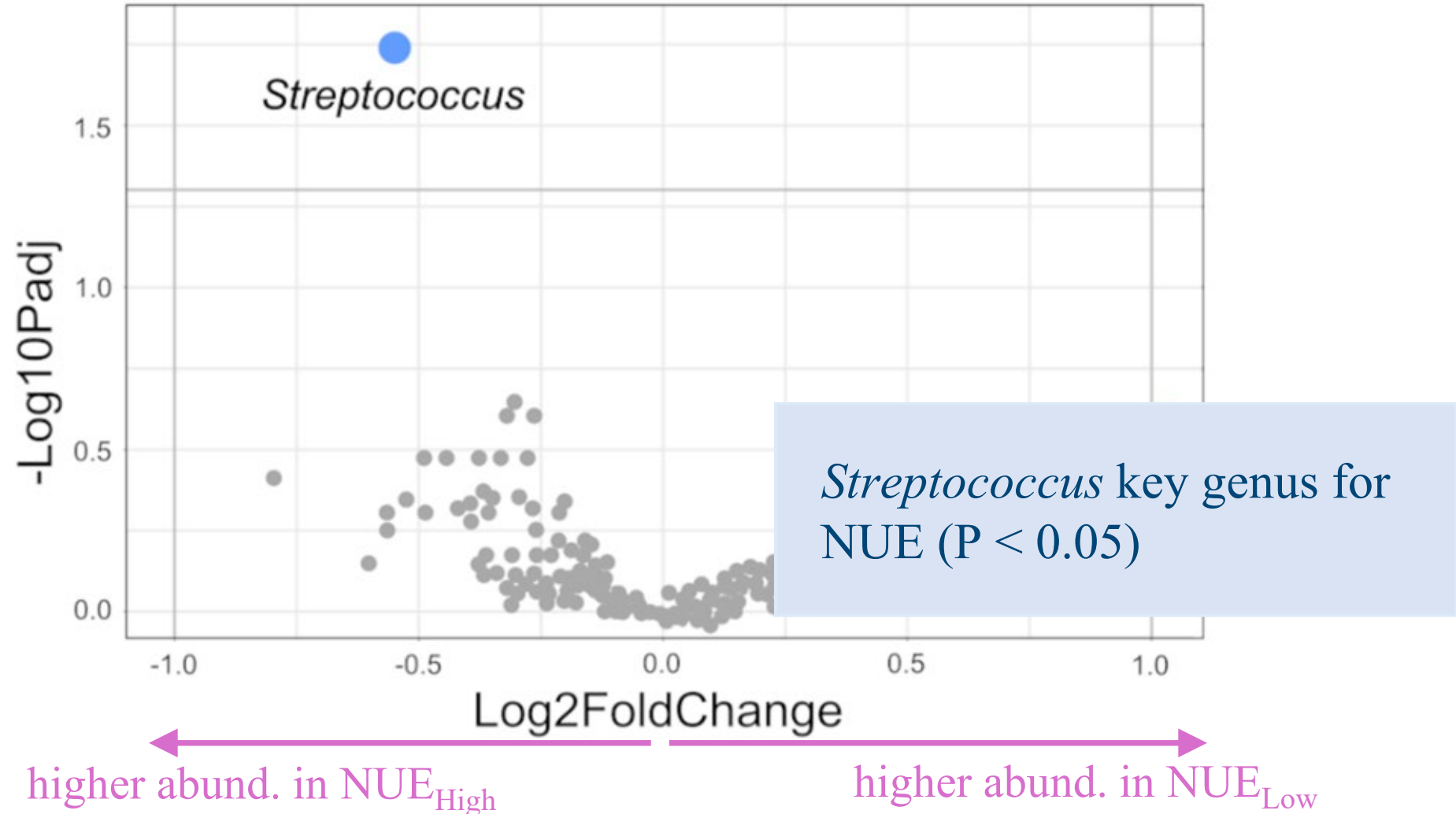
Results

LinDA model for the comparison of NUE_{High} and NUE_{Low} group in SP 1



Results

LinDA model for the comparison of NUE_{High} and NUE_{Low} group in SP 1

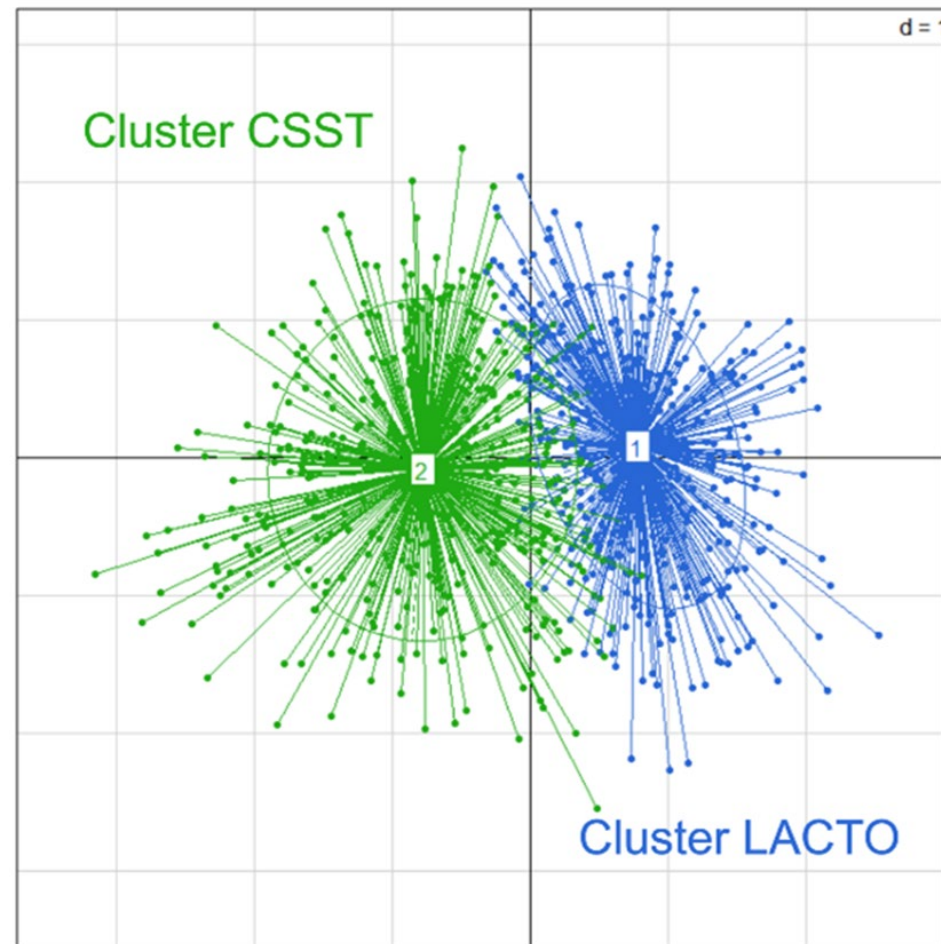


Results

Could we group the whole data set? (**both SPs**)

Cluster

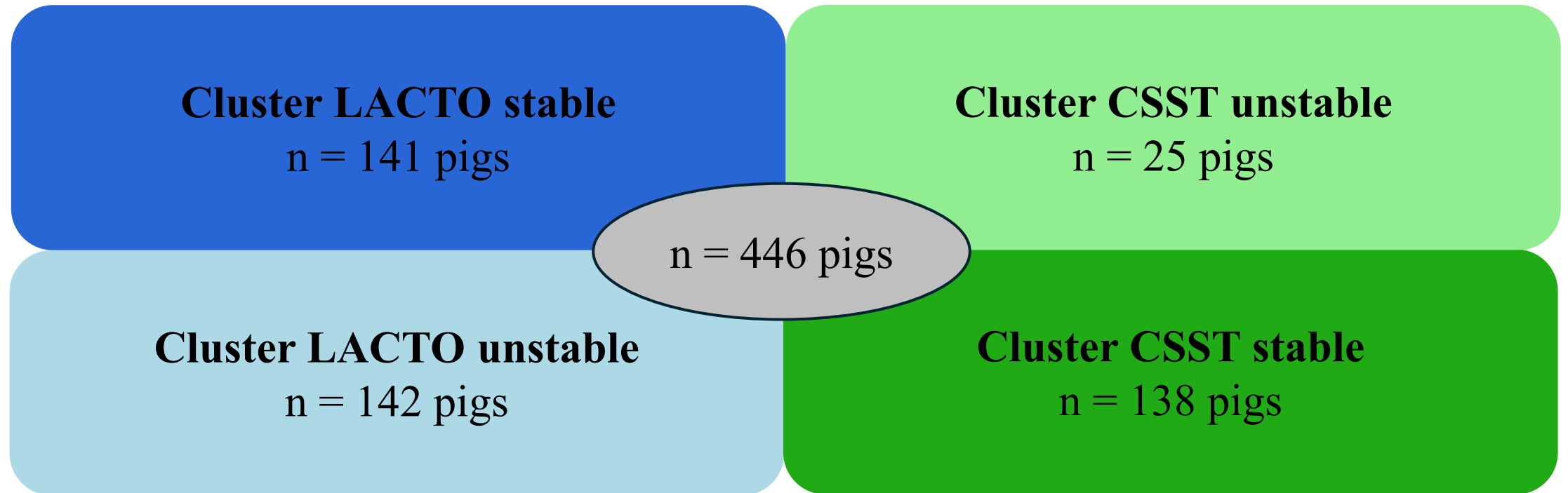
Clostridium sensu stricto



Cluster
Lactobacillus

Results

Stability from SP 1 to SP 2



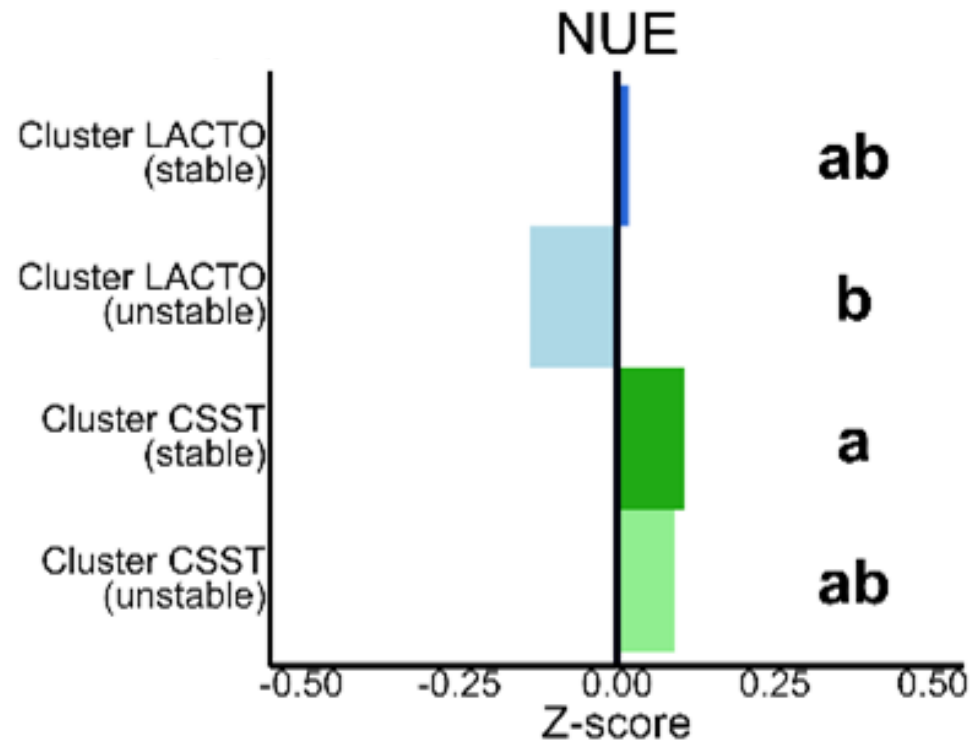
Cluster LACTO unstable: Cluster LACTO (SP 1) → Cluster CSST (SP 2)

Cluster CSST unstable: Cluster CSST (SP 1) → Cluster LACTO (SP 2)

Results

Is there a link to the performance characteristics? (**over both SPs**)

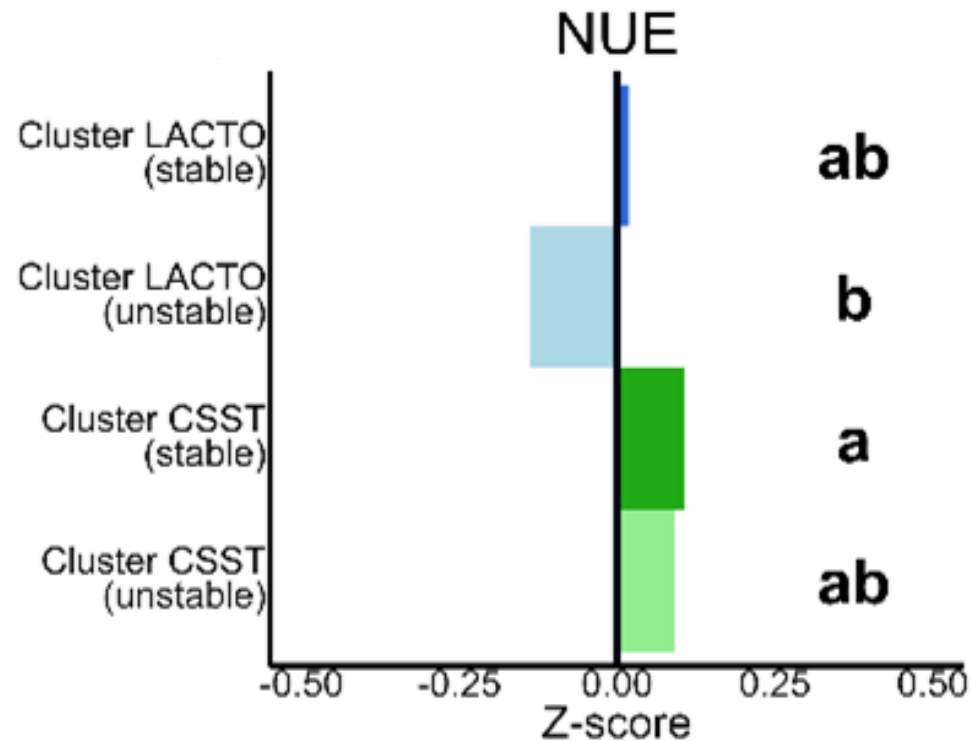
Performance characteristics



Results

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Performance characteristics

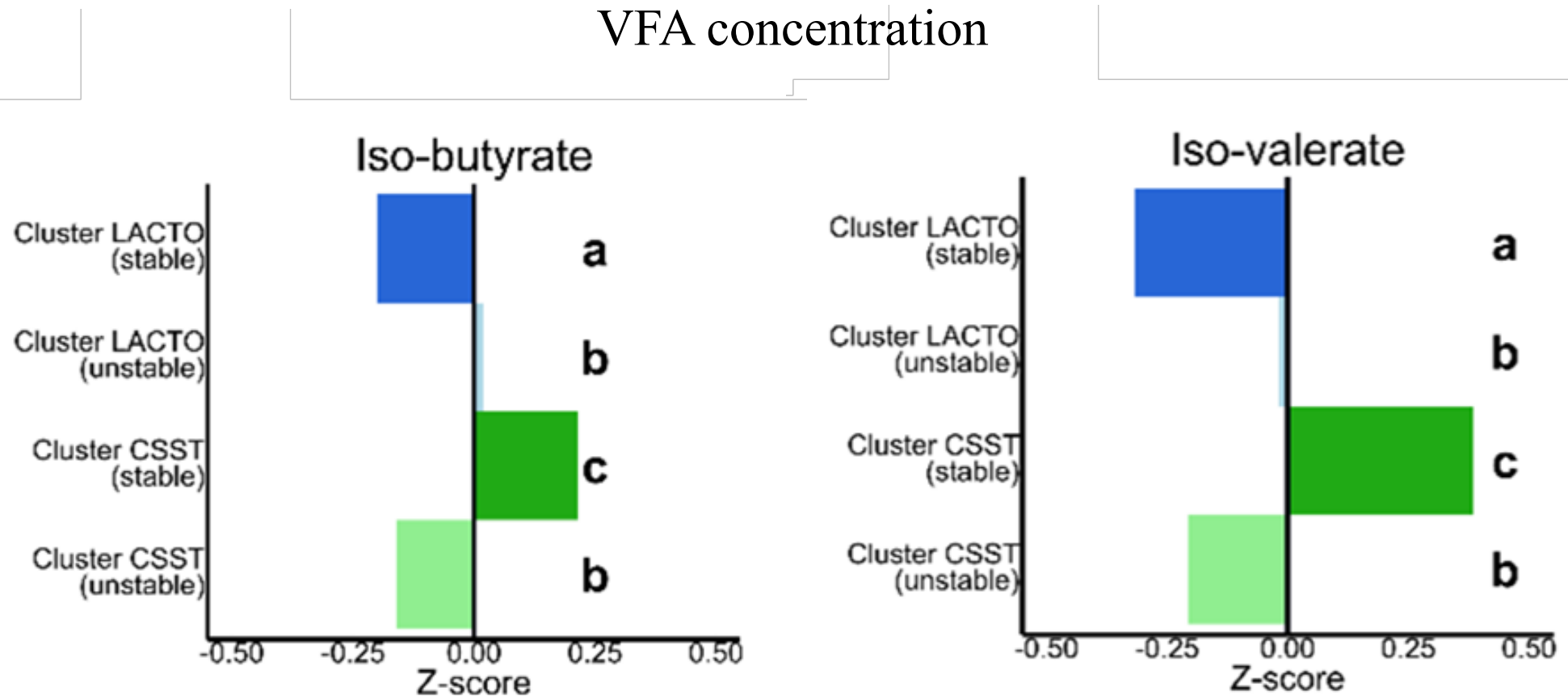


Cluster CSST (stable) lowest
ADG, DMI and **DNR** ($P < 0.05$)

No differences for **BW** and **G:F**
between subgroups ($P > 0.05$)

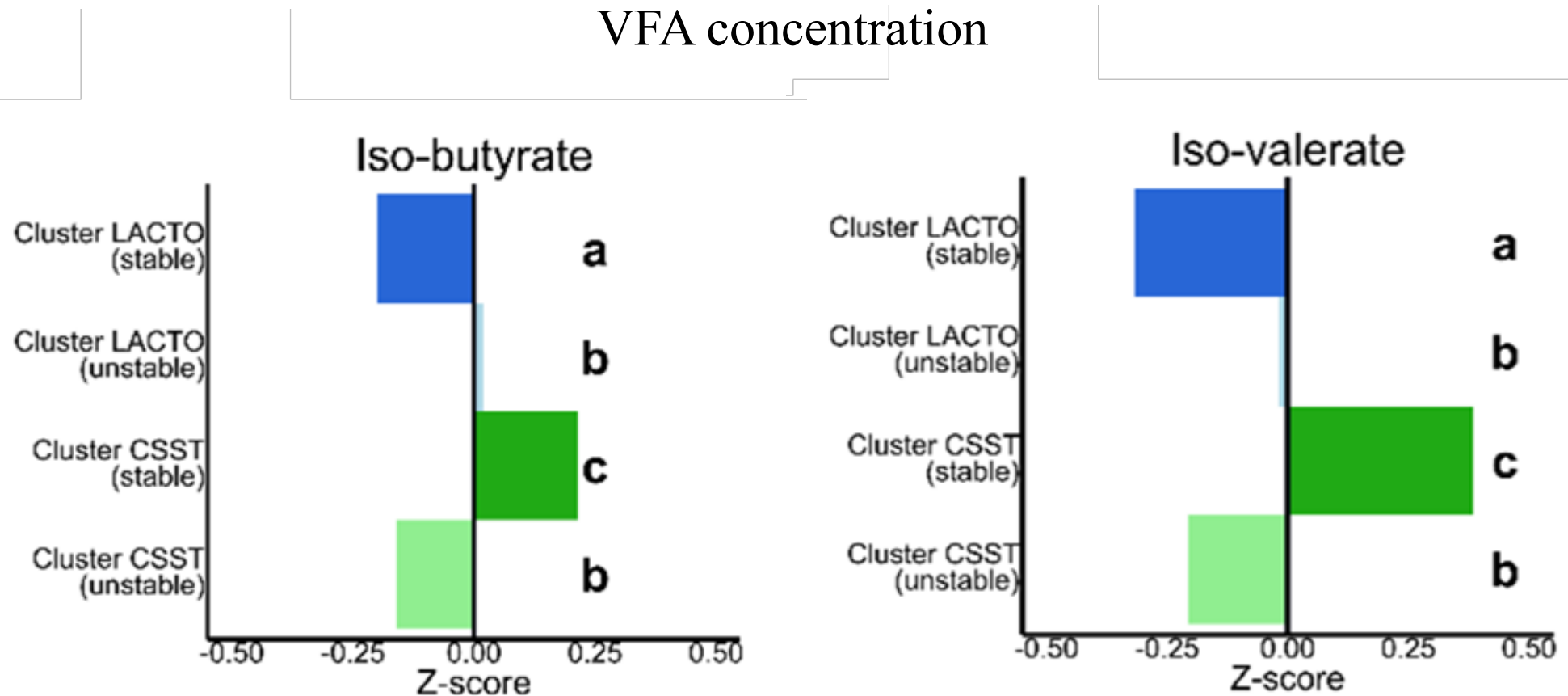
Results

Are there different VFA fermentation patterns? (**over both SPs**)



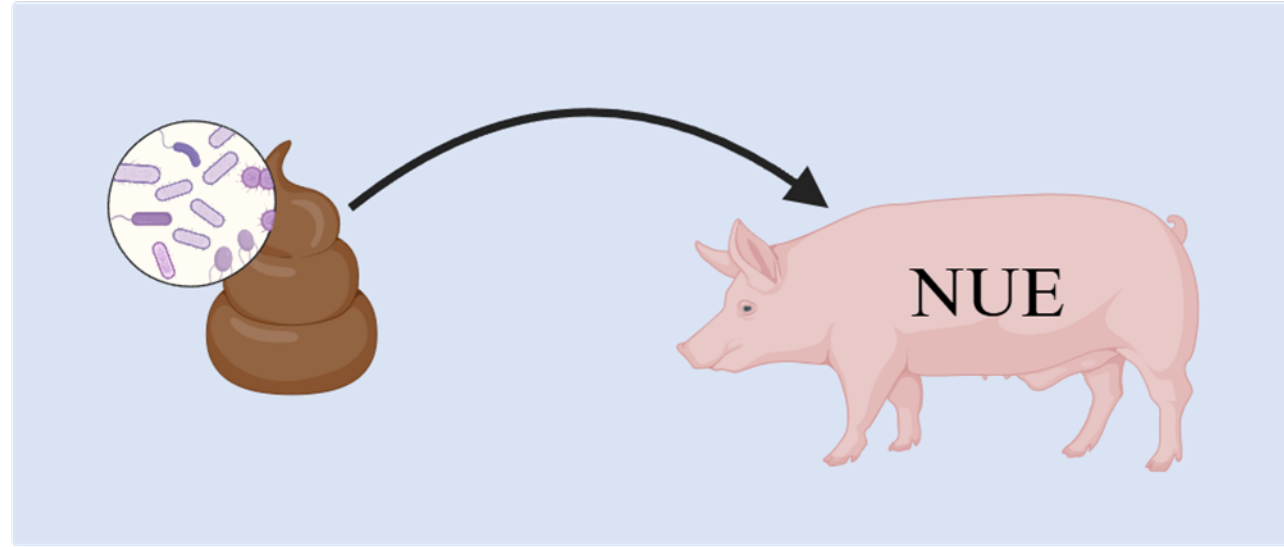
Results

Are there different VFA fermentation patterns? (**over both SPs**)

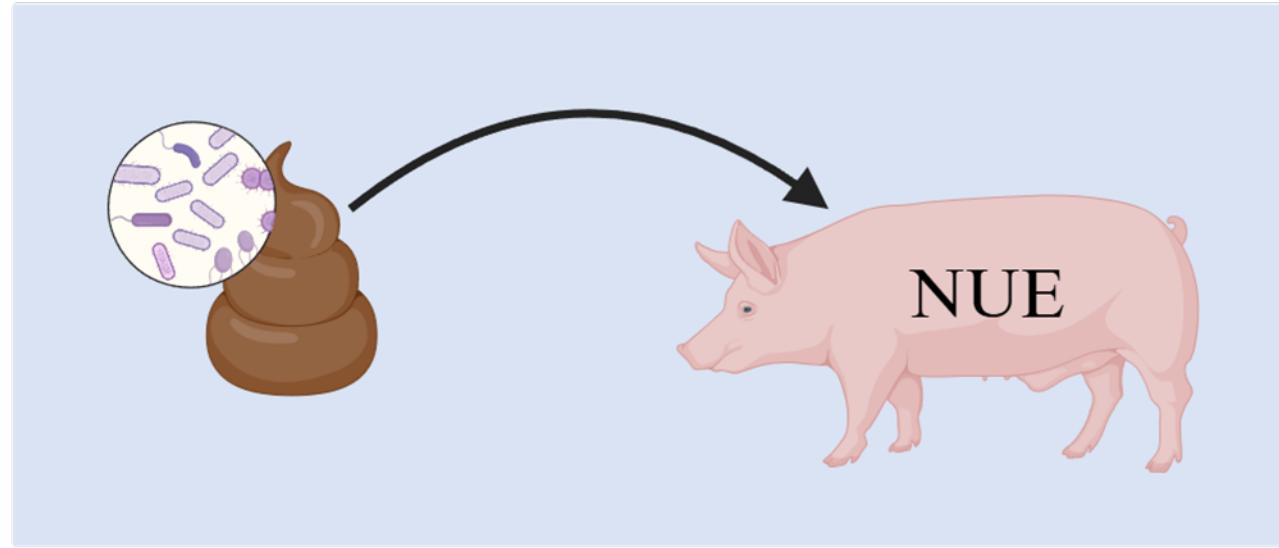


Cluster CSST stable had highest protein fermentation potential

Conclusion

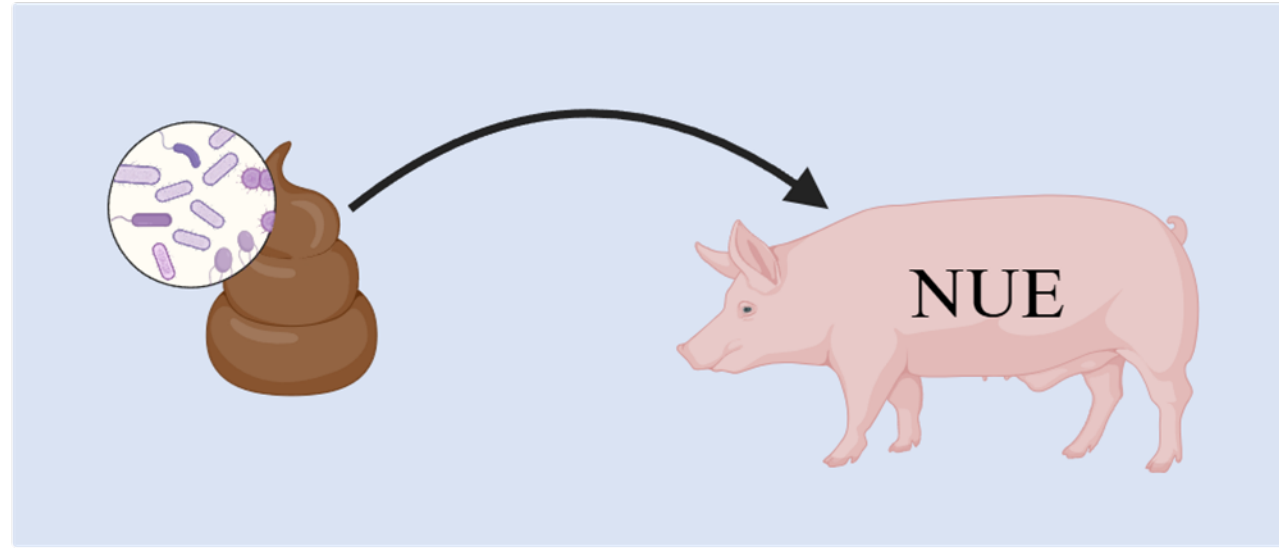


Conclusion



***Streptococcus* key genus for NUE in SP 1**

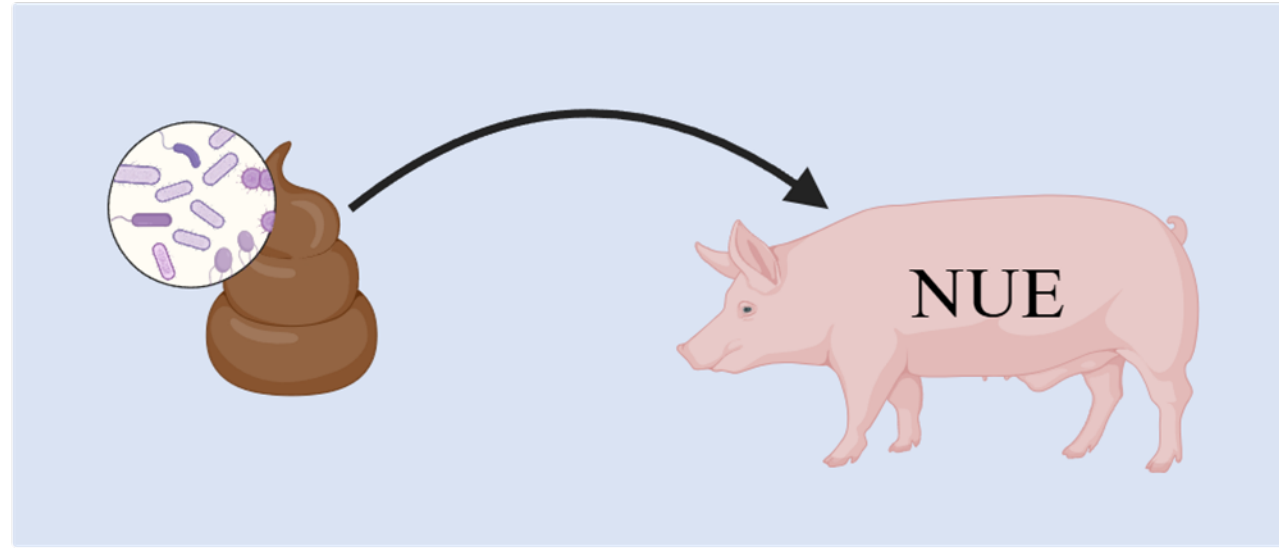
Conclusion



***Streptococcus* key genus for NUE in SP 1**

Stable subgroup of cluster CSST had highest NUE

Conclusion



Streptococcus key genus for NUE in SP 1

Stable subgroup of cluster CSST had **highest NUE**

Frontiers in Microbiology (2024):
Microbial signatures and enterotype clusters in fattening pigs: implications for nitrogen utilization efficiency

Acknowledgement

H. WILHELM SCHAUMANN STIFTUNG



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Thank you very much for your attention!

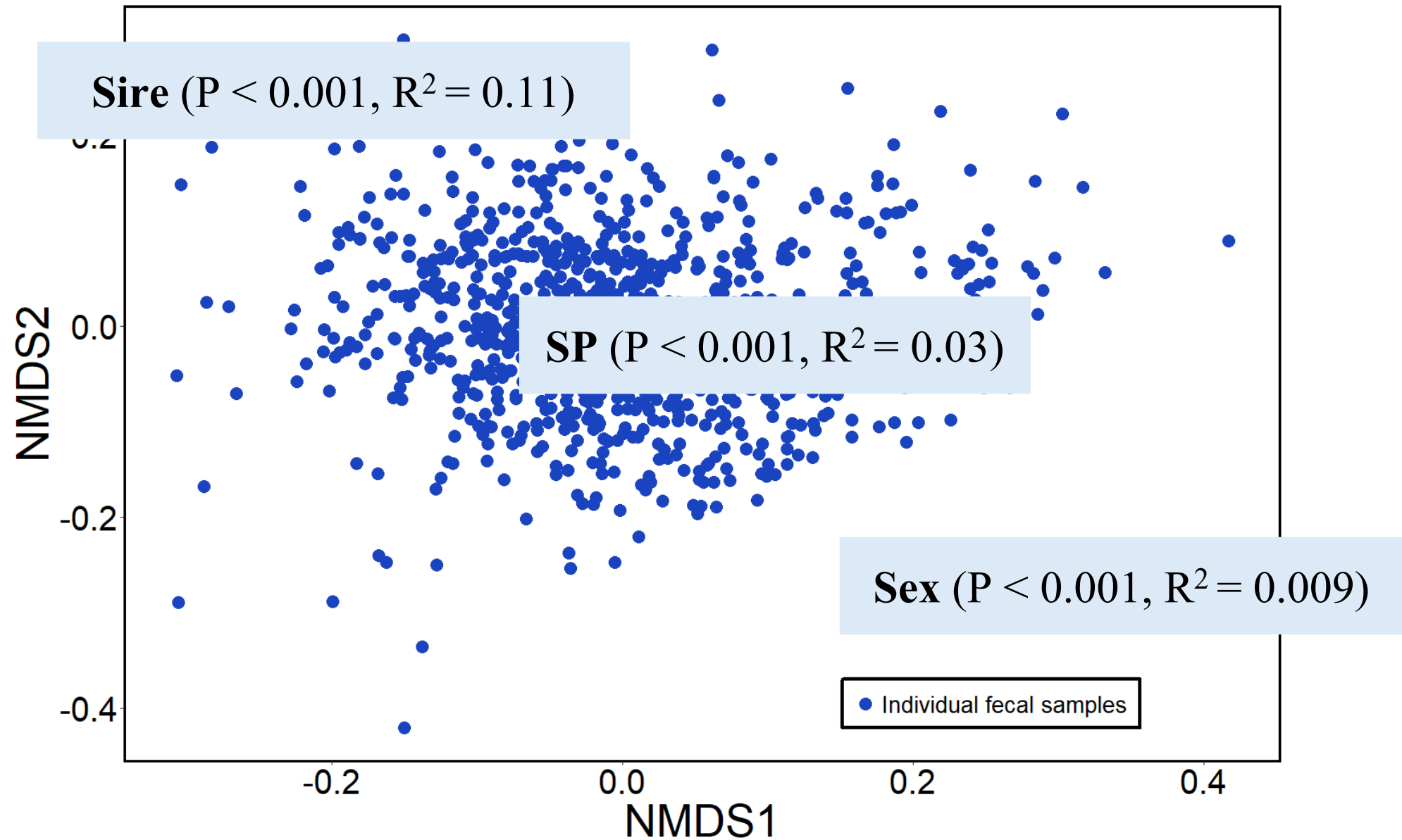
Supplementary

Table S1 Ingredient composition of the diets used in the two experimental phases.¹

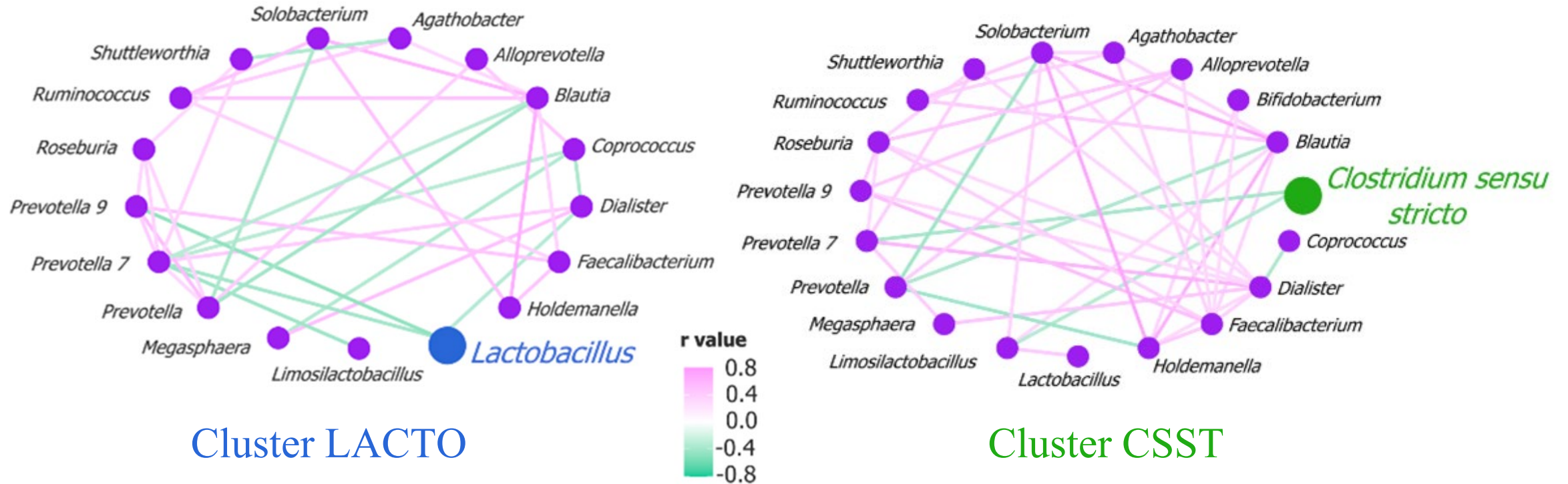
Ingredient (g/kg)	Starter phase	Grower phase
Wheat	430	430
Barley	300	402
Soybean meal	240	140
Soybean oil	3	5
Mineral-vitamin premix	27	23

¹Details of ingredient and analytical composition of the diets are contained in the companion paper (Berghaus et al. 2023)

Results



Results

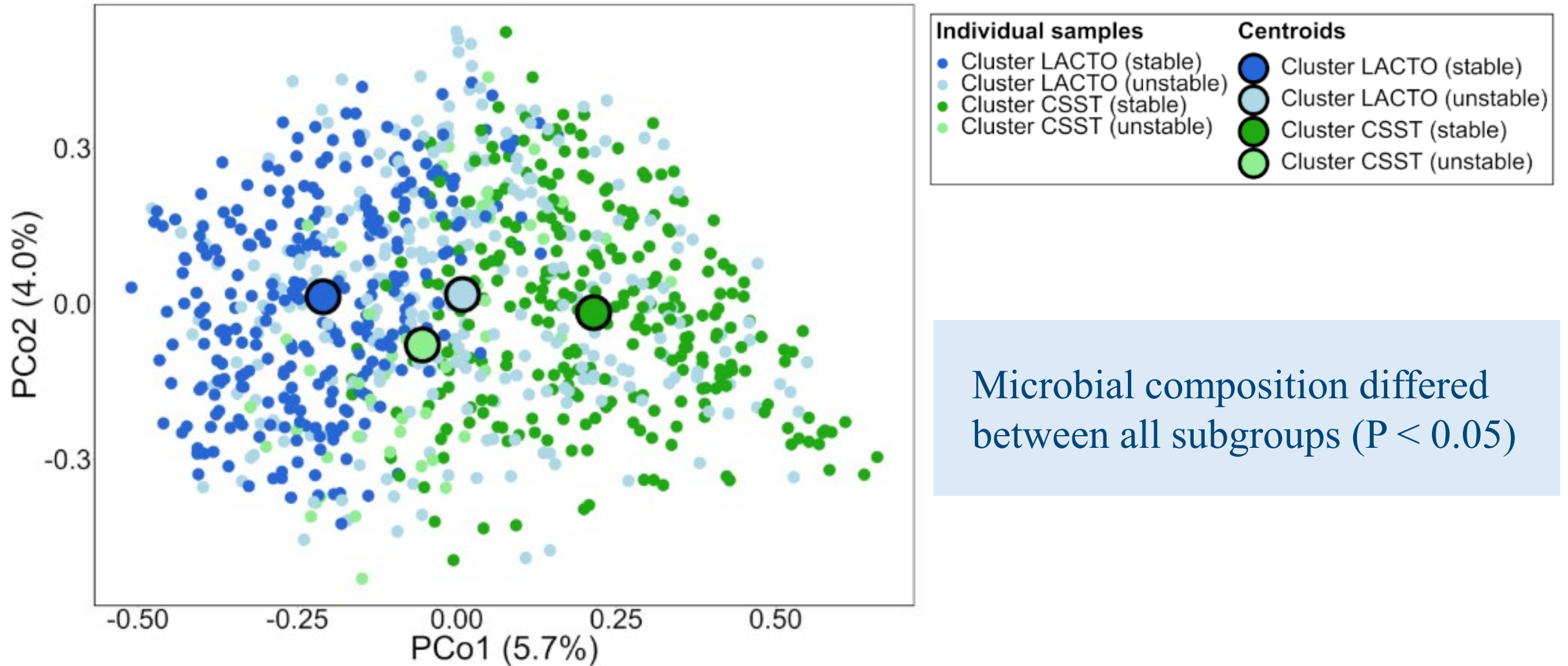


$$r > 0.3 \text{ or } r < -0.3 \text{ (} P < 0.0001 \text{)}$$

Both clusters are not group-driven!

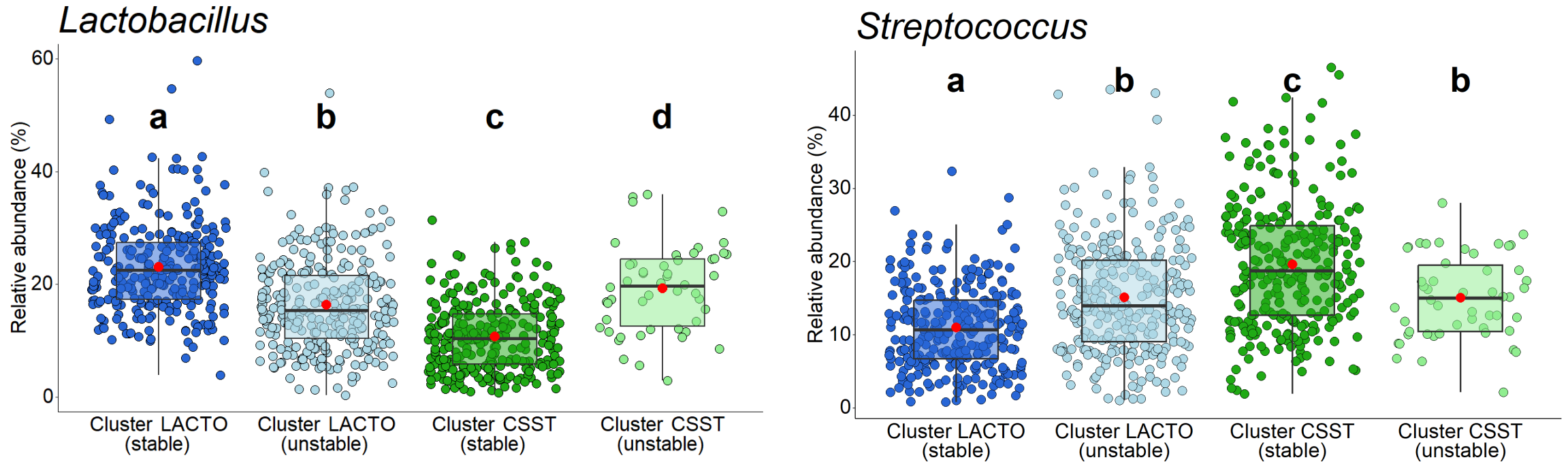
Results

Sample distribution within the subgroups of enterotype-like clusters



Results

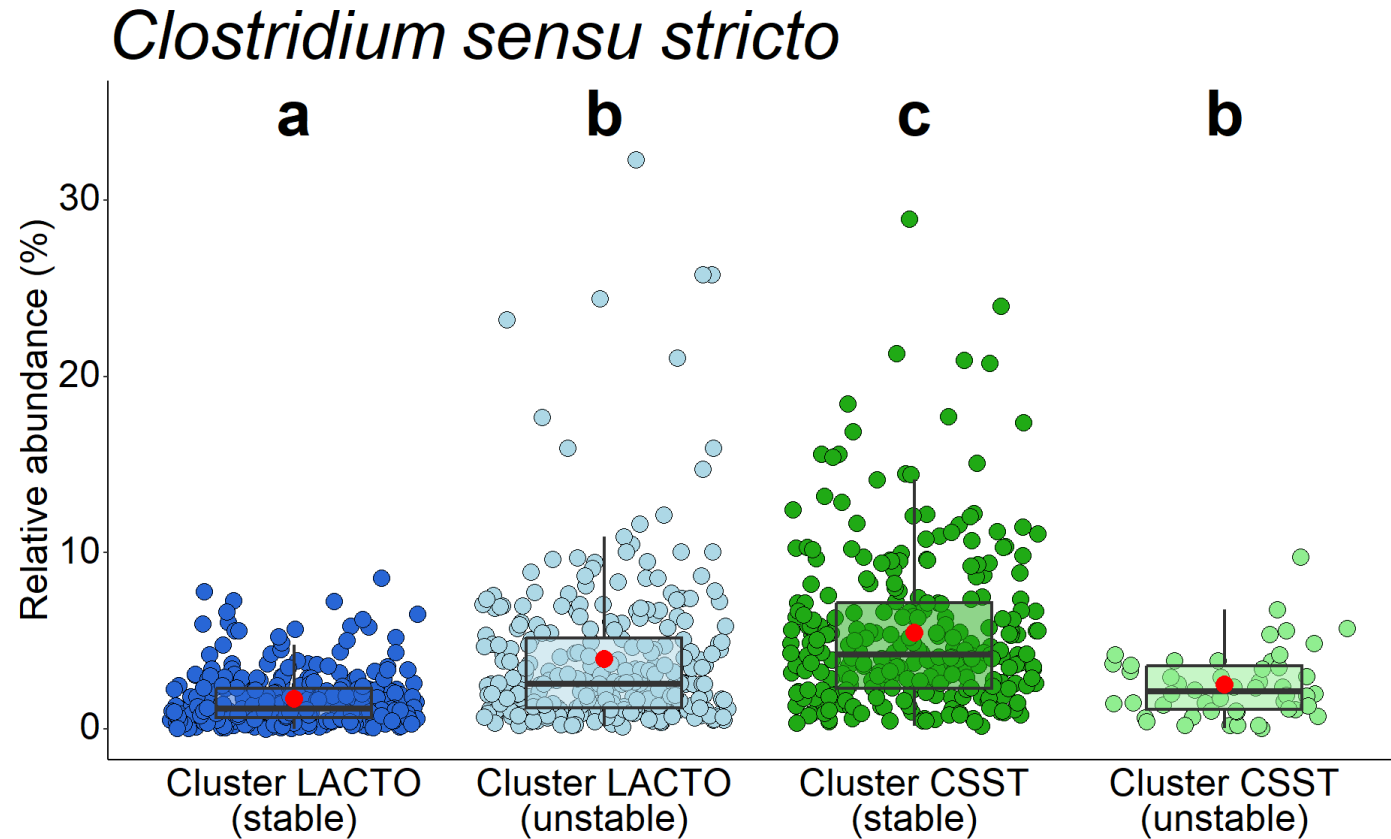
Relative abundance within the subgroups of enterotype-like clusters at the genus level



Lactic acid bacteria with varying proteolytic ability

Results

Relative abundance within the subgroups of enterotype-like clusters at the genus level



Genus less described in pigs