



## Early life profiling of weaning robustness using productive performance and gut microbiota composition



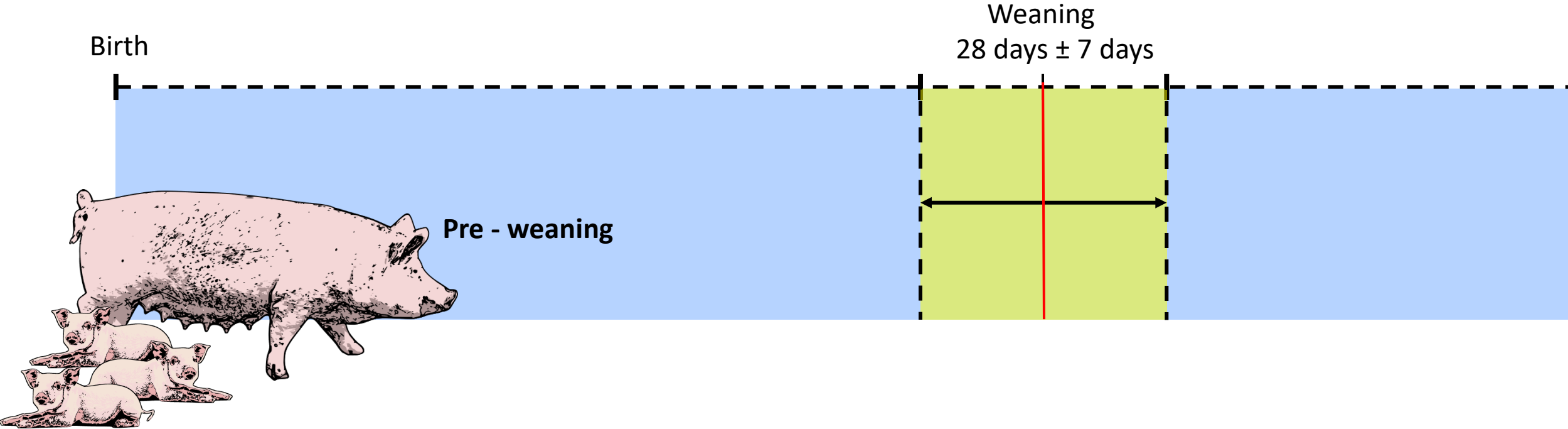
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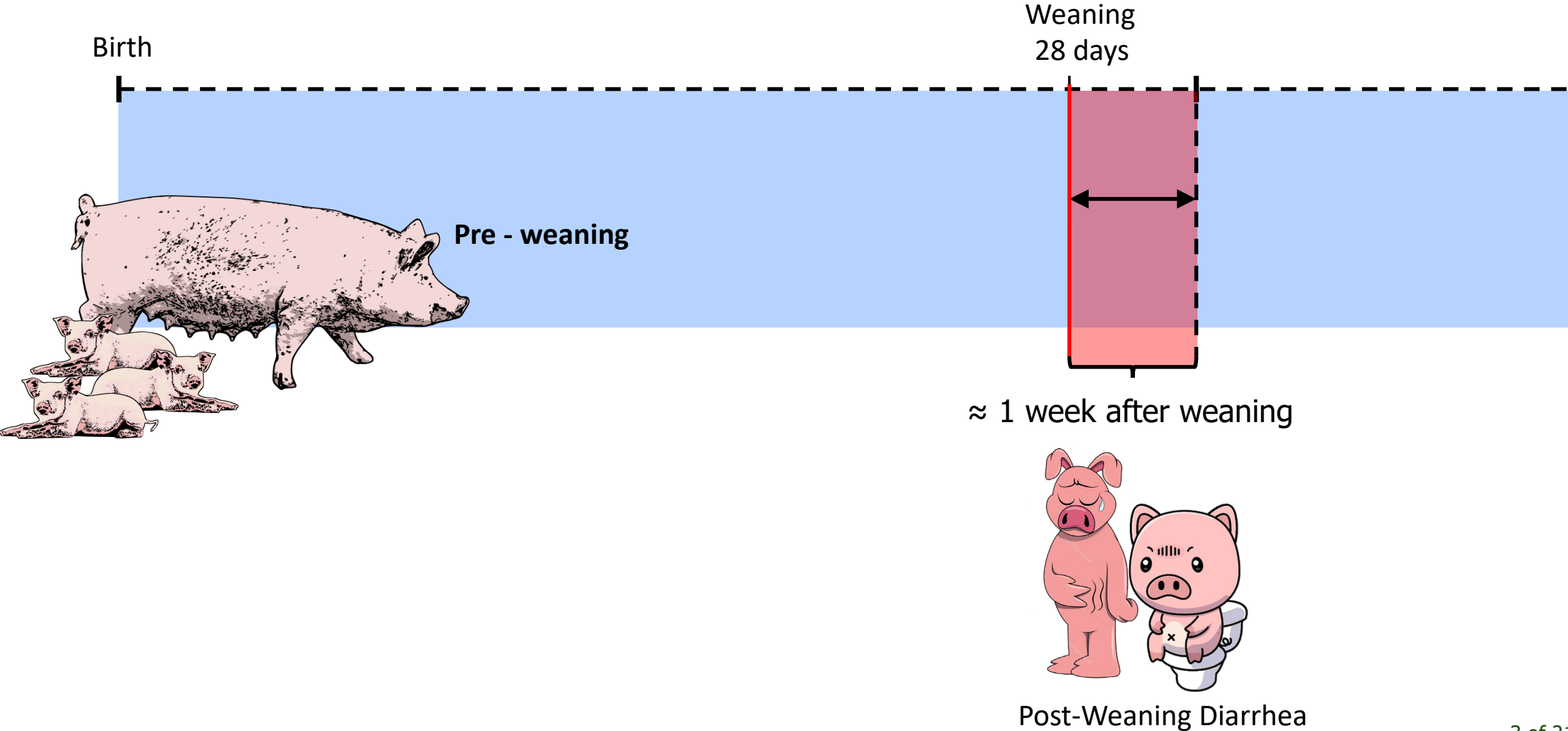
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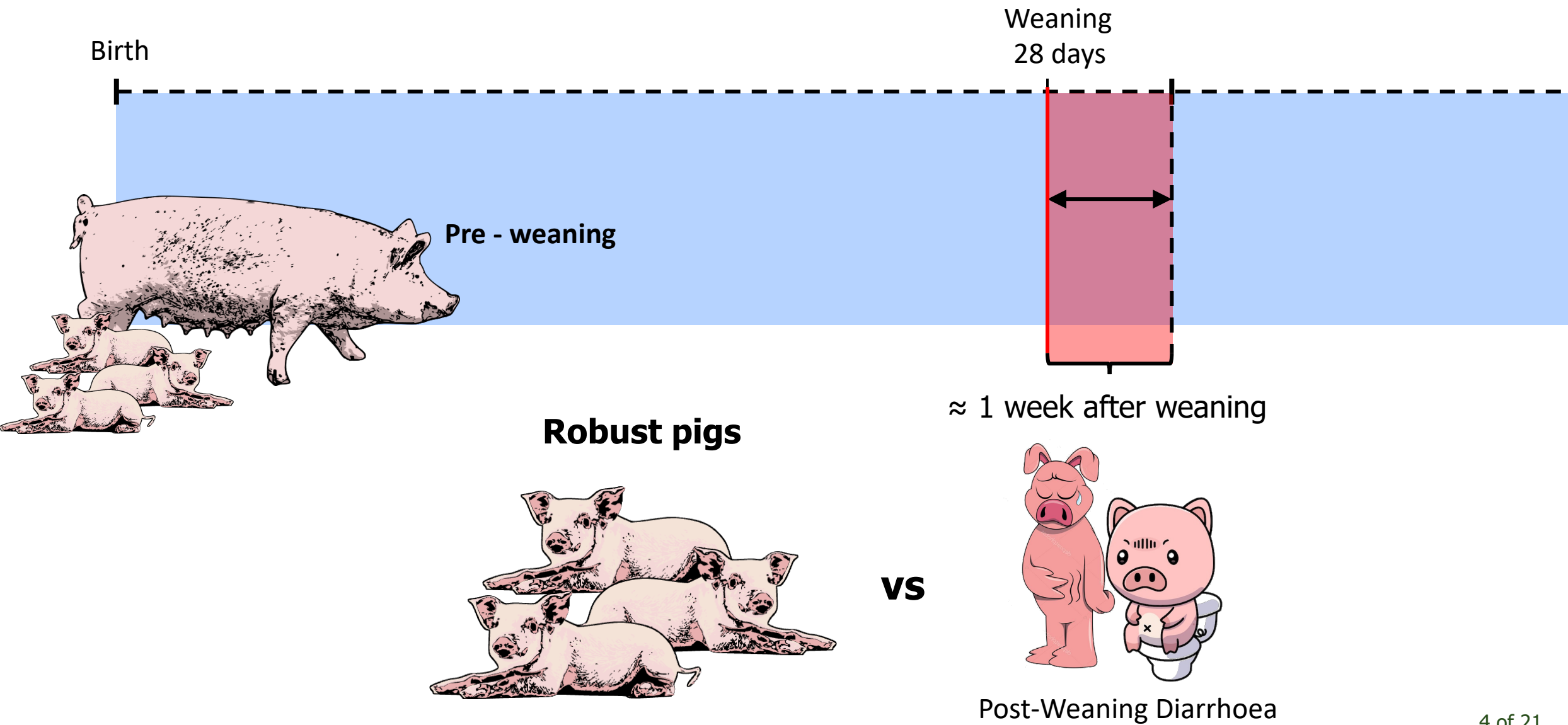
# Weaning



# Problem: Post weaning diarrhea

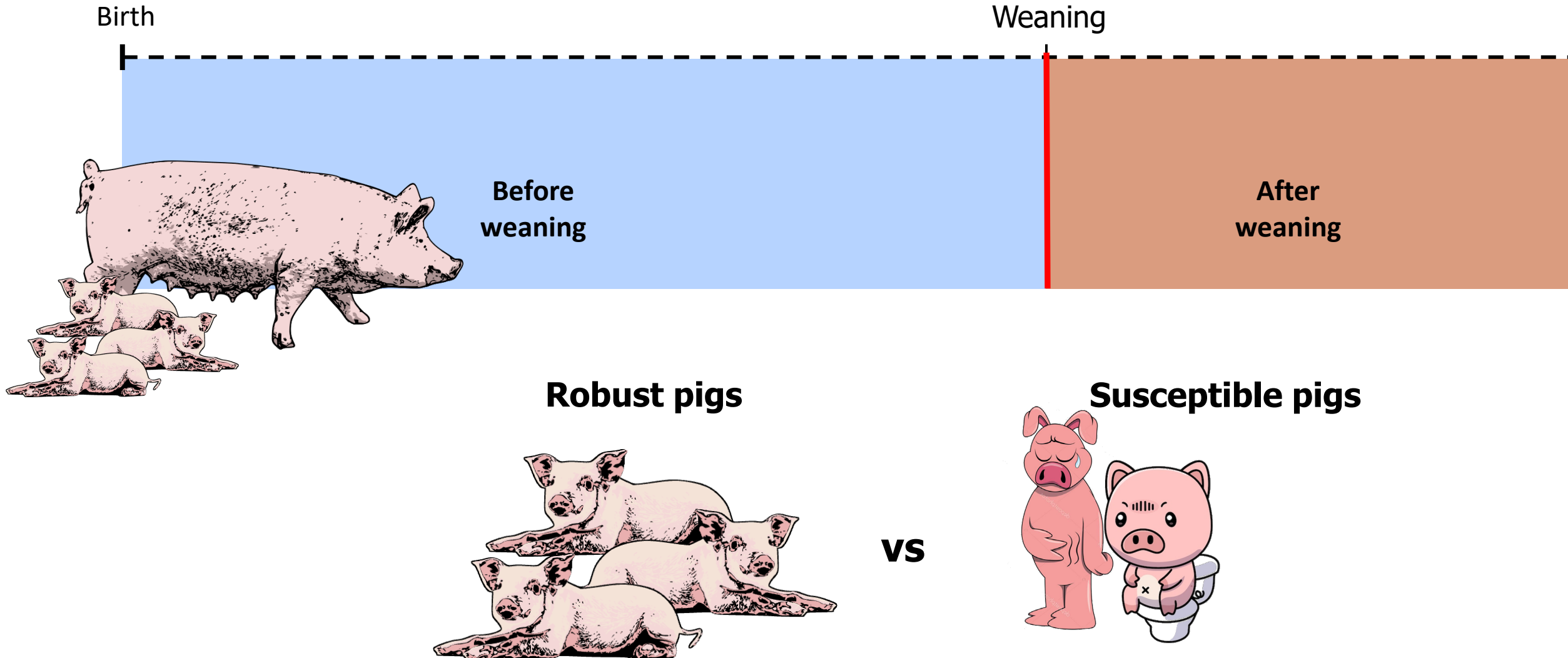


# Problem: Post weaning diarrhoea



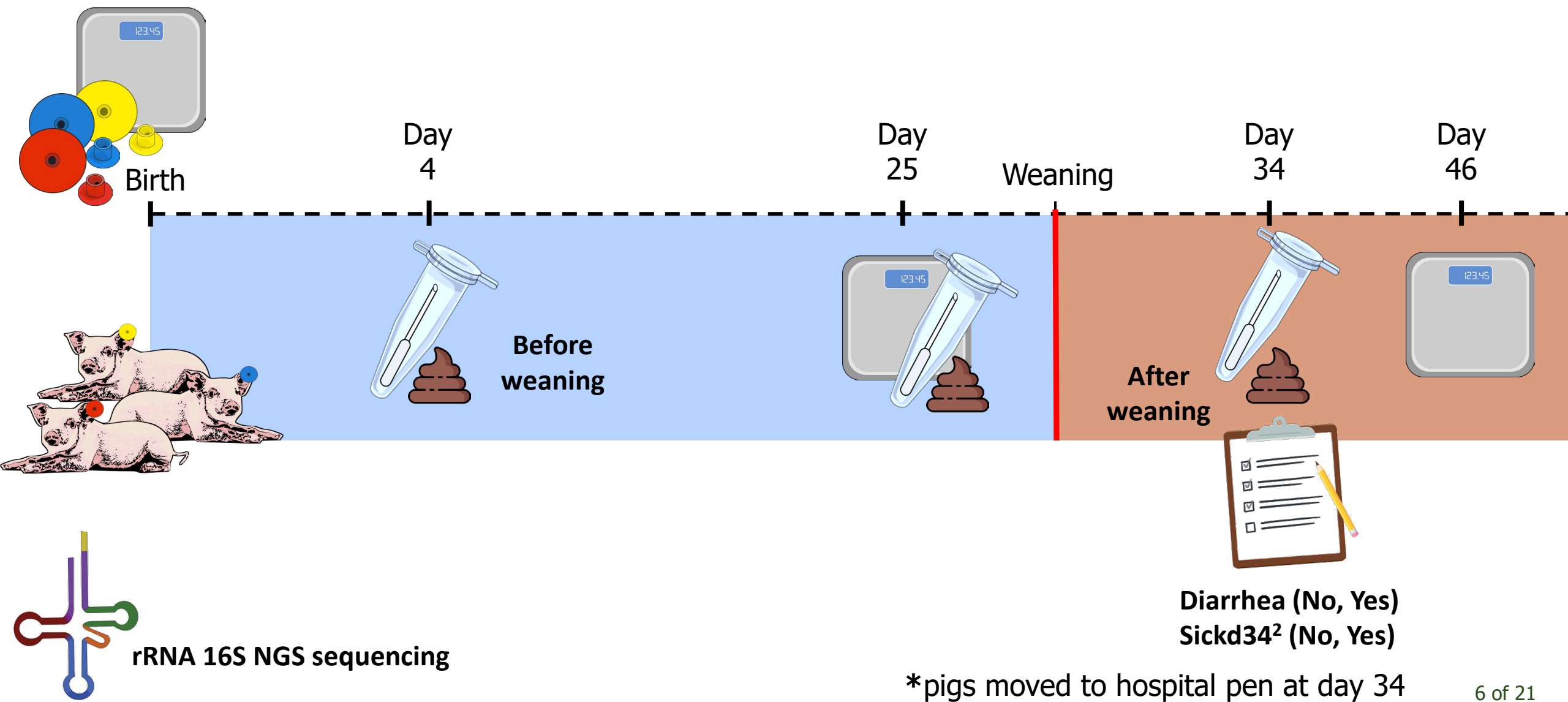
# Study pig microbiota before and after weaning

To find microbial taxa associated to pig robustness at weaning



# Study pig microbiota before and after weaning

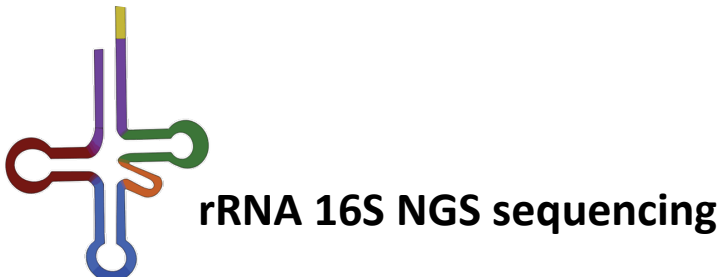
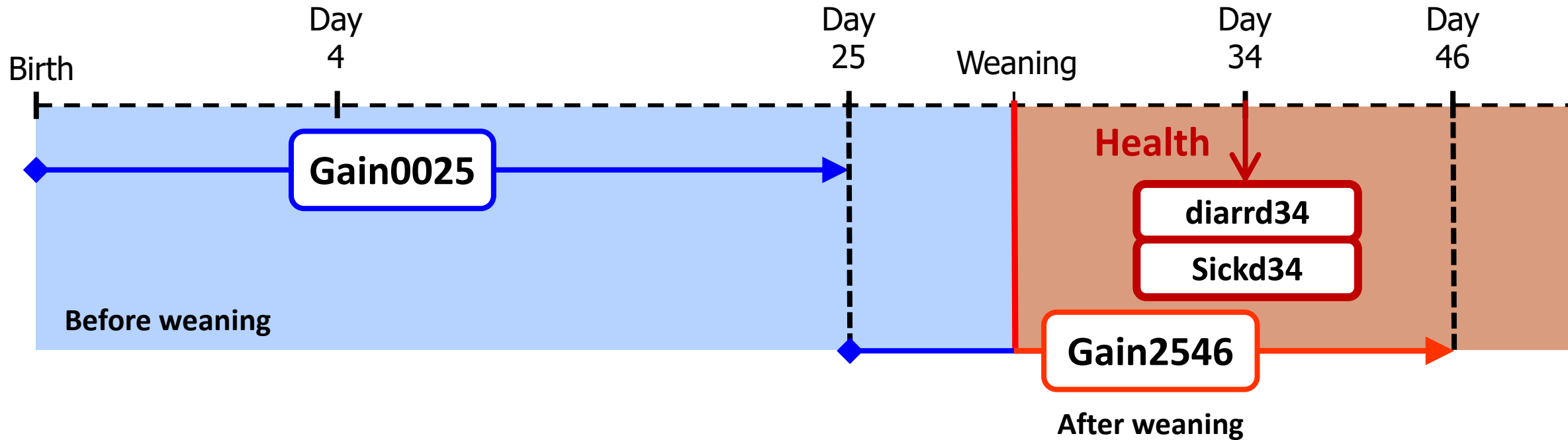
To find microbial taxa associated to pig robustness at weaning



# Study pig microbiota before and after weaning

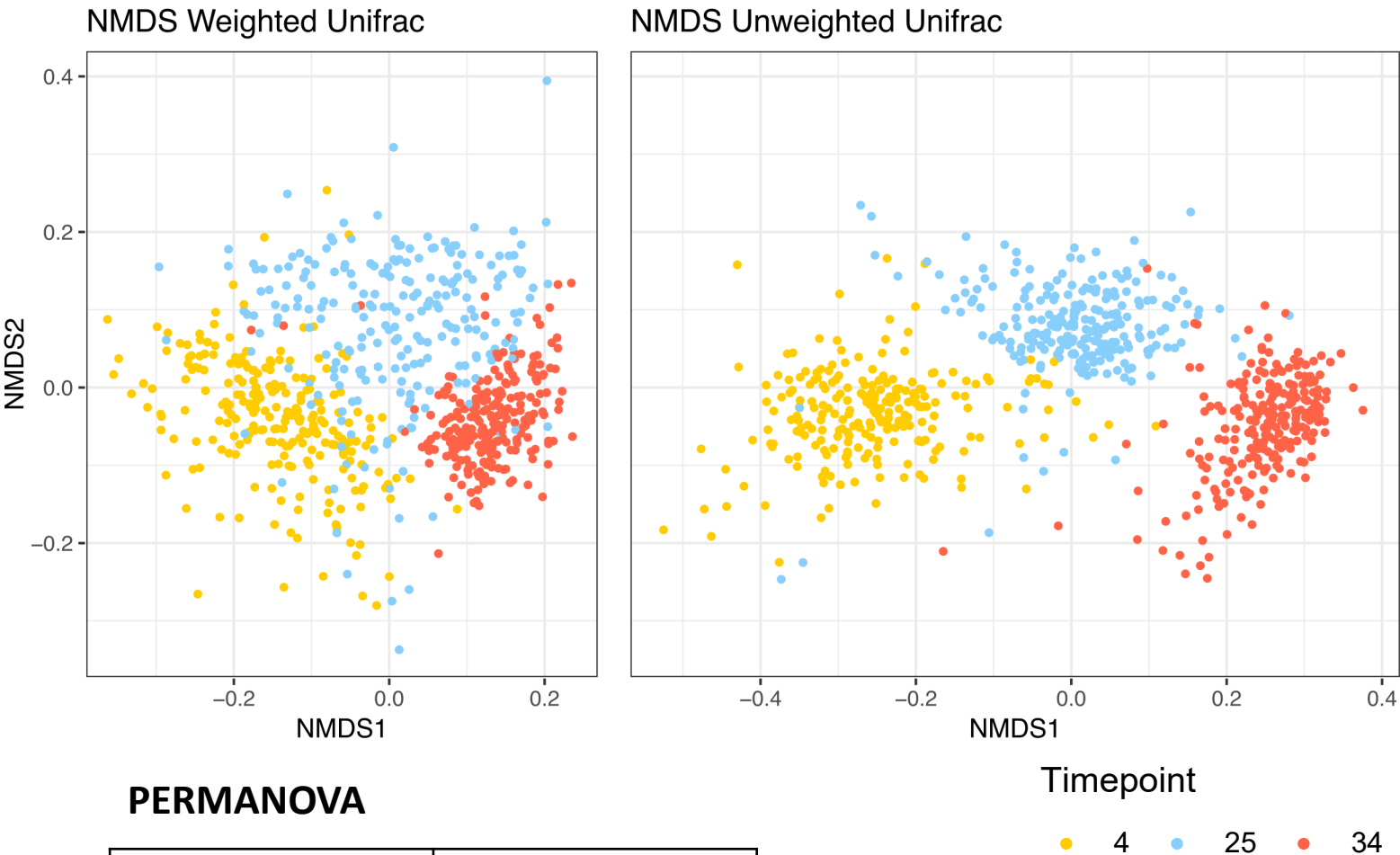
4 variables related to piglets robustness and microbiota:

- 2 performance related: Average daily gain (Gain) before (0025) and after weaning (2546).
- 2 health related: diarrhoea cases and sick pigs 1 week after weaning.



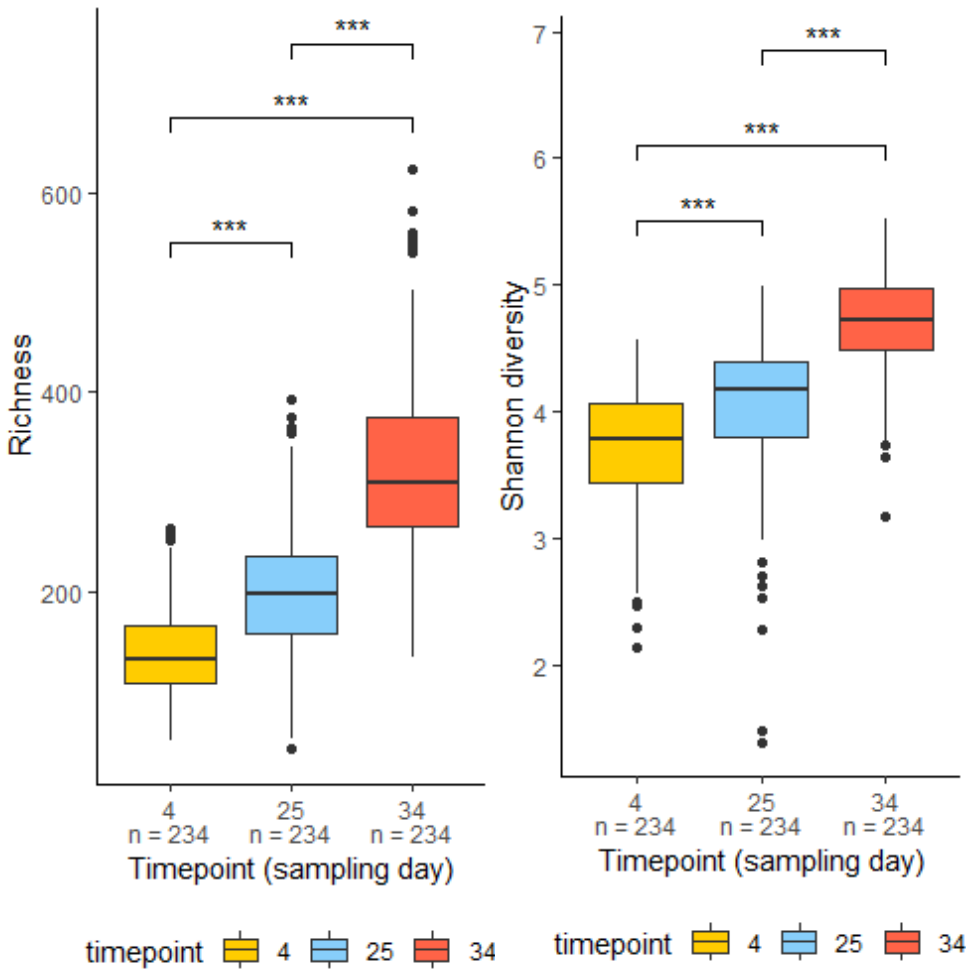
# Microbiota composition at each timepoint

## Beta-diversity



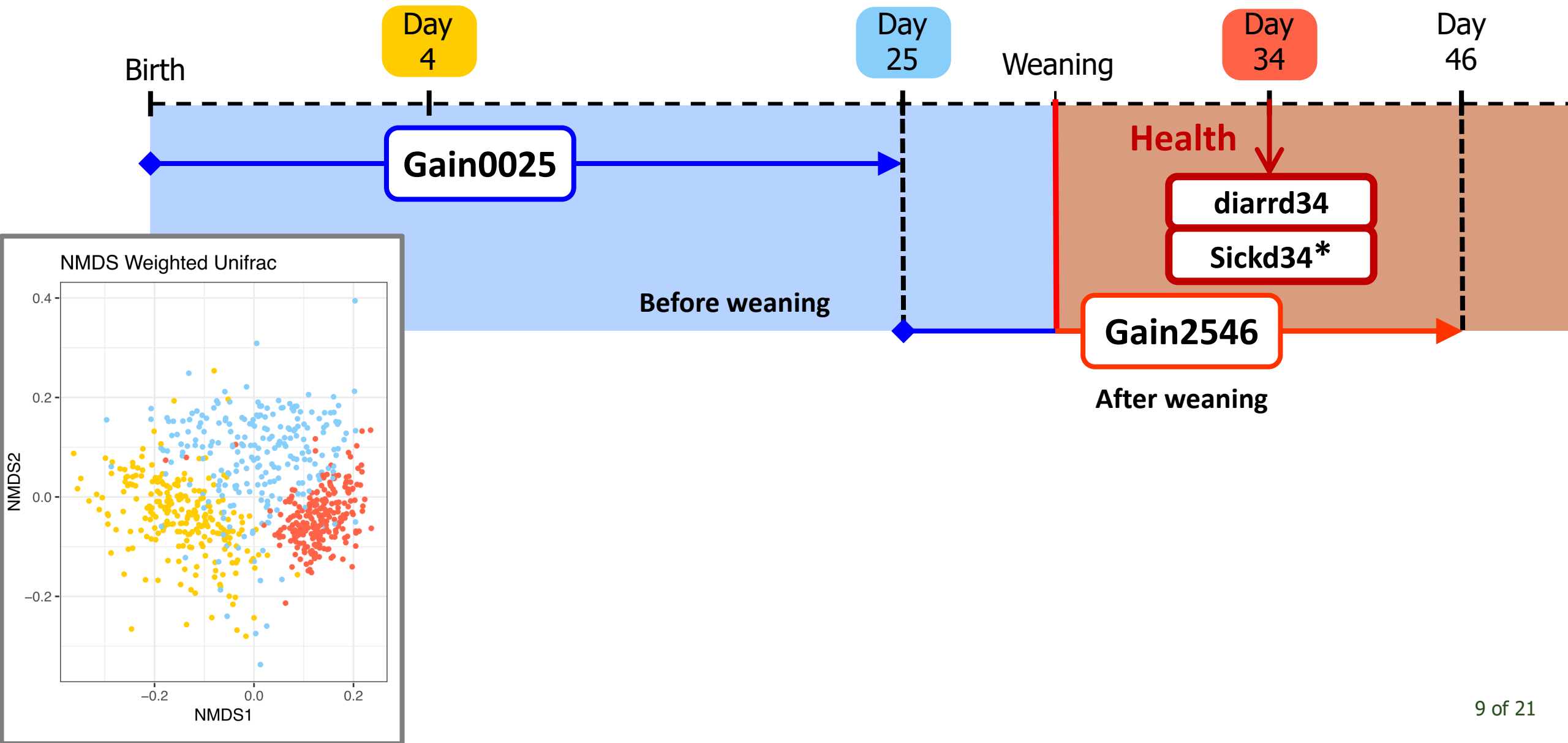
## Alpha-diversity

Pairwise Wilcoxon test.  $P < 0.001$

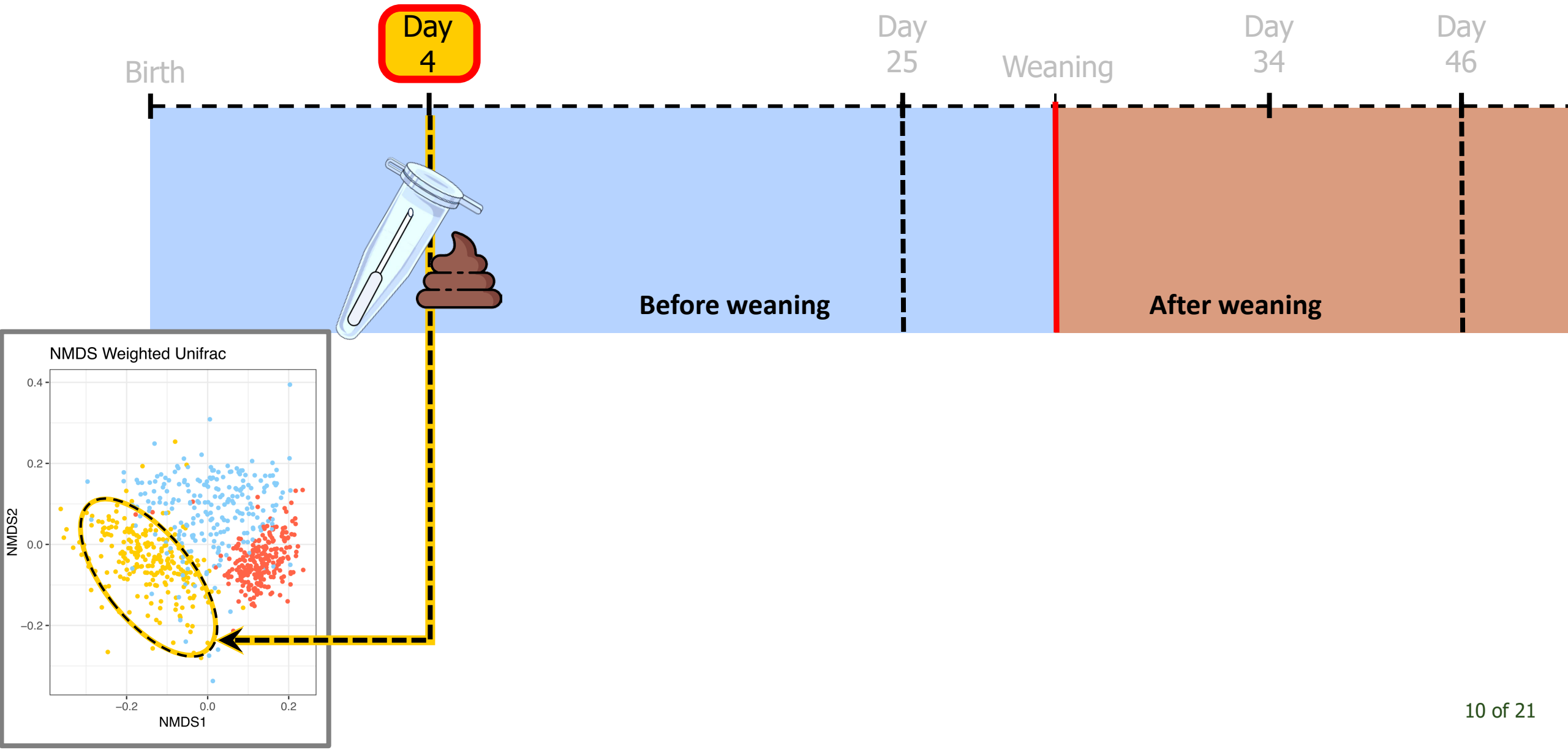


Microbiota diversity increases by age (Dong et al., 2023)

# Test variables impacting microbiota of each day



# Test variables impacting microbiota of day 4

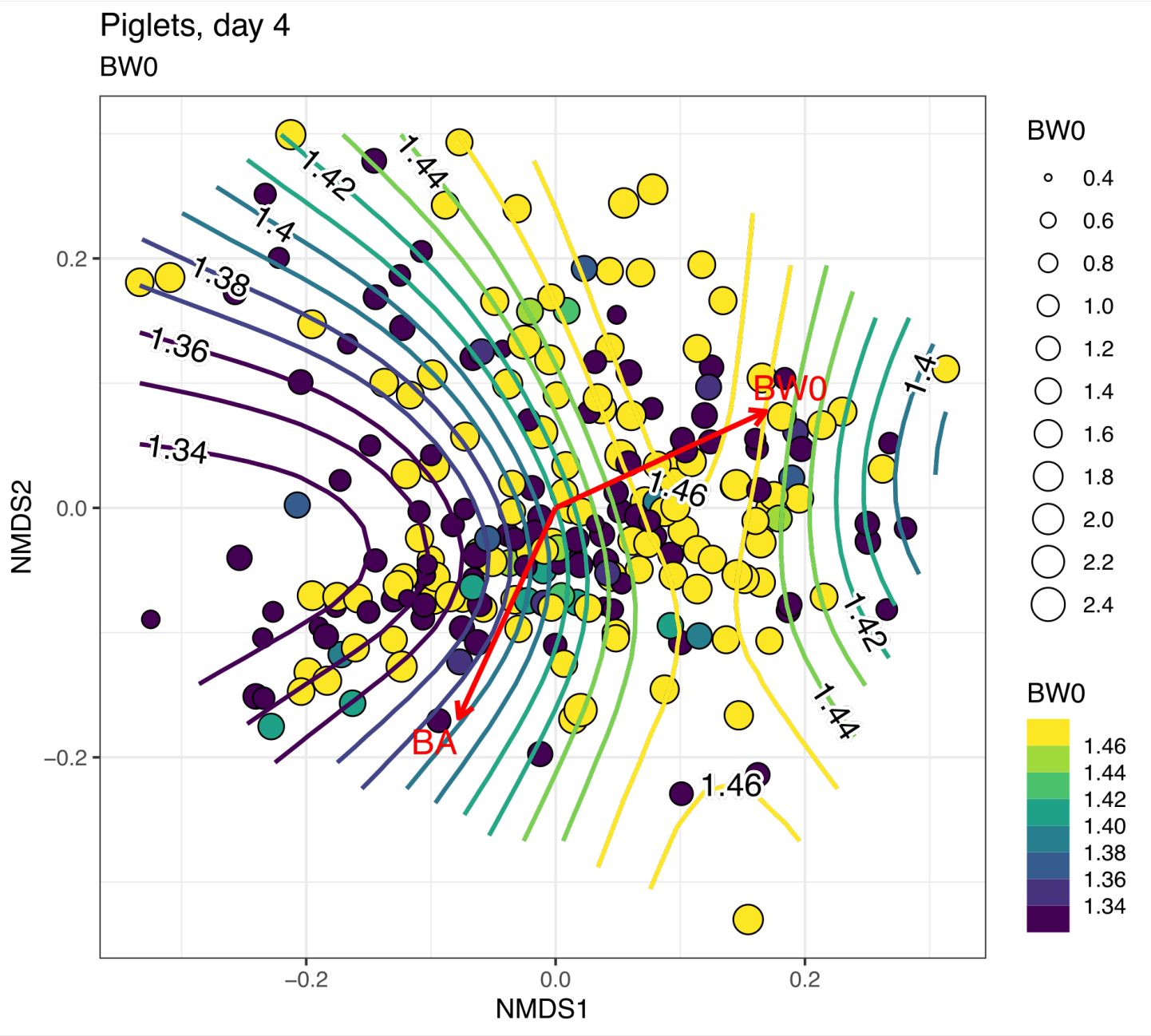


# Microbiota of day 4

Pigs with **higher BW0** have a **different microbiota**.

## PERMANOVA

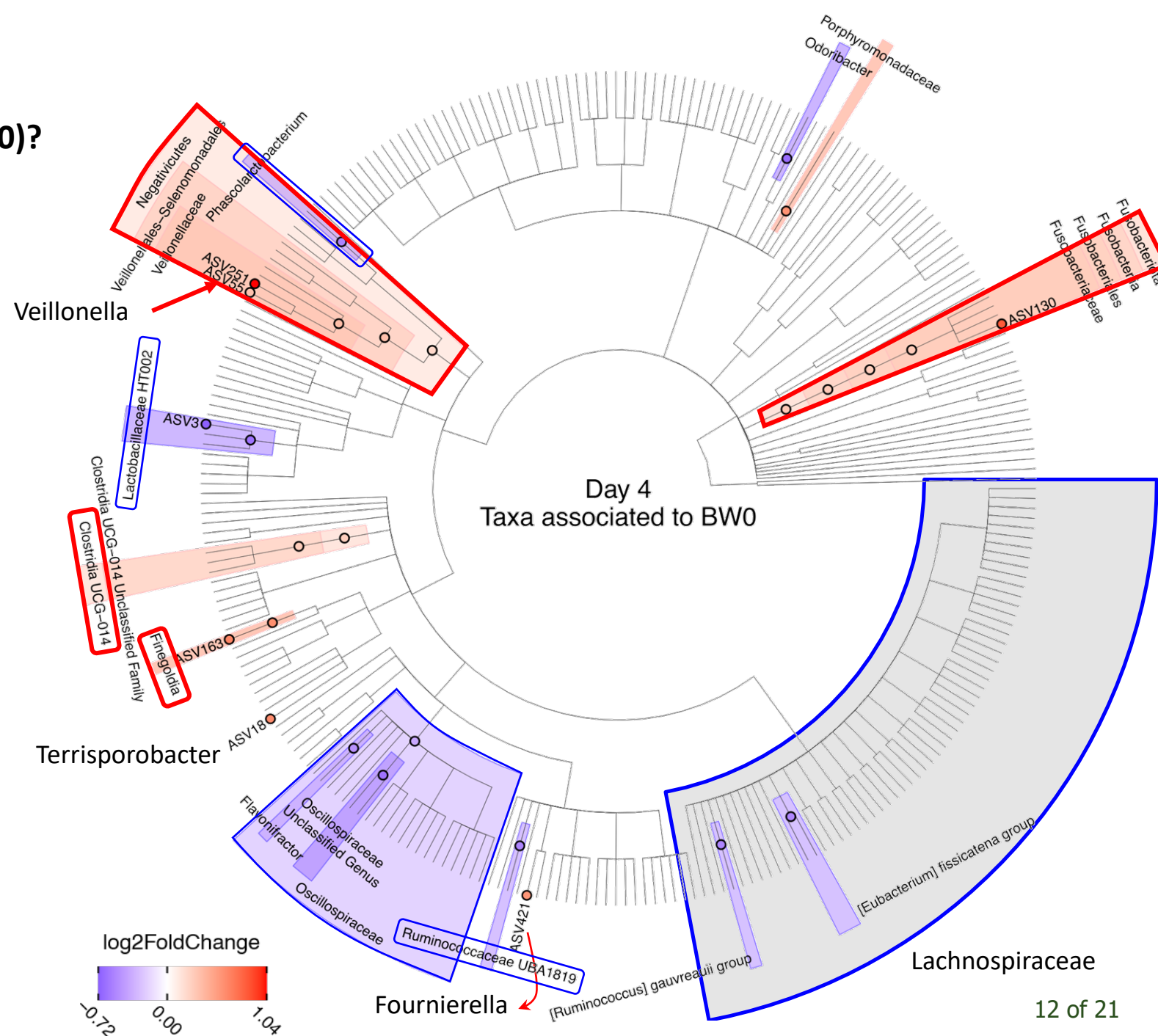
| day4             |                |
|------------------|----------------|
| Weighted Unifrac |                |
| Parity           | N.S            |
| BA               | 0.0193* (0.01) |
| BW0              | 0.0158* (0.01) |



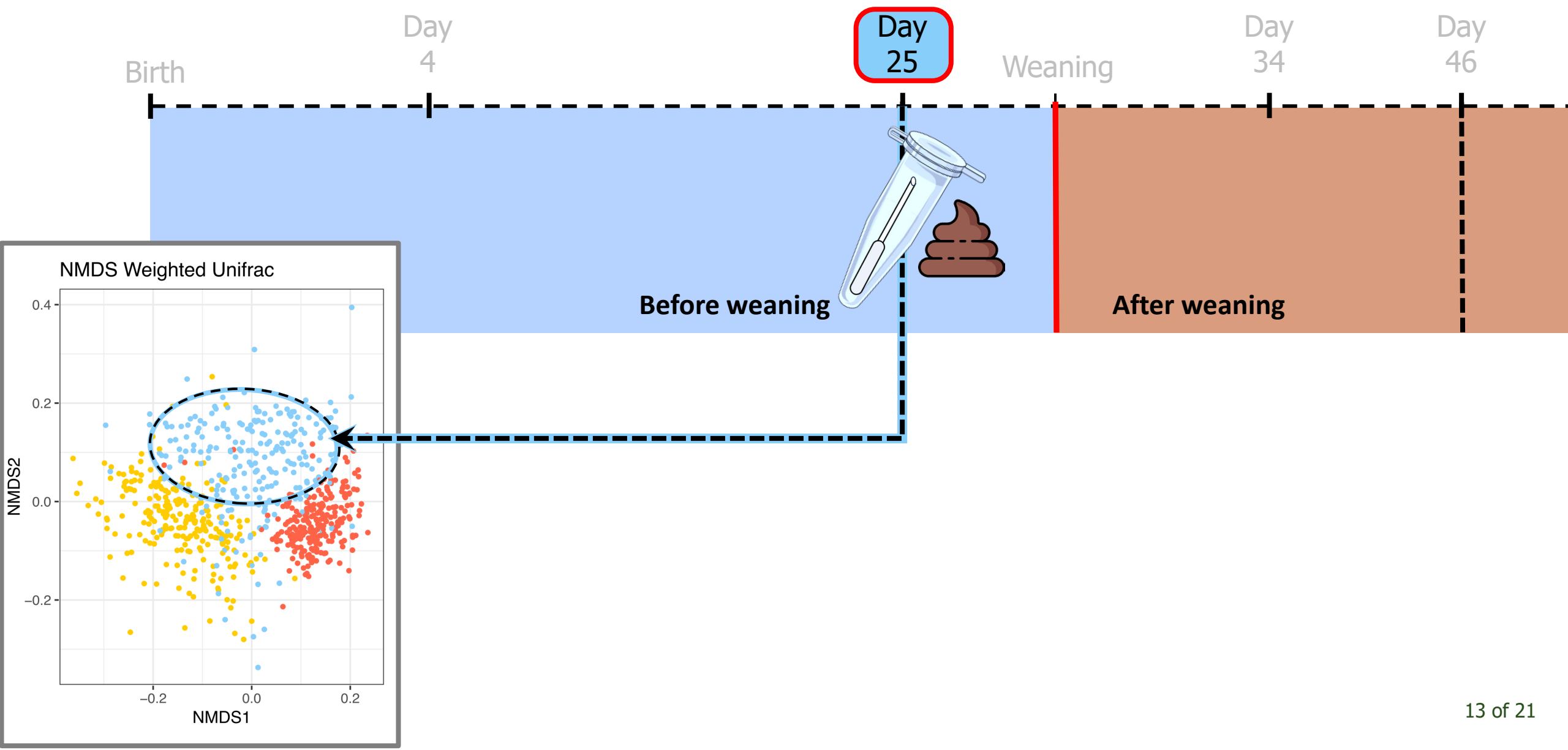
# Microbiota of Day 4

Which taxa are associated to Birth Weight (BW0)?

- **Heavier pigs at day 4:** *Veillonella*, *Fusobacterium*, *Clostridia* UCG-014, *Finegoldia*, *Fournierella*.
- **Lighter pigs at day 4:** *Oscillospiraceae*, *Lachnospiraceae*, *Lactobacillaceae* HT002, *Odoribacter*, *Phascolarctobacterium*.
- *Fusobacterium*, *Odoribacter*, *Terrisporobacter* and *Finegoldia*: common in suckling piglets (Chen et al., 2017; Li et al., 2017; Choudhury et al., 2021; Yang et al., 2021).



# Test variables impacting microbiota of day 25

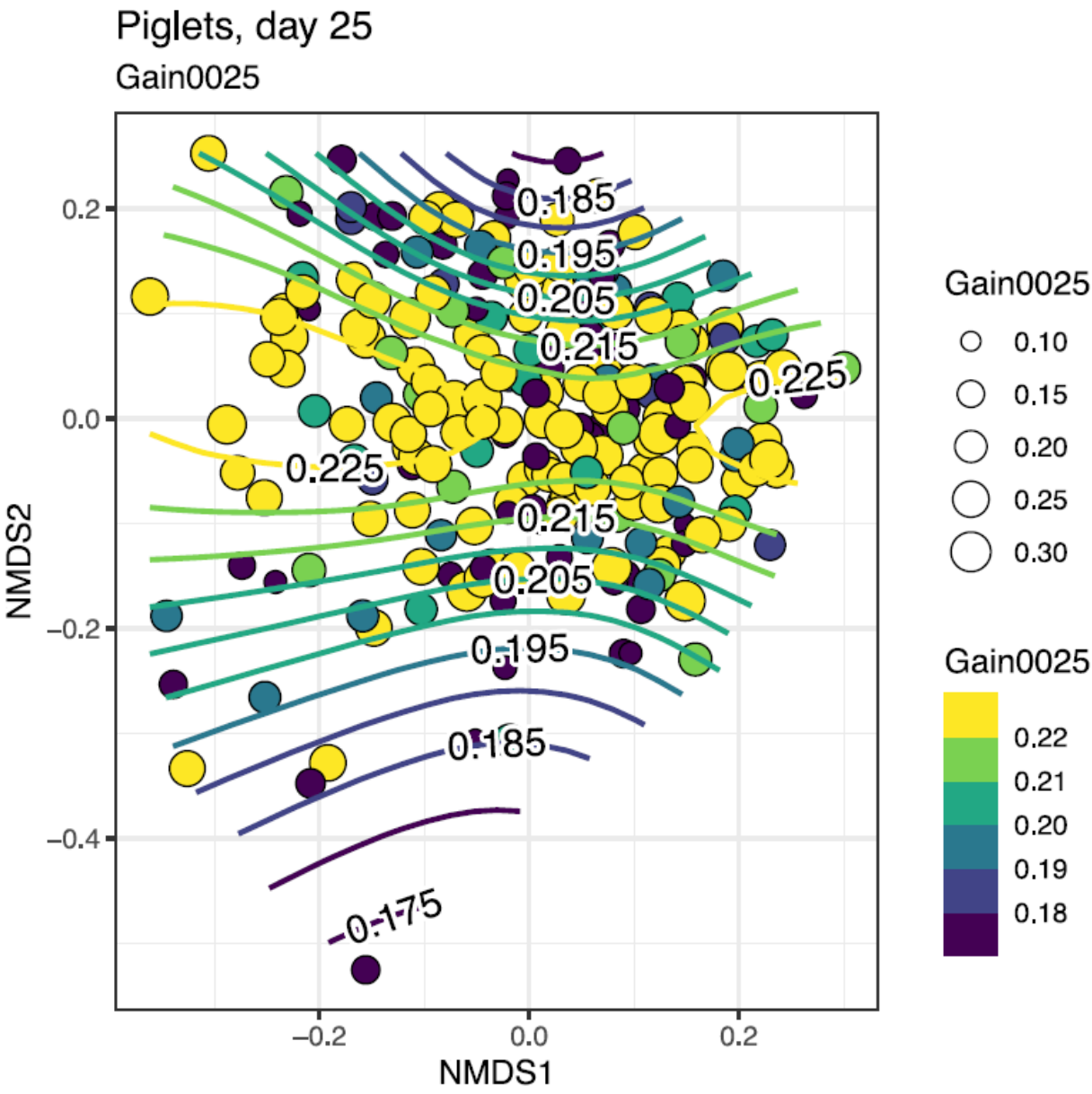


# Microbiota of Day 25

Microbiota of day 25 is impacted by **Gain0025** and **sickd34**

## PERMANOVA

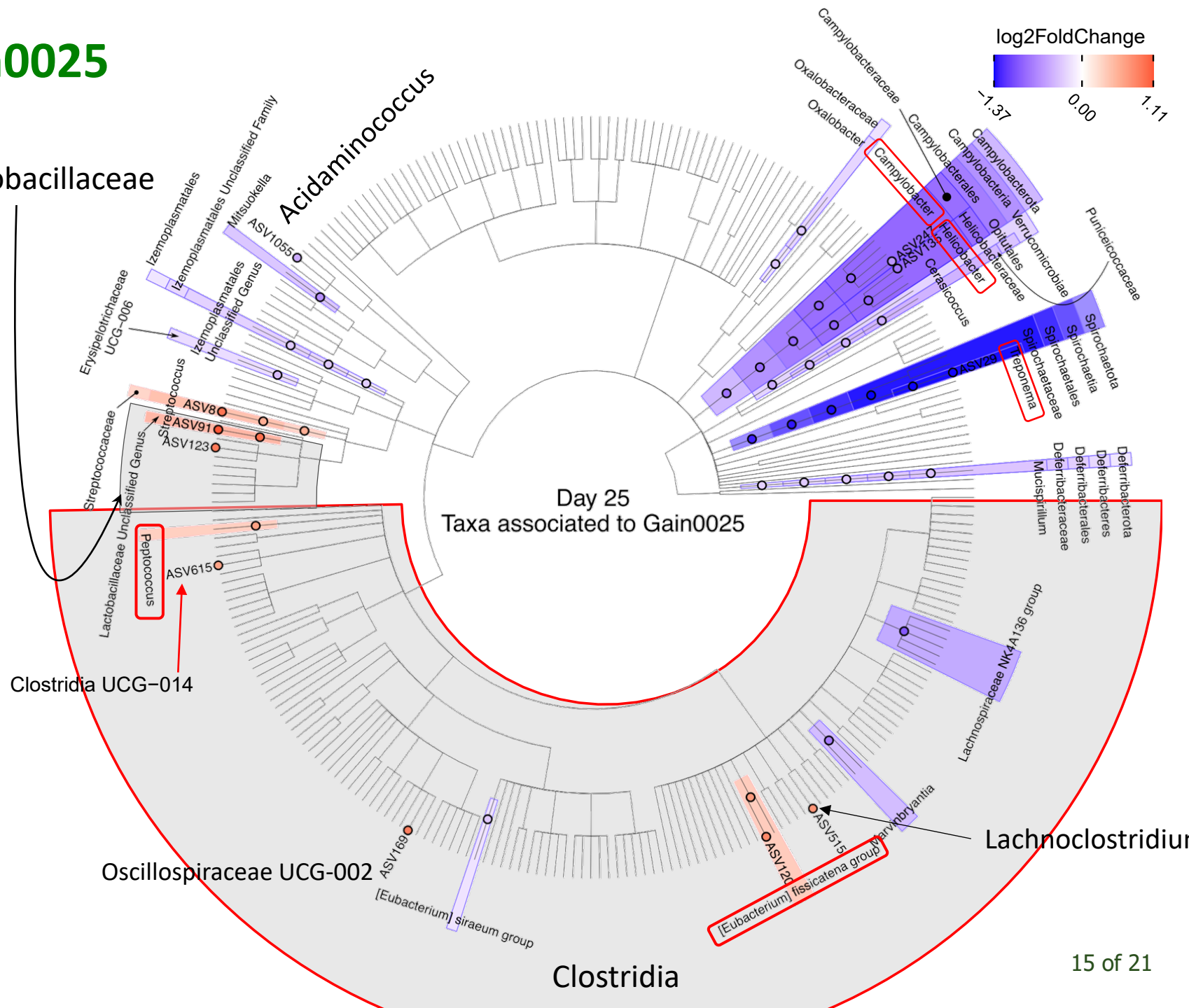
|                  | day25           |
|------------------|-----------------|
| Weighted Unifrac |                 |
| Parity           | N.S             |
| BA               | N.S             |
| sex              | N.S             |
| CF               | N.S             |
| Gain0025         | 0.0011** (0.01) |
| diarrd34         | N.S             |
| sickd34          | 0.0093** (0.01) |
| Gain2546         | N.S             |



## Microbiota of Day 25: Gain0025

## Taxa associated to Gain0025

- **Higher Gain0025:** *Lactobacillaceae*, *Lactobacillaceae*, *Streptococcaceae*, *Peptococcus*, *Clostridia* UCG-014, *Oscillospiraceae* UCG-002, *Eubacterium fissicatena* group, *Lachnoclostridium*.
- Link of *Lactobacillus*, *Streptococcus*, and *Peptococcus* with birth weight and average daily gain (Oh et al., 2020; Maltecca et al., 2021; Ding et al., 2019; Payen et al., 2023).
- **Lower Gain0025:** higher levels of *Campylobacter*, *Helicobacter*, *Treponema*, other taxa (Li et al., 2018; Payen et al., 2023).



## Microbiota of Day 25: sickd34

### Taxa associated to sick pigs at day 34, measured at day 25

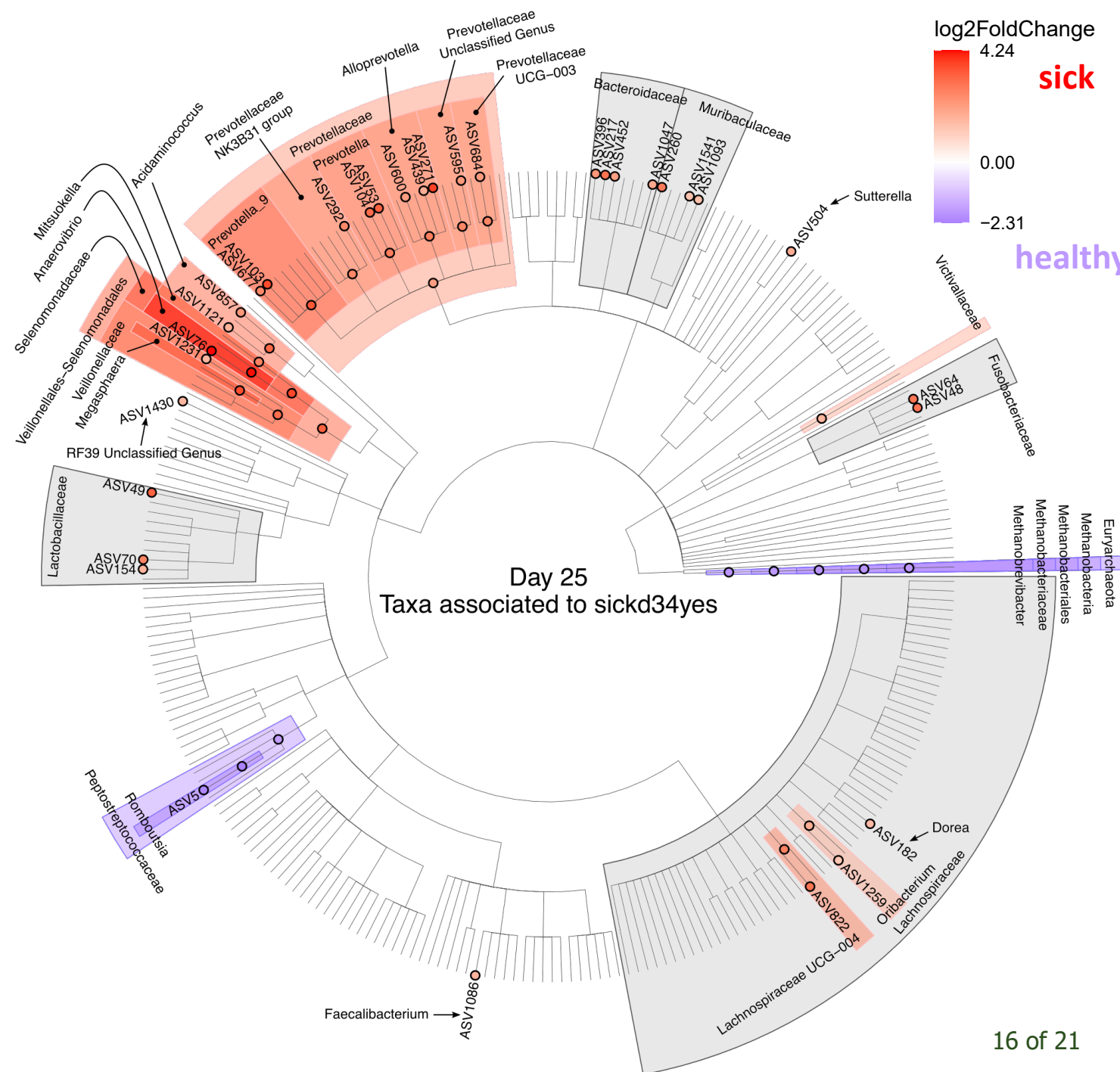
## Sick pigs:

↑↑↑ Veillonellaceae, Prevotellaceae,  
Acidaminococcus, Bacteroidaceae, Muribaculaceae,  
Fusobacteriaceae, Lachnospiraceae,  
Lactobacillaceae, Sutterella.

## Healthy pigs:

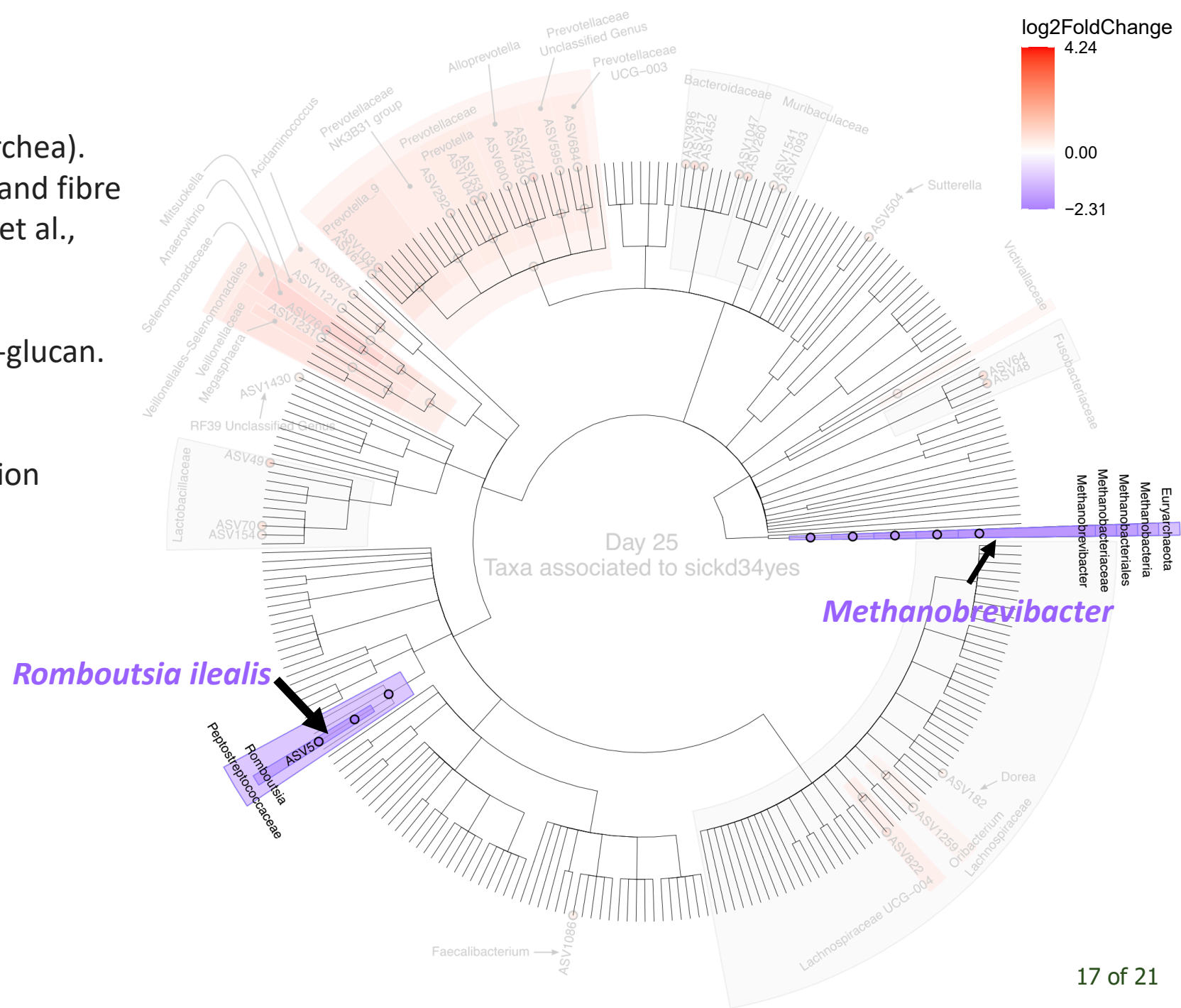
↑↑ *Romboutsia ilealis*, *Methanobrevibacter*.

- Unexpected results:
  - *Prevotellaceae* (mature microbiota).
  - *Lactobacillaceae*: beneficial effects in suckling pigs (Saladrigras et al., 2021; Nowland et al., 2022)
- *Prevotella*, *Bacteroides* and *Fusobacterium*: opportunistic infections in human or pigs (Gardiner et al., 2020; Tan et al., 2020; Tett 2021). Unknown role in this context.

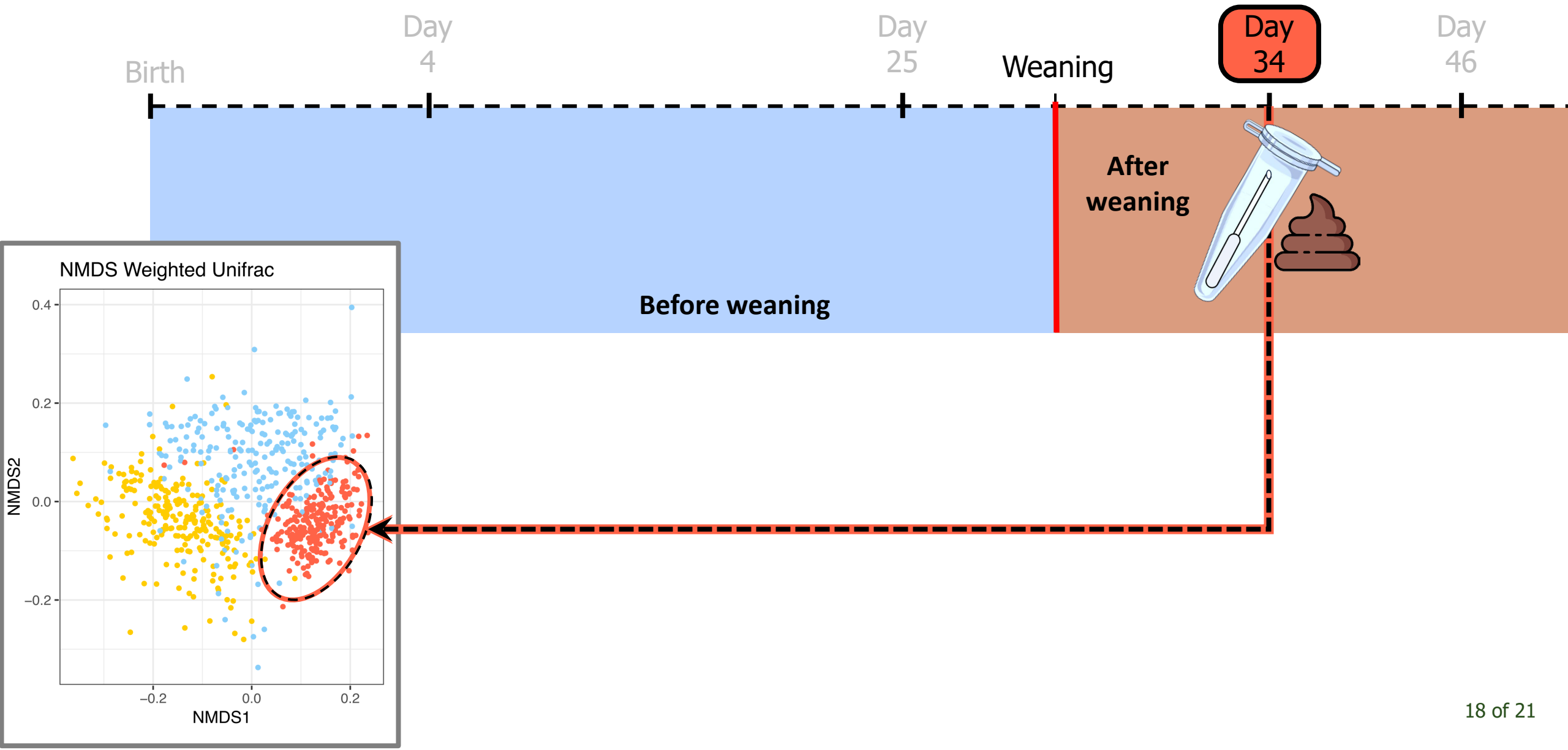


## Day 25: sickd34

- *Methanobrevibacter* (methanogenic archaea). Associated with better feed-efficiency and fibre digestibility (Gardiner et al., 2020, Niu et al., 2015)
- *Romboutsia ilealis*: produces its own  $\beta$ -glucan. (Chang et al., 2023).
- Both taxa: potential link with colonization resistance.



# Test variables impacting microbiota of day 34

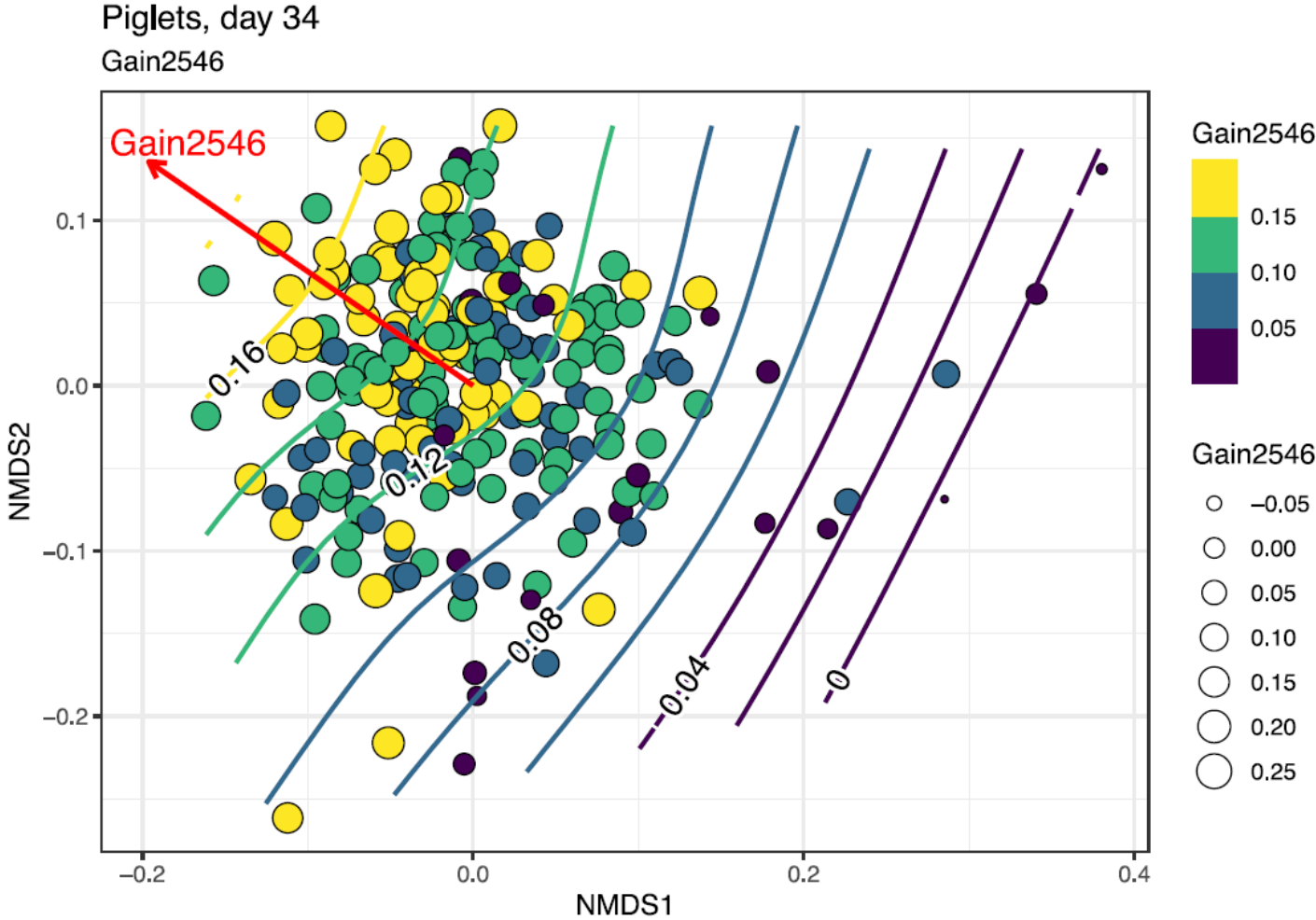


# Microbiota of Day 34

Microbiota of pigs at day 34 is impacted by **Diarrhoea** and **Gain2546**

## PERMANOVA

| Day34            |                  |
|------------------|------------------|
| Weighted Unifrac |                  |
| Sow.injected     | N.S              |
| Parity           | N.S              |
| BA               | N.S              |
| sex              | N.S              |
| BW0              | N.S              |
| CF               | N.S              |
| BWd25            | N.S              |
| Diarrd34         | 0.0019** (0.01)  |
| Sickd34          | N.S              |
| Gain2546         | <0.001*** (0.05) |

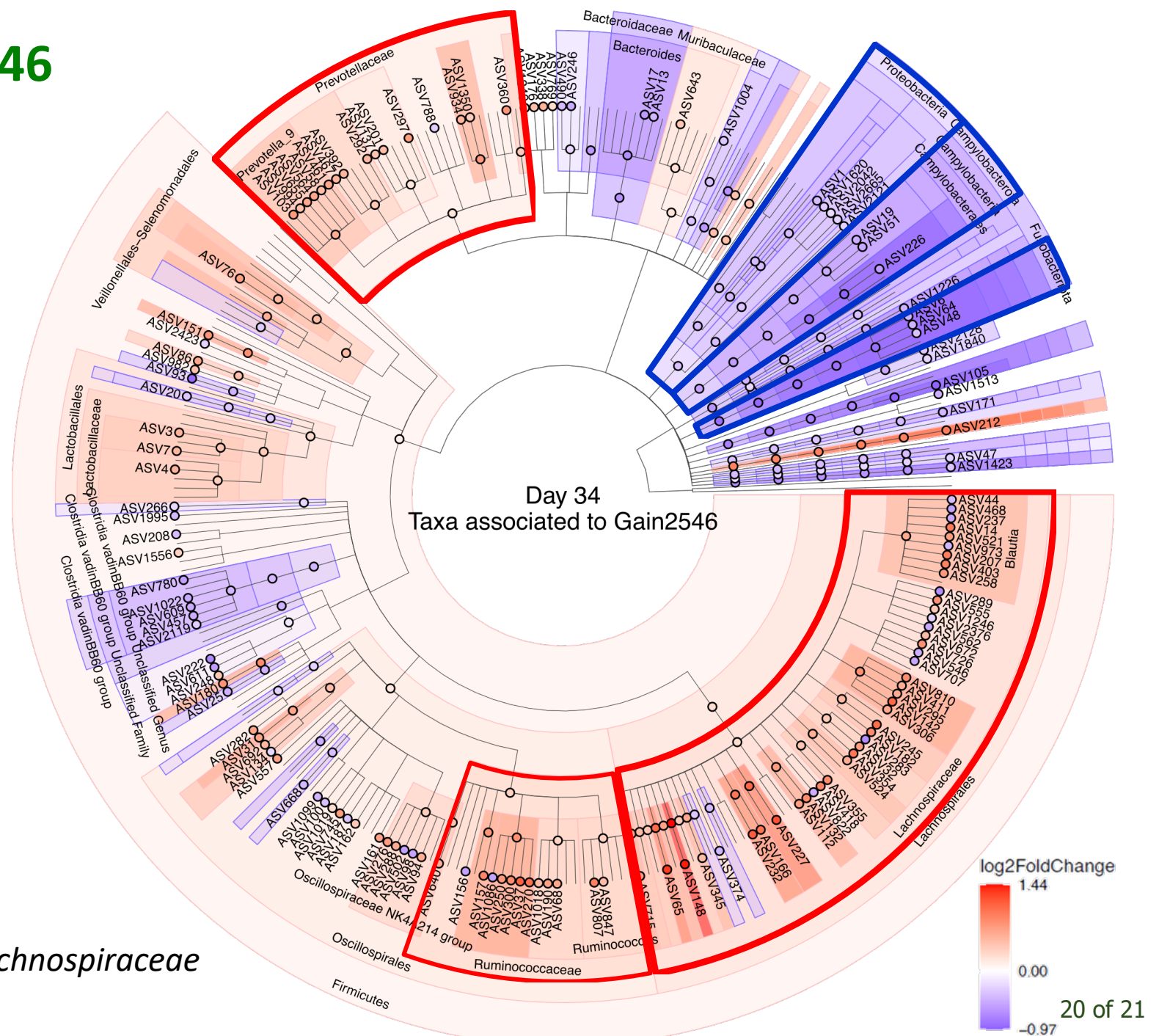


# Microbiota of Day 34: Gain2546

## Taxa associated to Gain2546

- **Higher Gain2546:** *Oscillospirales*, *Prevotellaceae*, *Lachnospiraceae*
- **Lower Gain2546:** *Proteobacteria*, *Campylobacterota* (*Campylobacter*, *Helicobacter*), *Fusobacteriota*.
- *Prevotellaceae*: improved performance (Ramayo-Caldas et al., 2015; Mach et al., 2015; Nowland et al., 2022)
- *Ruminococcaceae*: associated with better **lactation growth** (Mach et al., 2015; Gaukroger et al., 2020).
- *Ruminococcaceae* and *Lachnospiraceae* linked to **resilience against post-weaning diarrhea**. SCFA-producers (Dou et al., 2017; Holman et al., 2017; Luise et al., 2021, Beaumont et al., 2021, Ortiz Sanjuán et al., 2022).

**Here:** *Prevotellaceae* + *Ruminococcaceae* + *Lachnospiraceae* simultaneously.

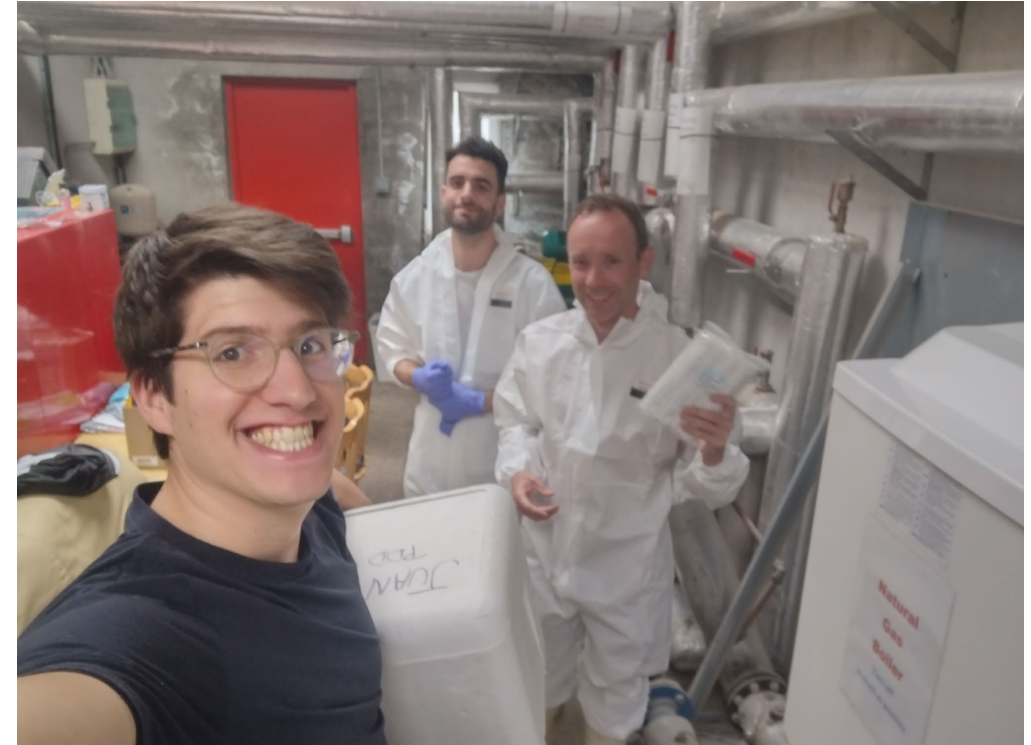


# Take home messages

1. Early differences in microbiota composition can be detected at 4 days of age. These differences are shaped by birth body weight.
2. Microbiota composition can explain differences in growth performance, especially in the first week post weaning (day 34).
3. Microbiota composition before weaning is associated to risk of sickness after weaning.
4. Future measures should aim to modulate robustness associated taxa such as those in families *Prevotellaceae*, *Ruminococcaceae*, *Lachnospiraceae* or *Lactobacillaceae*, as well as exploring the role of other taxa such as *Methanobrevibacter* and *Romboutsia ilealis* in pigs microbiota.

# Thank you

Thanks to EAAP for the opportunity of presenting the results of this study. And thanks to all the coauthors of this study.



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