

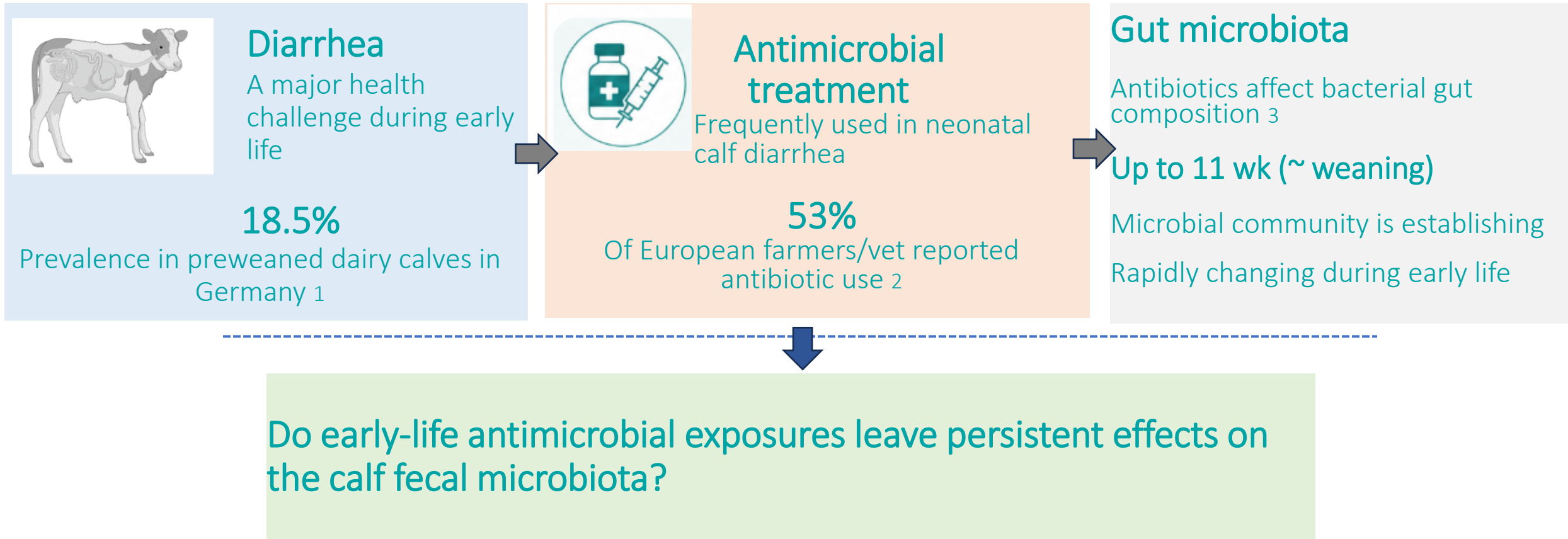
➤ Early-life antimicrobial treatment has long-term effects on the fecal microbiota of dairy calves

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2 UEP, INRAE, 2019. Unité Expérimentale du Pin

➤ Gastrointestinal disorders



Potential consequences for microbiota development and host health and performance

➤ Objective

- To evaluate the long-term effects of early-life antimicrobial treatments on the fecal microbiota of calves

➤ METHODS

Study design and sample collection – *Observational longitudinal cohort study*

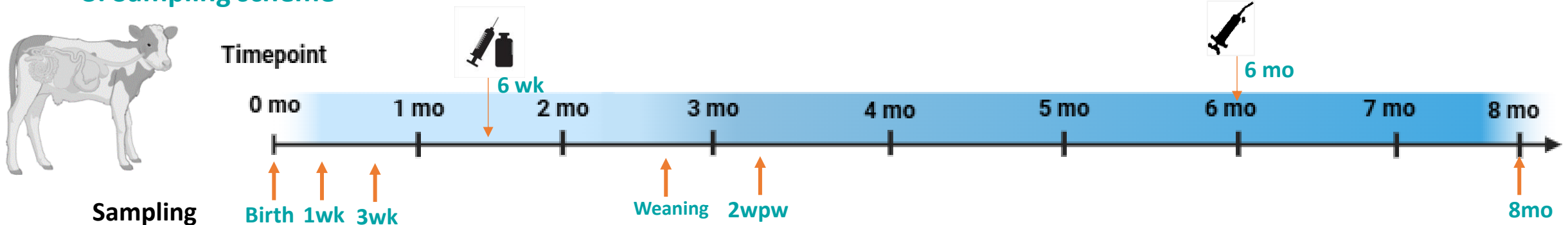
1. Animals

- 20 calves selected from a cohort of 63 (health record based selection)
- 2 breeds: Holstein (n=10), Normande (n=10)
- Balanced health status within breed: diarrhea (n=5)/healthy (n=5)

2. Antimicrobial treatment:

- Holstein + diarrhea => broad spectrum antibiotics (IM, pre-weaning – 6 wk)
 - Normande + diarrhea => coccidiostats (oral, post-weaning – 6 mo)
- => Breed and treatment type are cofounded

3. Sampling scheme



=> 120 fecal samples total, 16S rRNA gene amplicon sequencing (target bacteria)

4. Long term evaluation:

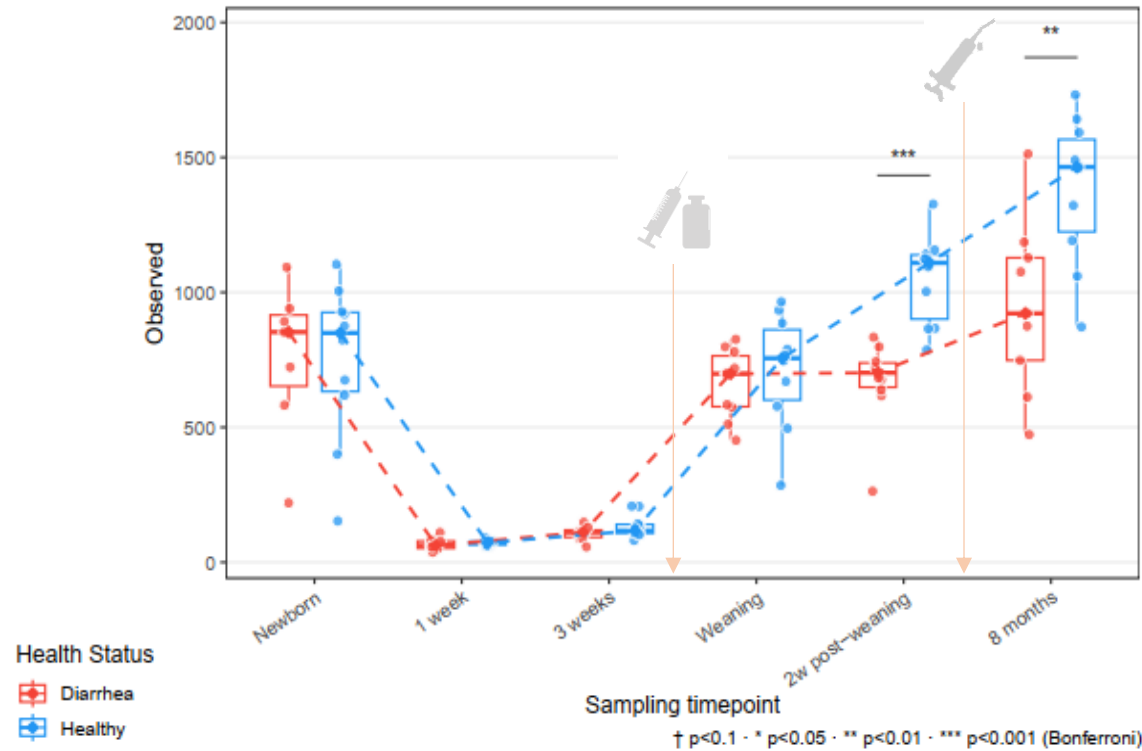
Assessed at 8 mo (all calves clinically healthy) – most disorders resolved by 6 mo

➤ RESULTS: Fecal bacteria

Alpha diversity — Fecal bacteria

Healthy vs Diarrhea across sampling timepoints

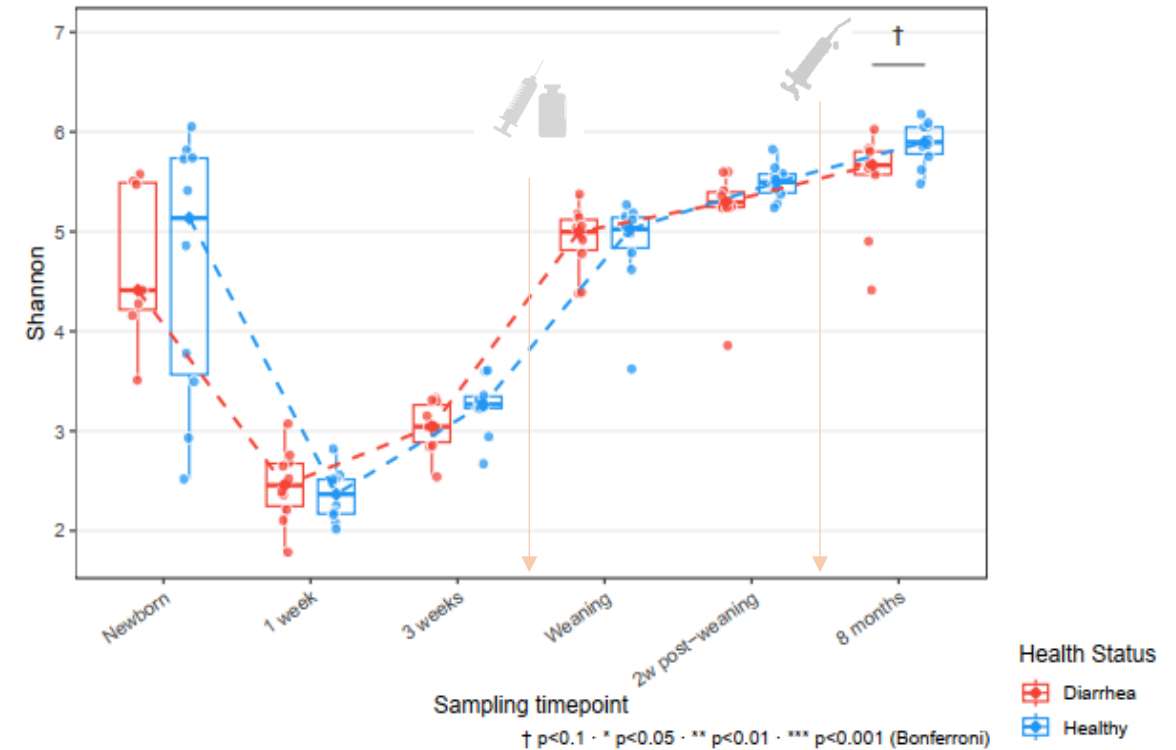
Alpha diversity — Observed



In diarrhea calves the richness was affected

No Breed × Health status interaction

Alpha diversity — Shannon

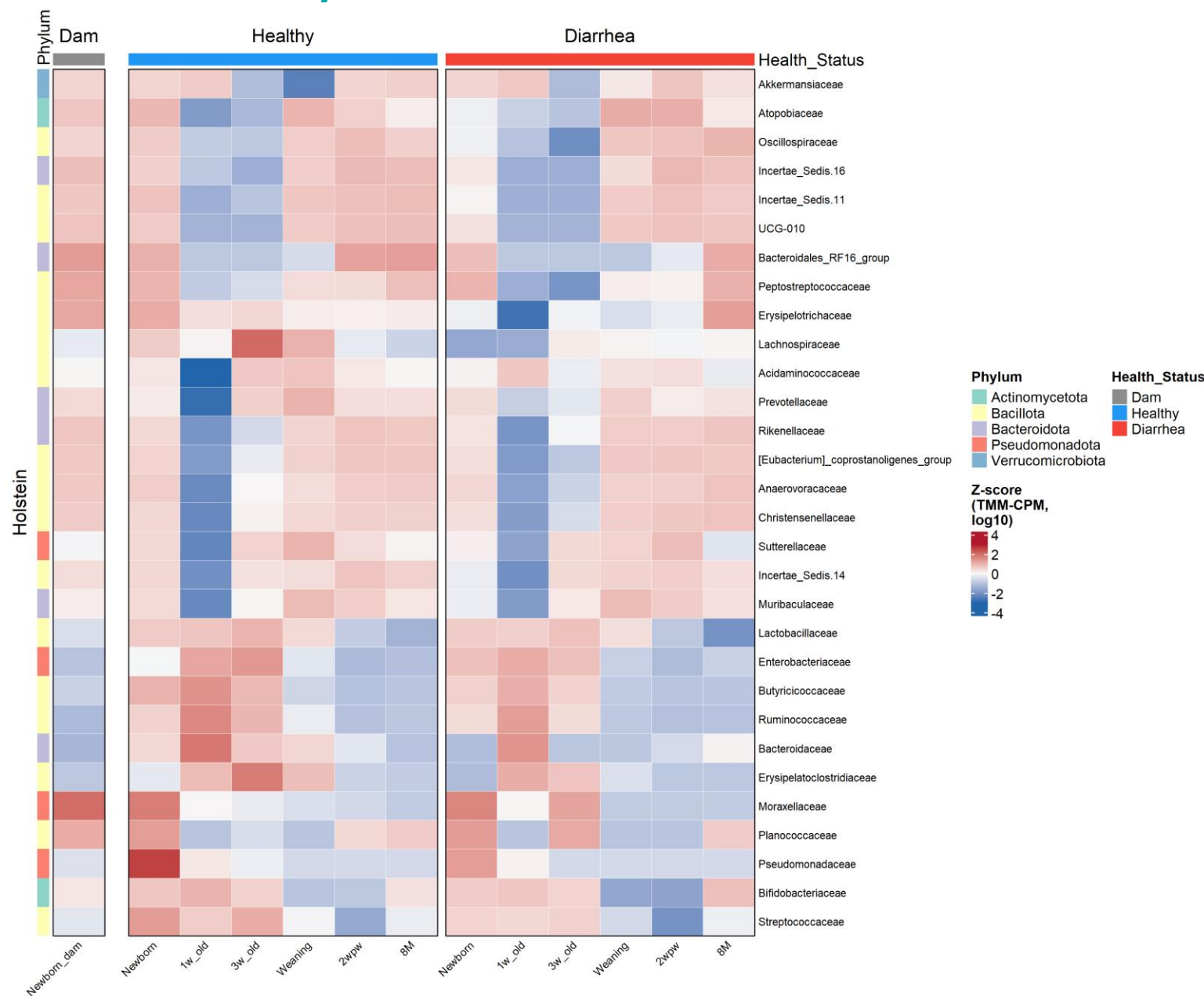


In diarrhea calves Shannon diversity was not impacted

Diarrhea calves that received antimicrobials present a reduced species number without impact on the global diversity

➤ RESULTS: Bacterial composition at Family level

The similar patterns of alpha diversity in healthy & diarrhea calves are confirmed by heatmap analysis on the family level

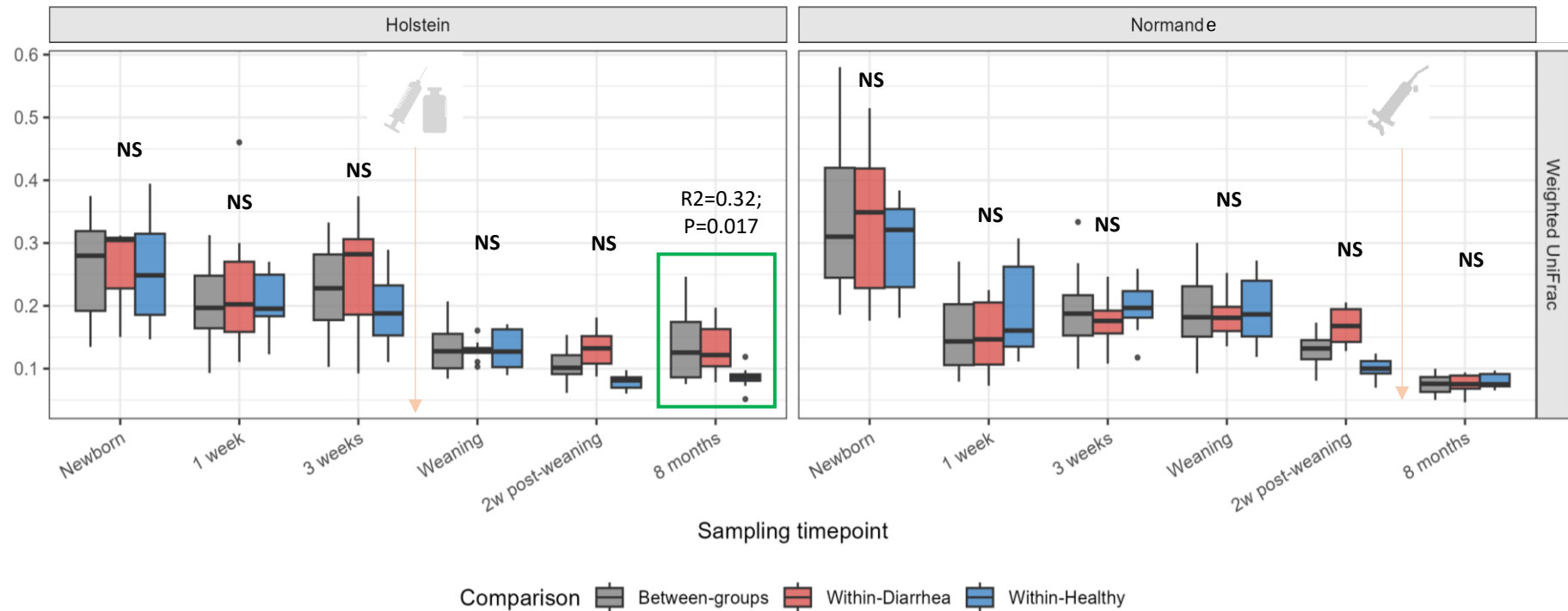


➤ RESULTS: Fecal bacteria

Beta diversity

Pairwise UniFrac distances by breed — Fecal bacteria

Within-Healthy vs Within-Diarrhea vs Between-groups, across sampling timepoints



Fecal microbiota diverges between healthy and diarrhea calves at the age of 8 months, but only in Holstein calves treated with systemic antibiotics

Individual fecal bacterial communities became progressively more similar with age, consistent with a shared trajectory of microbial community maturation.

➤ RESULTS: Growth by breed *from birth to 810 days of life by physiological stage and health status*

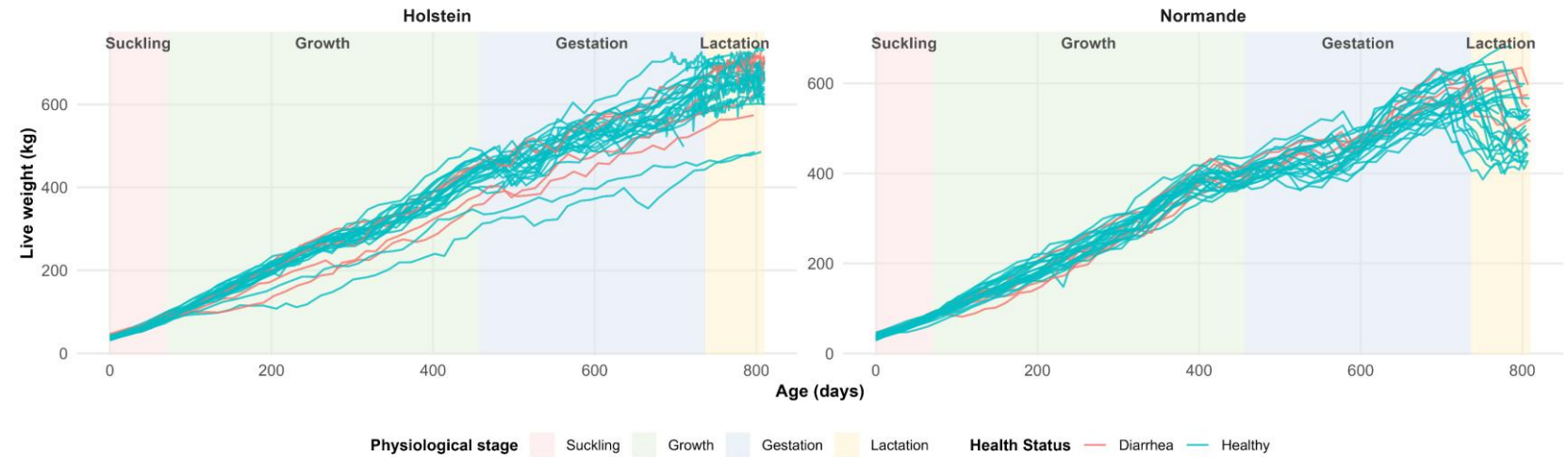
Individual growth trajectories overlap between healthy and diarrhea-affected calves in both breeds

Body weight parameters

Full cohort calves, n=63

A

Live weight curves with physiological stage windows



Holstein diarrhea calves trend slightly lower

B

Live weight curves with physiological stage windows

selected calves, n=20



➤ RESULTS: Growth by breed *from birth to 15 months by health status and breed*

selected calves, Holstein n=10; Normande n=10

Diarrhea-affected Holstein calves are lighter and more variable at the growth stage, a breed-specific effect

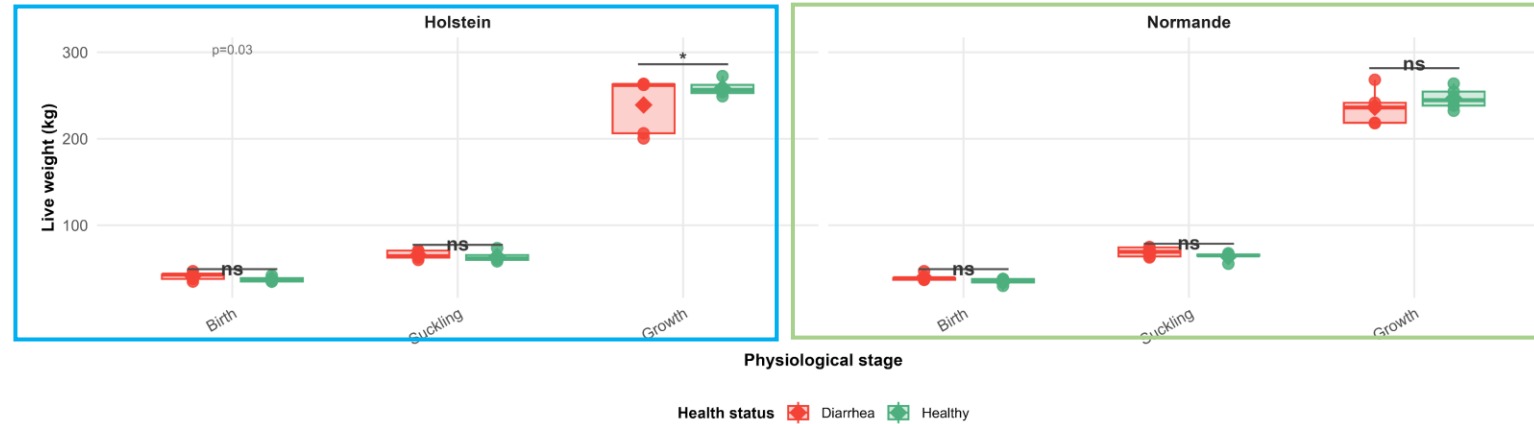
Normande calves shows no differences

Body weight parameters

A

Live weight by health status and physiological stage

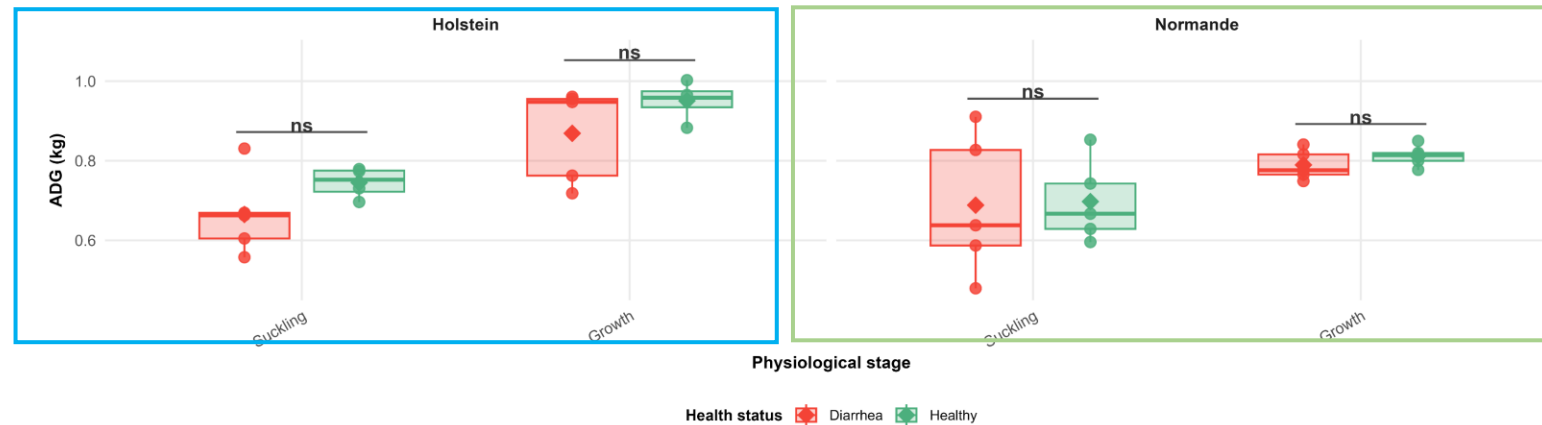
Diamond = model mean (95% CI) | Ribbon = loess | *p<0.05 **p<0.01 ***p<0.001 ns = not significant



B

ADG by health status and physiological stage

Diamond = model mean (95% CI) | Ribbon = loess | *p<0.05 **p<0.01 ***p<0.001 ns = not significant



➤ Summary

1. Early-life antimicrobial treatment is associated with long-term changes in fecal bacteria composition, most evident in the Holstein calves that received systemic antibiotics
2. The same group that received systemic antibiotics also shows lower and more variable body weight at the growth stage, paralleling the microbiota effect
3. Stratifying by breed controls for breed differences, but within Holstein, diarrhea and antibiotic exposure still cannot be separated.



➤ Acknowledgments



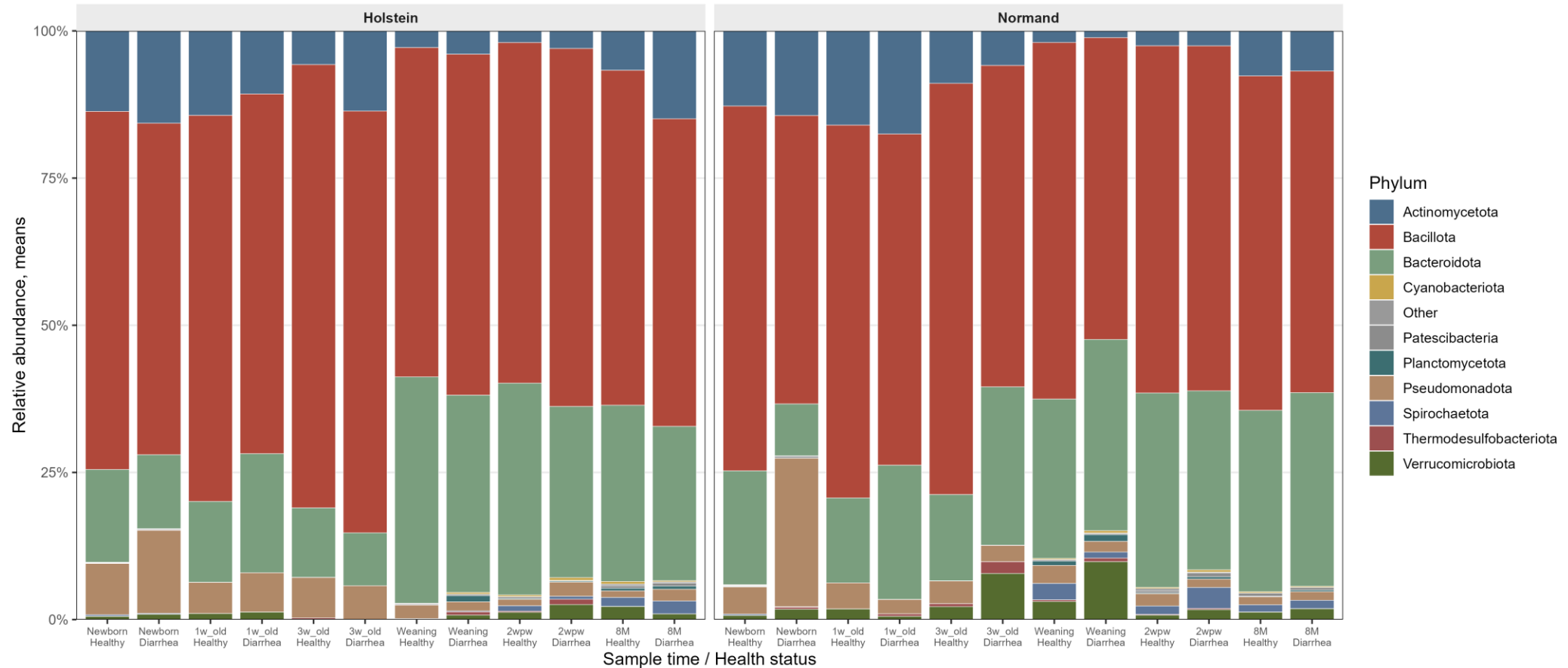
We acknowledge the support by the EU Horizon 2020 research and innovation program under grant agreements 101000213-HoloRuminant.

Thank you for your attention!

➤ RESULTS: Bacterial composition

Age-associated shifts in bacterial composition (Phylum level)

Healthy vs. Diarrhea



Expected age-driven phylum succession (Pseudomonadota → Bacillota → Bacteroidota), consistent across breeds, no phylum-level signature for health status