To what extent rumen microbiota composition is host-driven?

An experimental approach in goats

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Context

- Understanding of the symbiotic association between the host animal and its rumen microbiota is essential
- Each adult animal harbors its own microbiota => suggest a significant impact of the host on its microbiota composition
- High **specificity** and **resilience** of the rumen microbiota within its host in lactating cows (Weimer et al., 2010, 2017)

Context

- Understanding of the symbiotic association between the host animal and its rumen microbiota is essential
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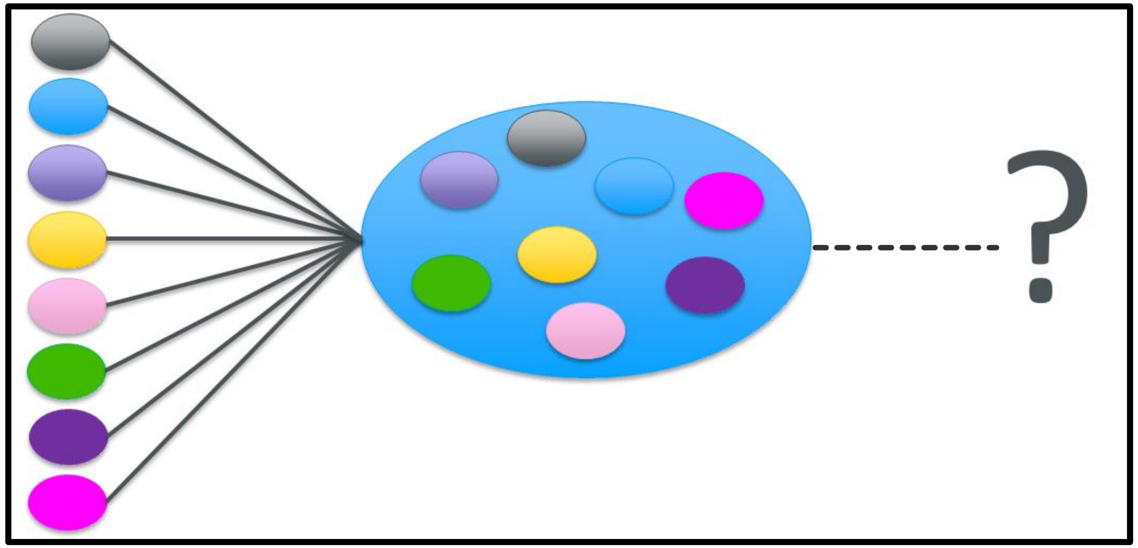
Aim of the trial

- Test the **existence of a sustained host specificity** in the rumen microbiota composition
- => **original experimental approach** :
  - emptied rumens of adult goats, pooled all the rumen contents and refilled each goat with the pooled rumen microbiota
  - tracked the microbiota compositional changes and compare the individual microbial equilibriums reached



Goat 1 microbiota

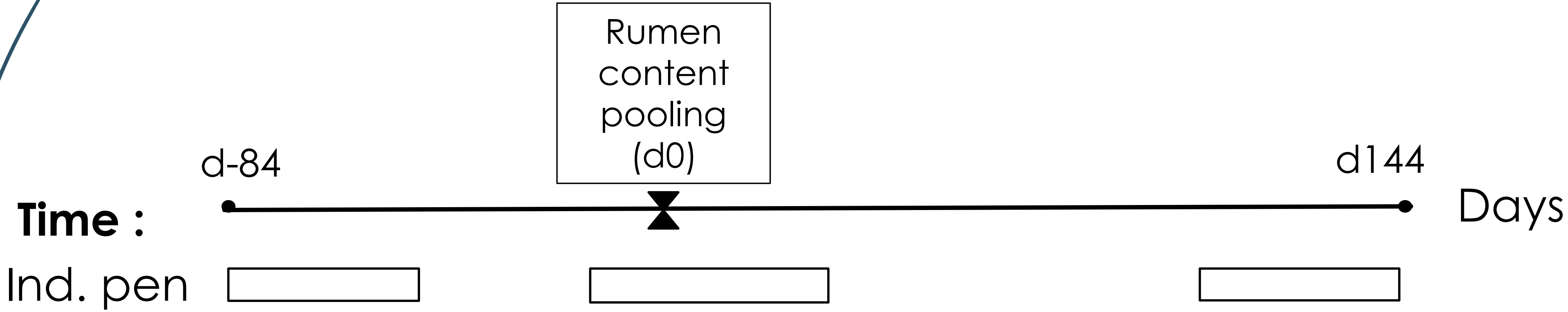
Goat 2 microbiota

Goat n-1 microbiota

Goat n microbiota

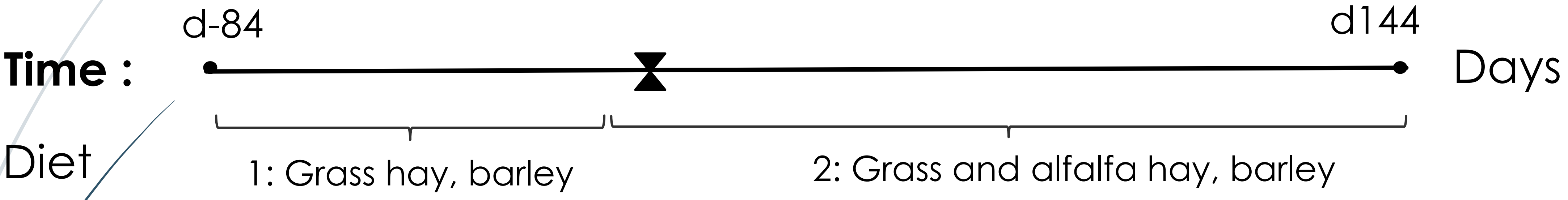
Trial: Animals

- 12 dry dairy goats (3 Saanen, 9 Alpine)
- Raised in similar conditions from birth
- Rumen cannulated
- During 7.5 months
- 3 periods in individual pen



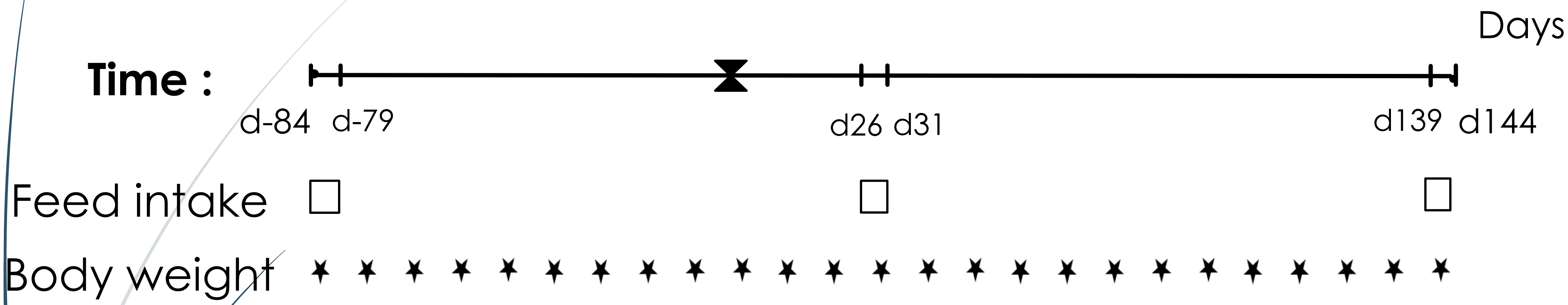
Trial: Diets

- 2 diets rich in fiber, of similar nutritional composition
- Quantities given adjusted to each goat's BW



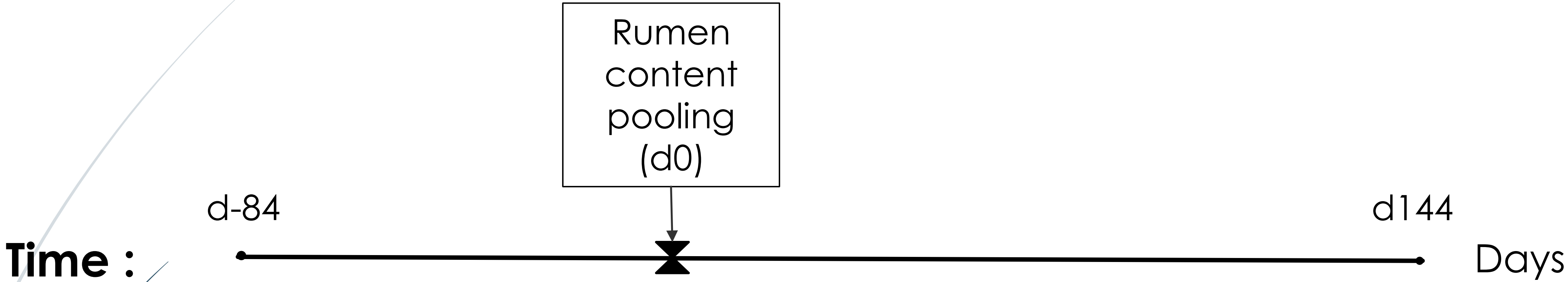
Nutritional composition	1	2
NDF (%DM)	59	56
ADF (% DM)	33	30
Starch (% DM)	8.6	8.4
Crude protein (% DM)	7.5	7.0

Trial: Goat traits



	BW (kg)	DMI (kg/d)
Mean	53.1	1.23
Standard deviation	6.9	0.10

Trial: rumen content pooling procedure



Rumen content pooling (d0)

Time :

d-84

d144

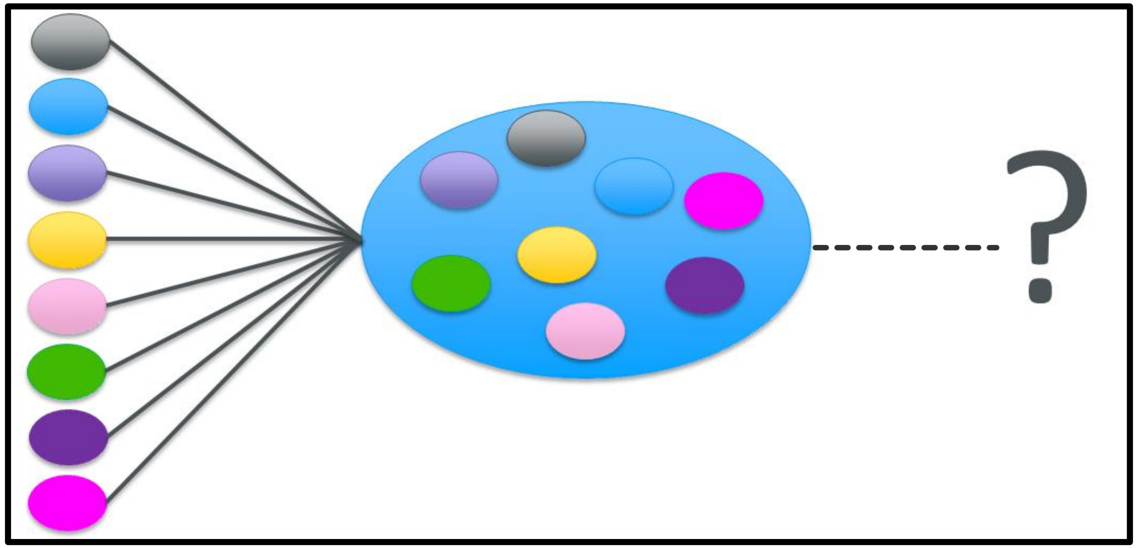
Days

Goat 1 microbiota

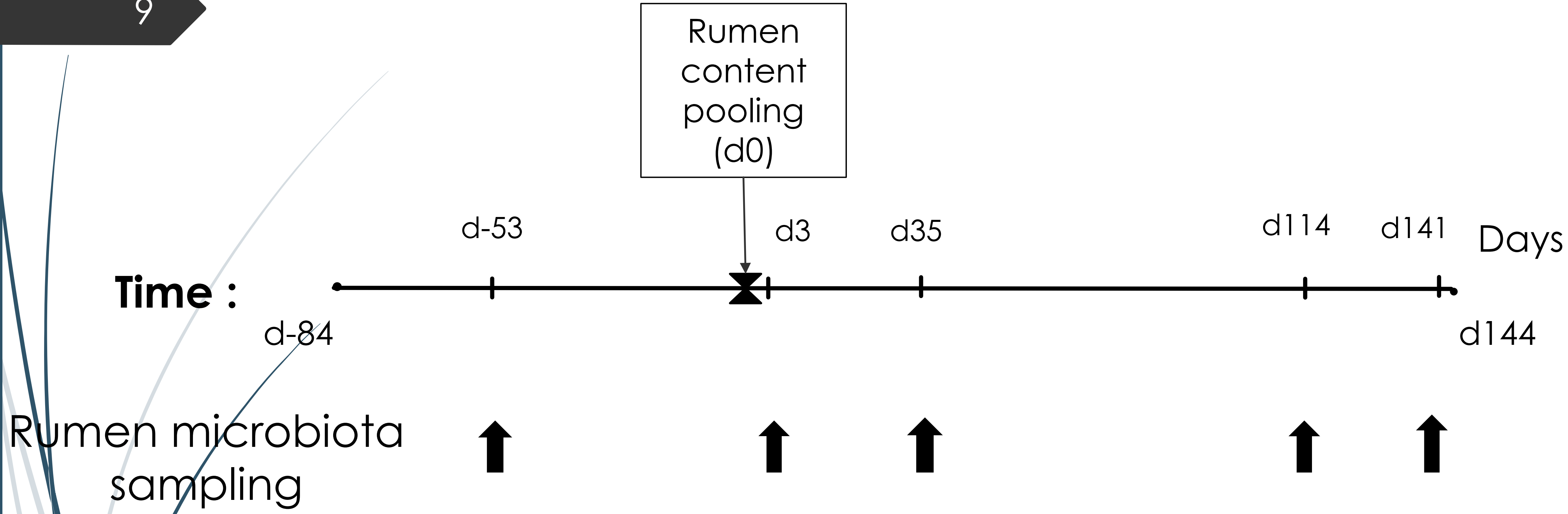
Goat 2 microbiota

Goat n-1 microbiota

Goat n microbiota



Trial: Rumen microbiota composition analysis



Rumen content pooling (d0)

Time :

d-84

d-53

d3

d35

d114

d141

d144

Days

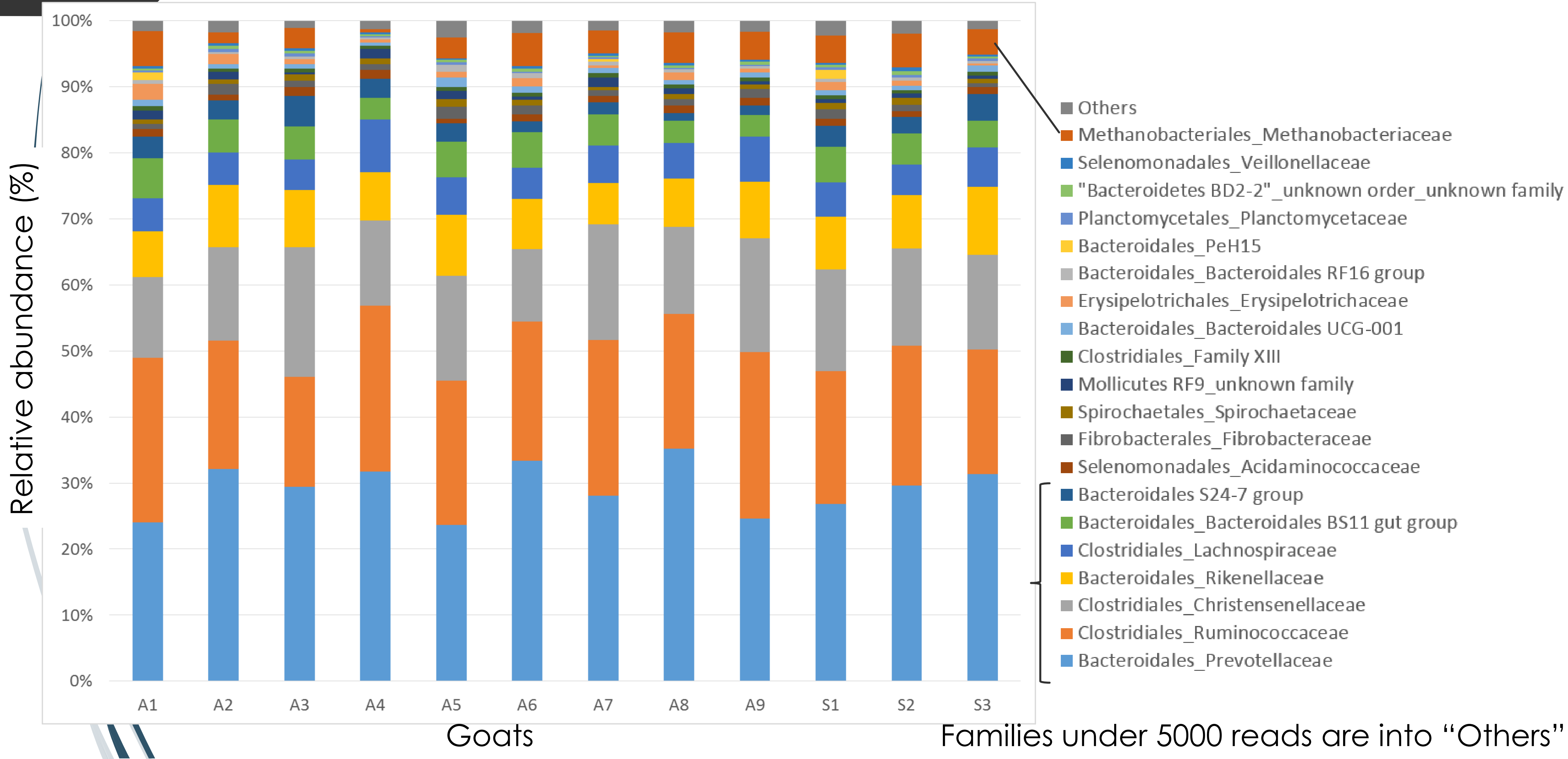
Rumen microbiota sampling

- V4-V5 regions of archaeal and bacterial 16S rRNA genes
- Miseq Illumina sequencer
- Sequence processing with FROGS pipeline under Galaxy
- Taxonomic affiliation of the 1 488 OTUs detected on the database SILVA 16S v128

Results

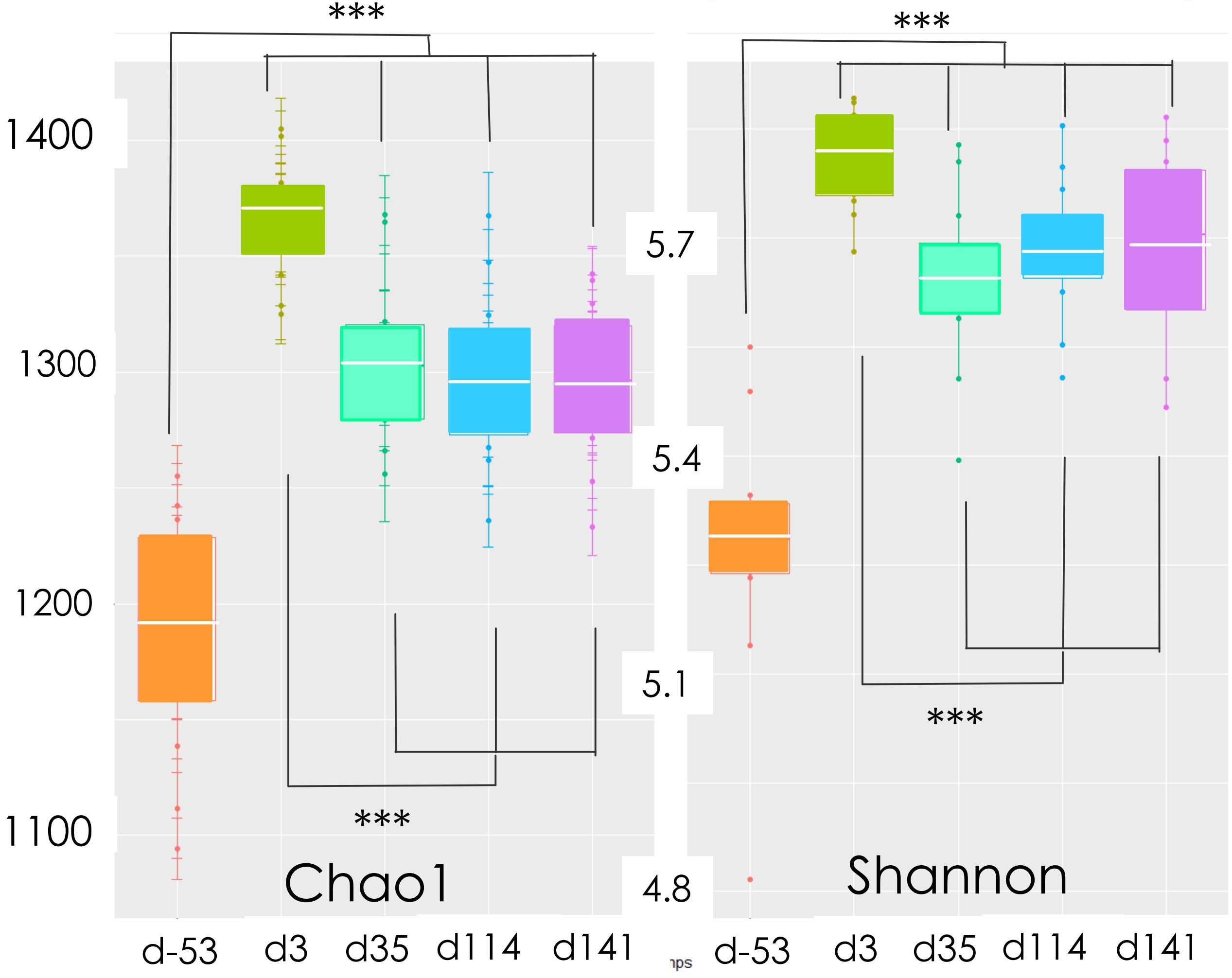
- Individual rumen bacterial and archeal composition at family level before rumen content pooling
- Diversity at species level
  - Alpha-diversity
  - Beta-diversity (Compositional, Phylogenetic)
- Modification of rumen microbiota composition at genus level relative to
  - Days
  - Goats

Individual rumen bacterial and archaeal relative abundances at family level at d-53



Families under 5000 reads are into "Others"

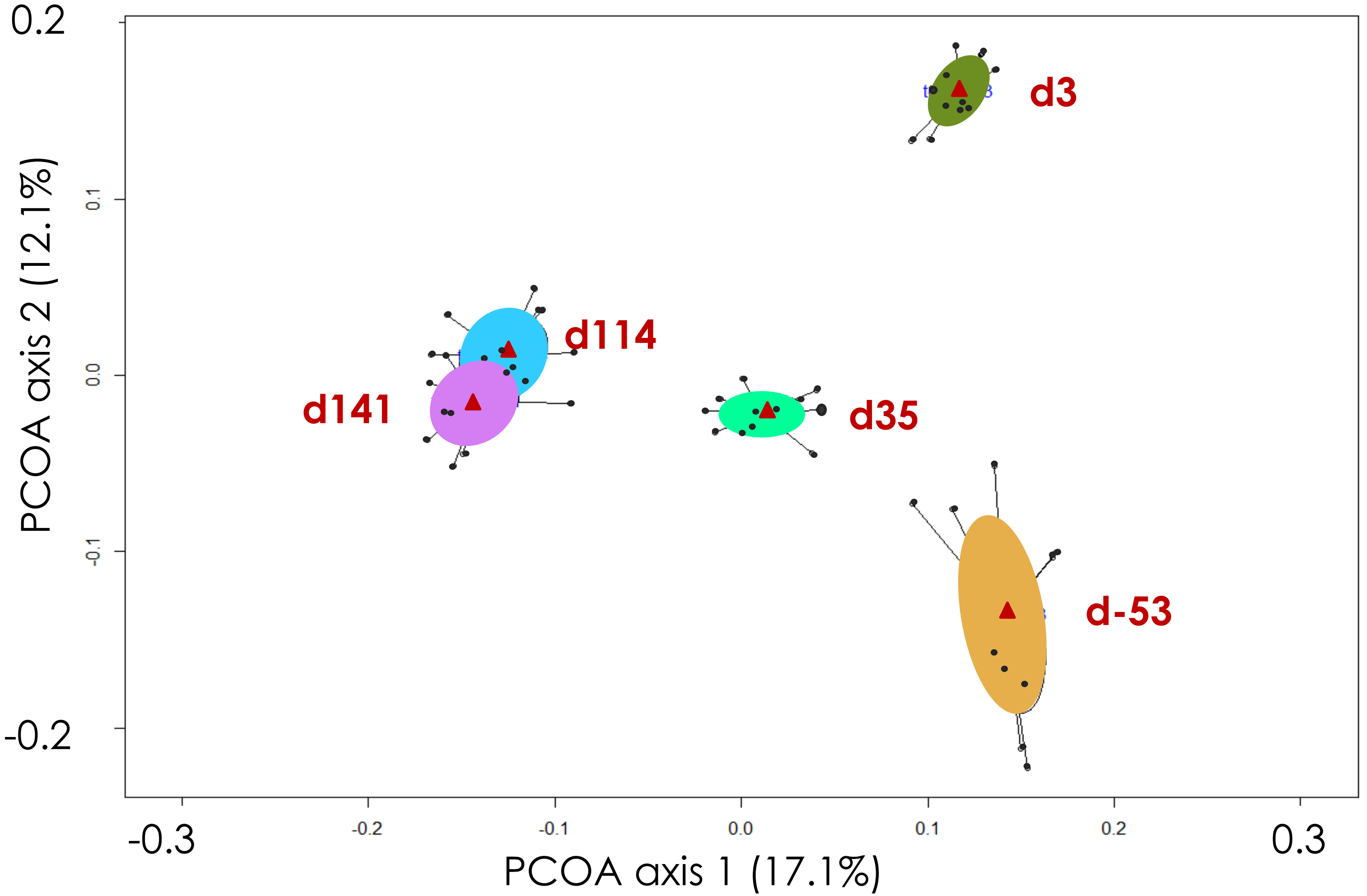
α–diversity (OTUs level)



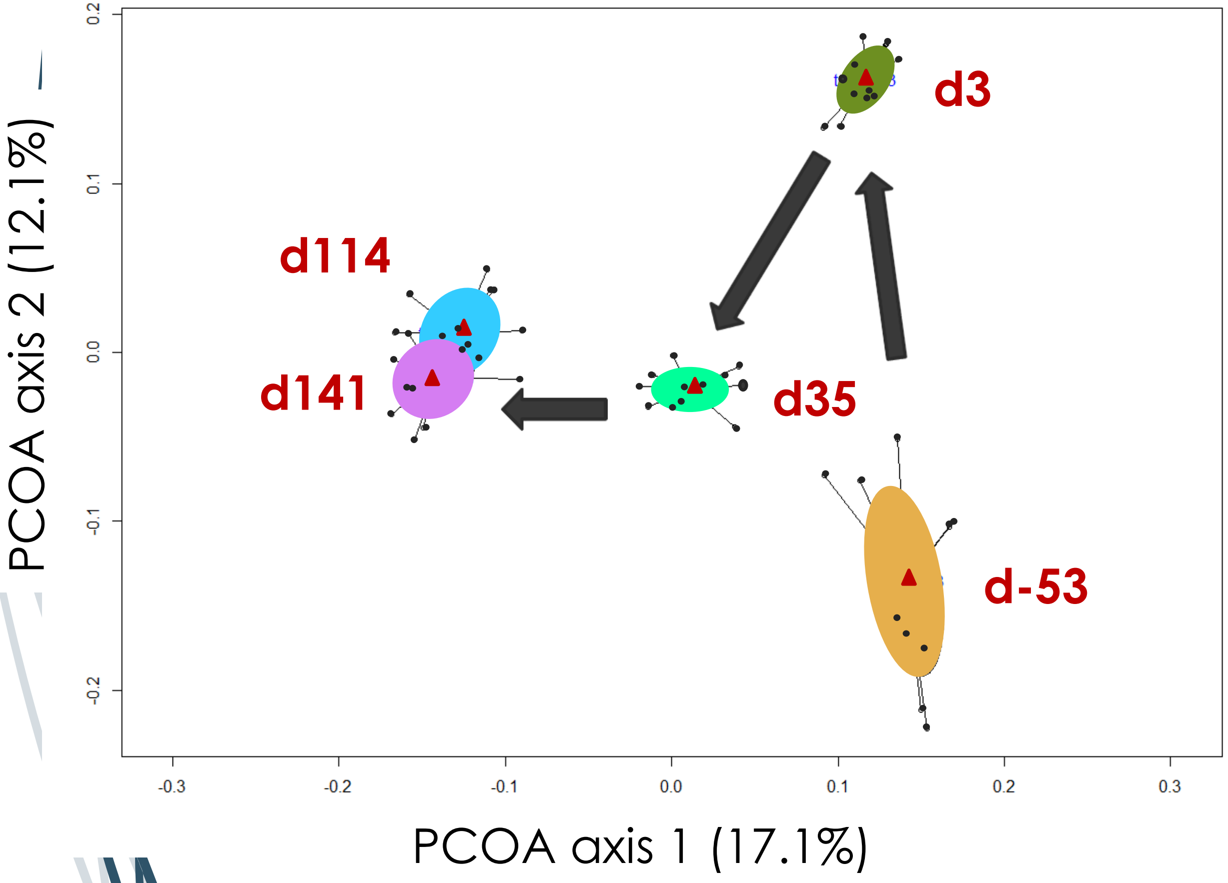
- At d3, increased α–diversity which stabilized at a higher level at d 35, d114 and d141
- Decreased variability of α–diversity indexes at d3 compared to d-53

Compositional β−diversity (OTUs level)

Principal **Co**ordinates **A**nalysis (**PCoA**)of rumen microbiota samples based on OTUs community dissimilarities (Bray Curtis)



Compositional β–diversity (OTUs level)

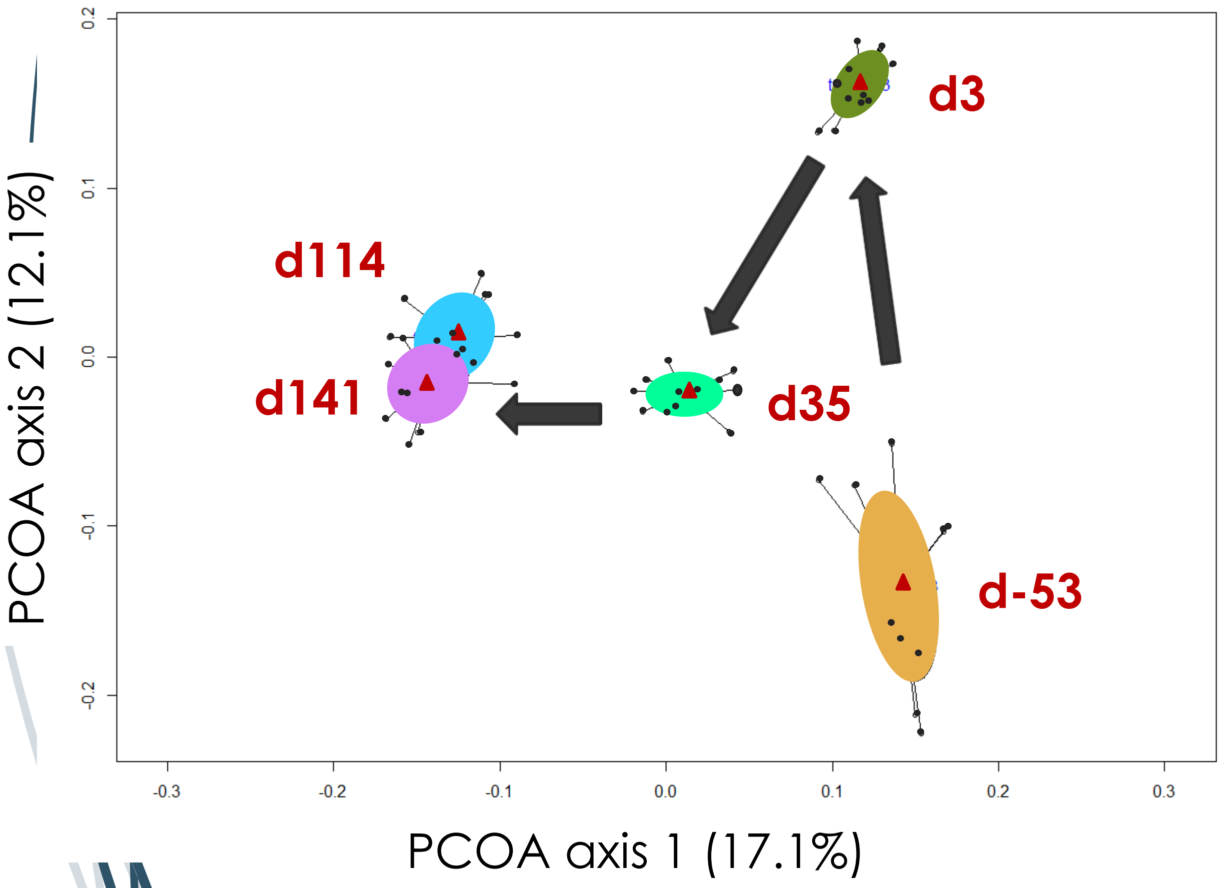


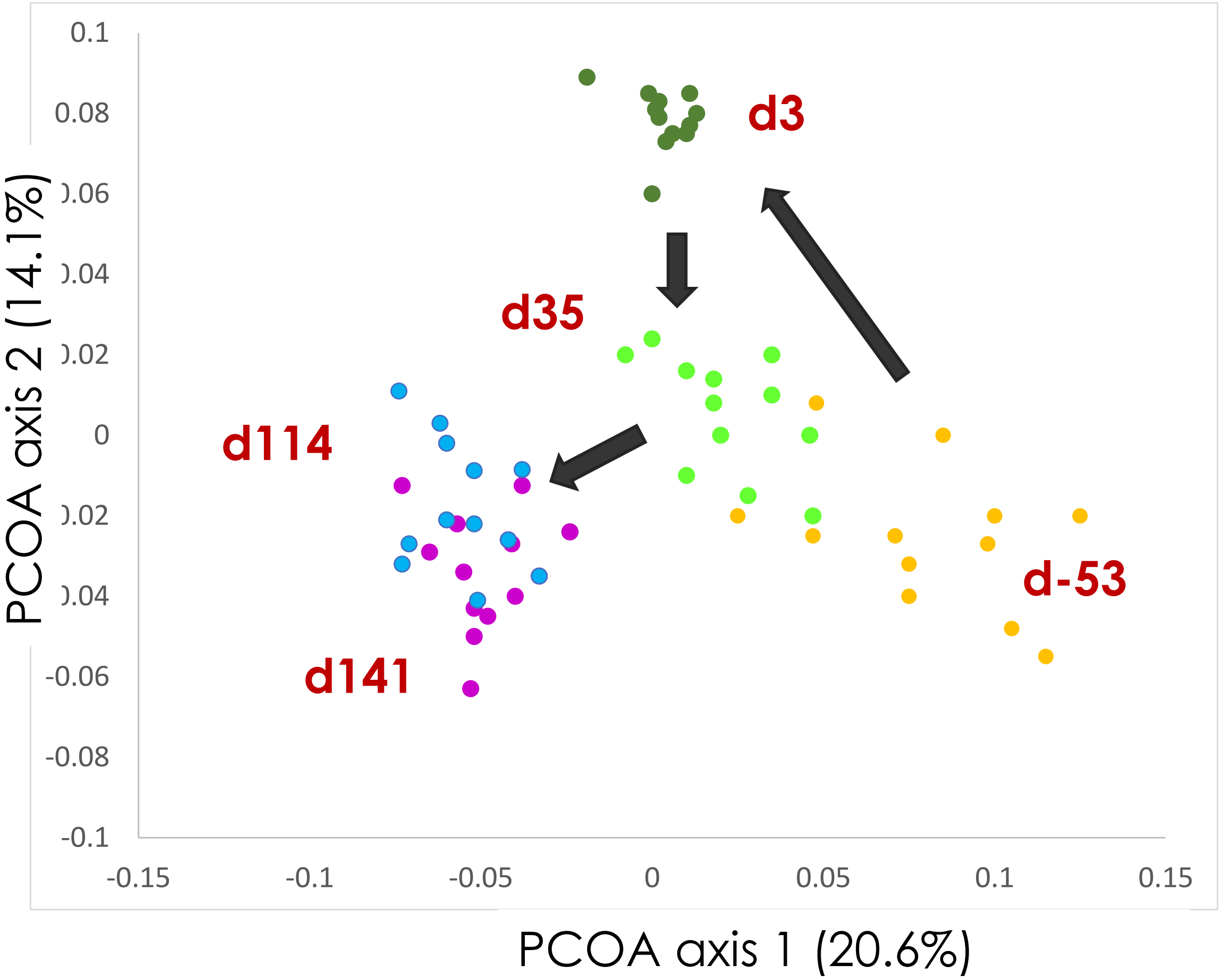
Analysis of similarity testing ranked bray-Curtis dissimilarity indices between days

	d-53	d3	d35	d114	d141
d-53		**R=0.61 (P=0.001)**	**R=0.78 (P=0.001)**	**R=0.90 (P=0.001)**	**R=0.89 (P=0.001)**
d3			**R=0.94 (P=0.001)**	**R=0.97 (P=0.001)**	**R=0.99 (P=0.001)**
d35				**R=0.95 (P=0.001)**	**R=0.95 (P=0.001)**
d114					R=0.04 (P=1)

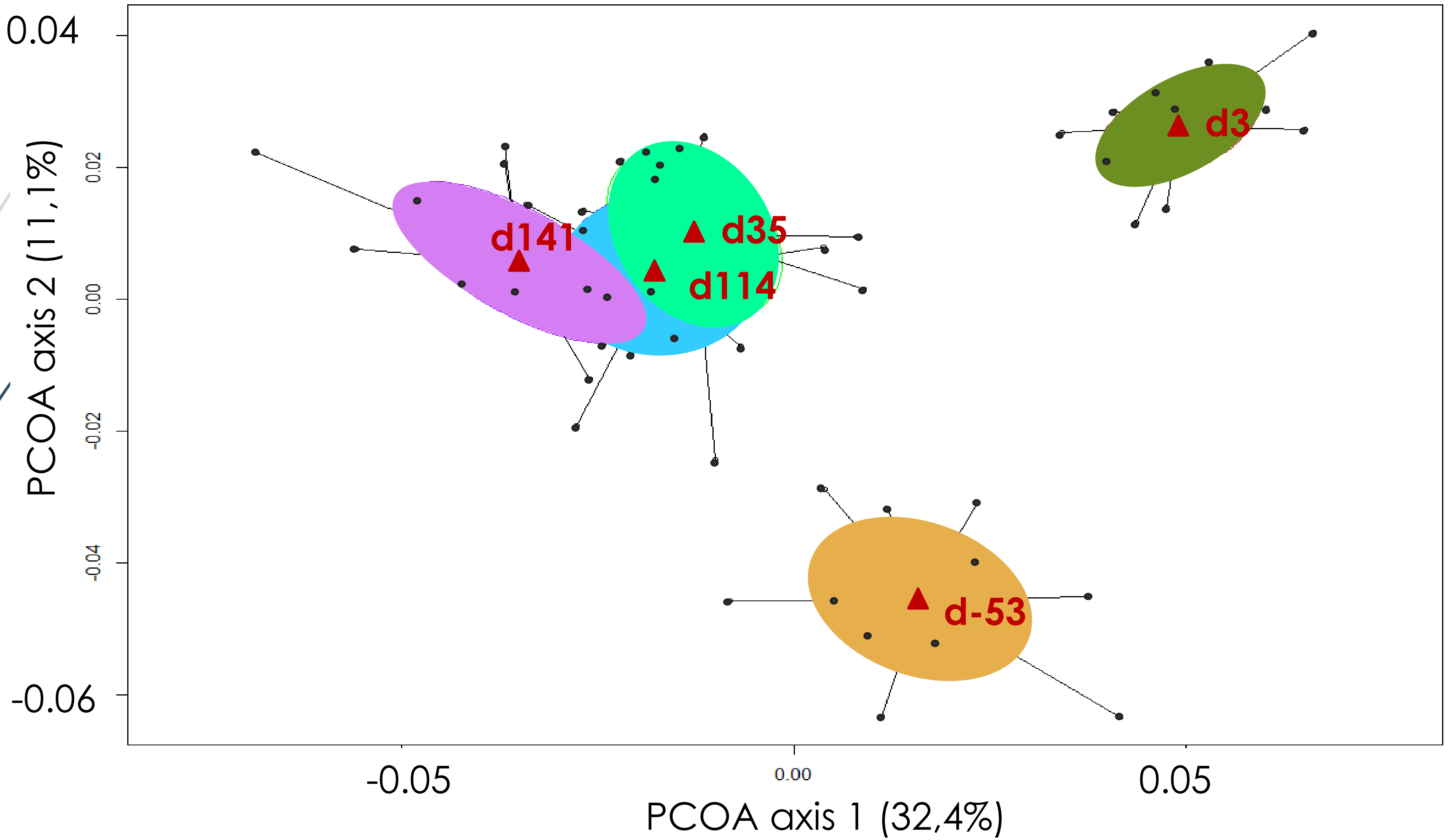
Phylogenetic β–diversity at OTUs level

PCoA of rumen microbiota samples based on weighed unifrac distance

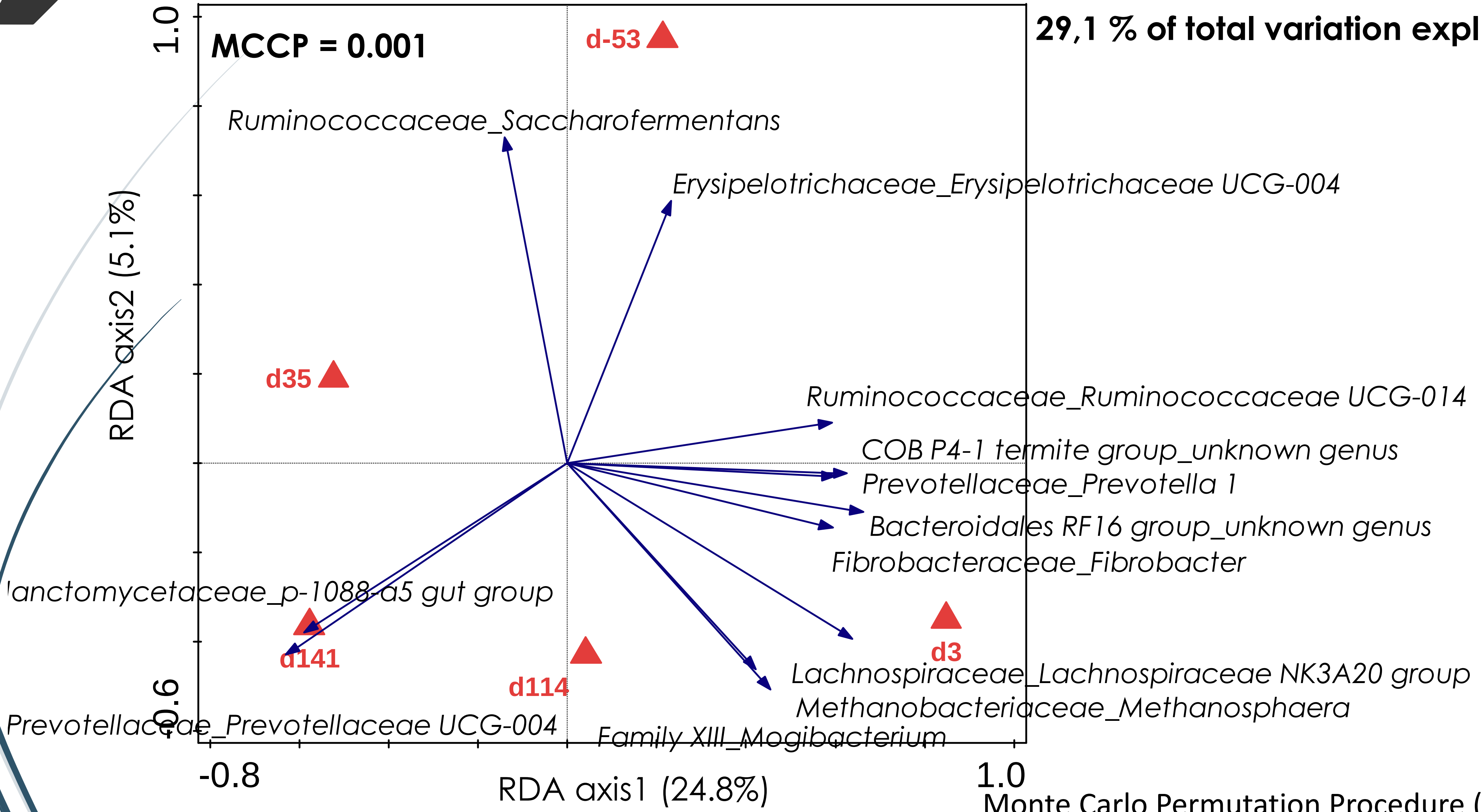




PCoA of rumen microbiota samples based on Bray Curtis distance at genus level



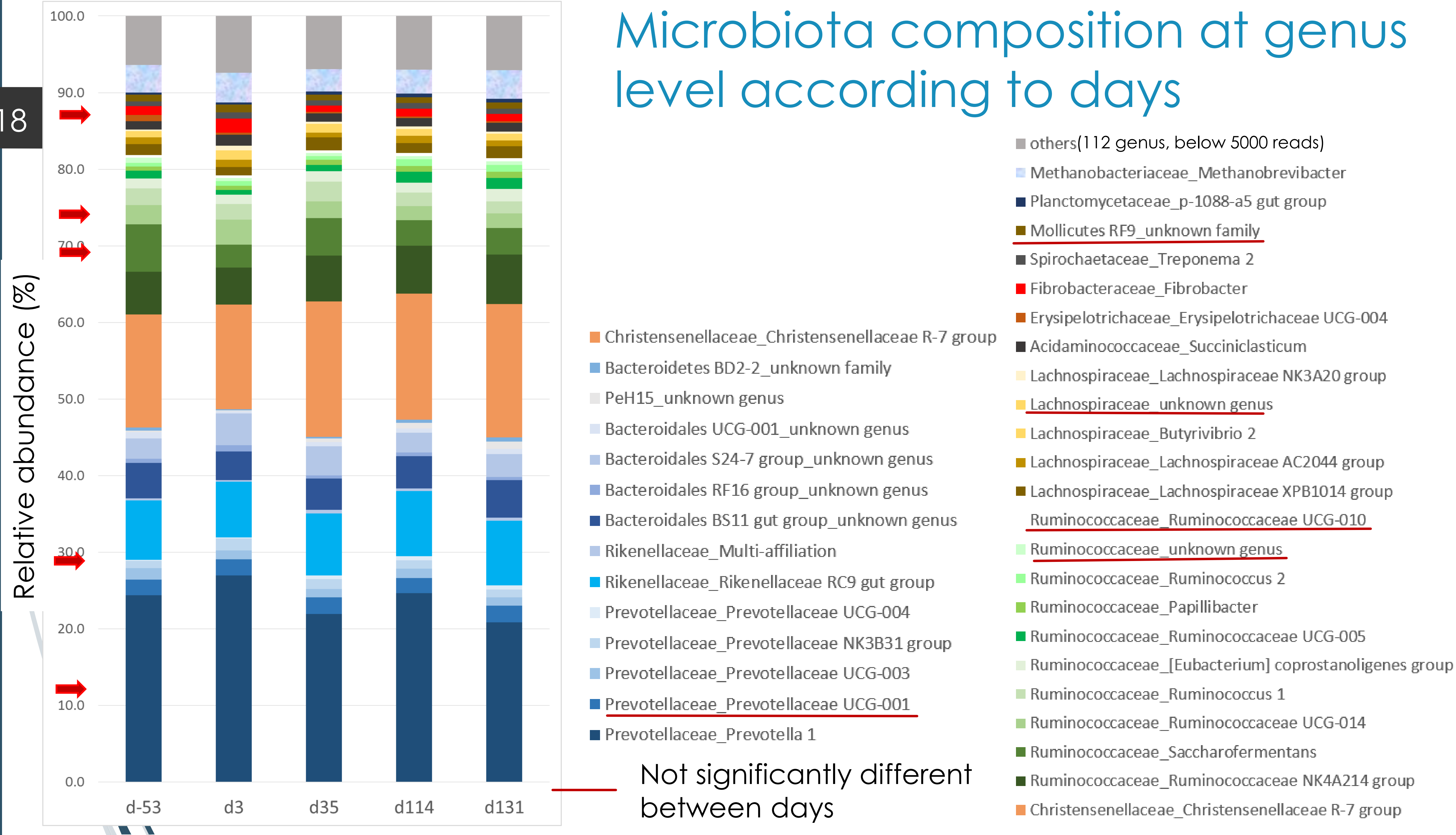
Biplot of RDA of rumen microbiota composition relative to days (genus level)



29,1 % of total variation explained

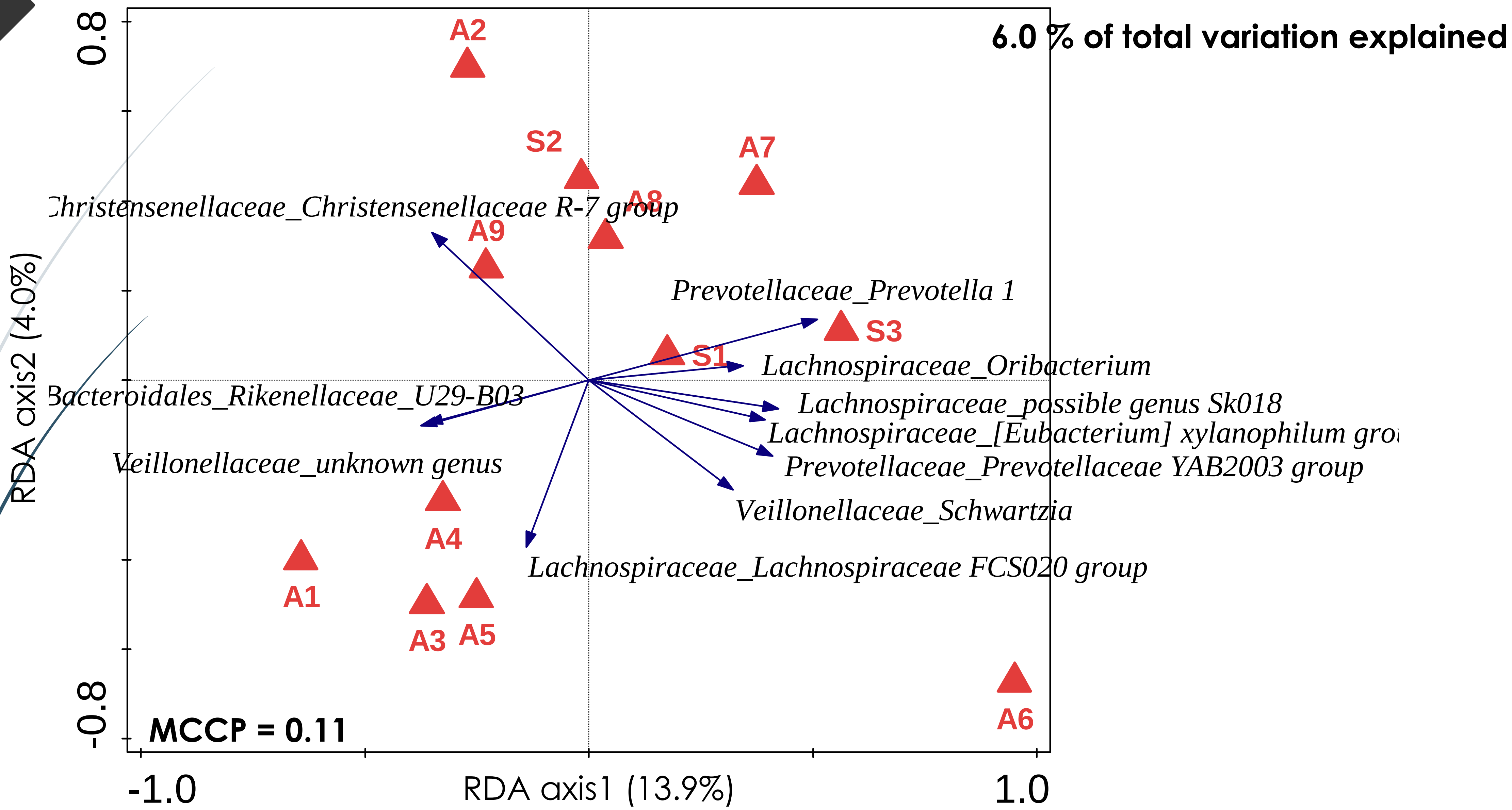
Monte Carlo Permutation Procedure (MCPP)

Microbiota composition at genus level according to days



Not significantly different between days

Biplot of RDA of rumen microbiota composition relative to goats (genus level)



Monte Carlo Permutation Procedure (MCPP)

Conclusion 1

- Increased α-diversity after reinoculation which stabilized at a higher level than before reinoculation
- β-diversity:
  - Clear clustering pattern based on days with no return to original state
  - Goats impacted microbial composition to a much lower extent
- Contrary to Weimer et al., no resilience was observed. Instead all rumen microbiota exhibited a high structural plasticity.

Functional redundancy?

Conclusion 2

- From the reinoculation step to 5 months later, the 12 ecosystems evolved following a **common pattern** in which hosts played a minor role
- In stabilized rumens, can host-dependent variables explain the structural microbiota differences?

Take home message

In dry goats fed high fiber diets, rumen microbiota composition was more environnementally and diet-driven than host-driven

Thank you for your attention