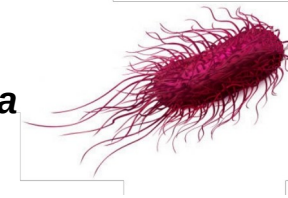


➤ Construction of a large genome catalog of microbial community of cattle

S. Teseo, Ph. Ruiz, P. Sapountzis

Pathogènes
Alimentaires
Zoonotiques

DEC
Listeria



Fonctions
Métaboliques
du Microbiote
et Dysbioses

Polyphénols
Xénobiotiques
SII



Aliment

PAZ



Animal

MICROBIOTE



Galéniques
Innovantes

Probiotiques
Prébiotiques
Substances actives

Homme

FM2D



GALINN

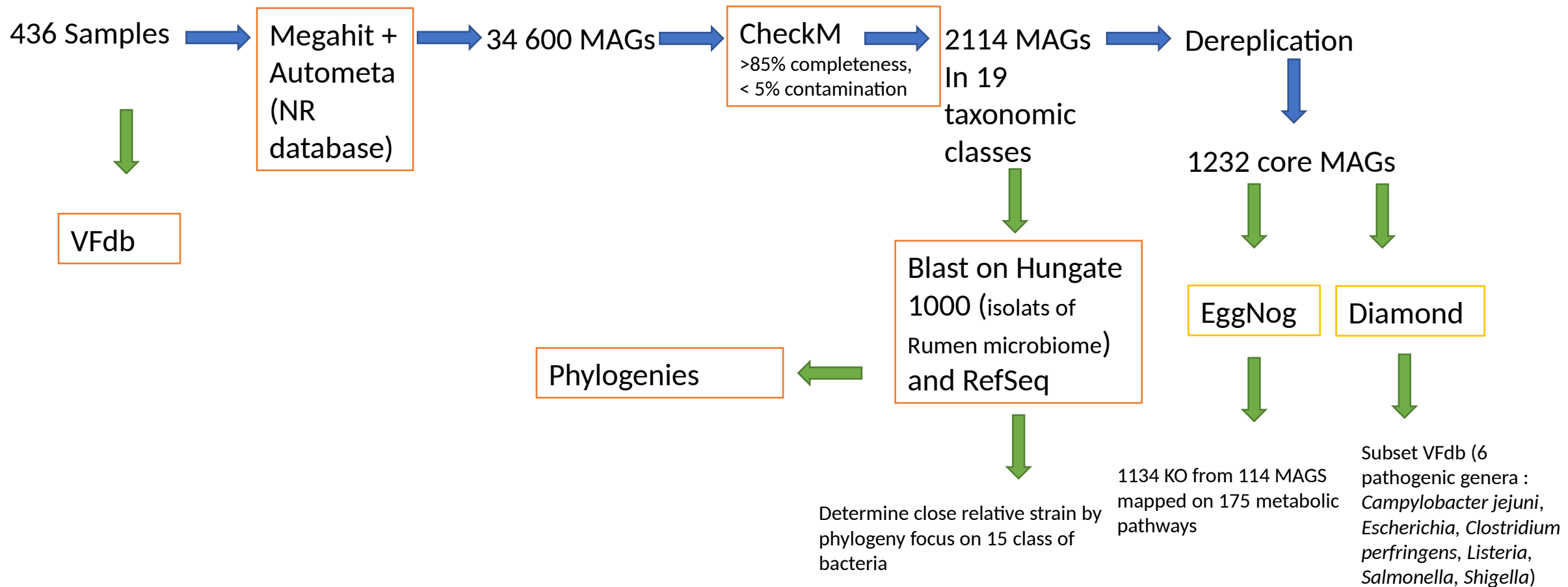
> Objective

- Generate a global high quality MAG catalog that can cover up the fecal (proxy of intestine) bacterial symbionts that can be used as a reference.
- Characterize the core microbiota and reconstruct their metabolic functions.
- Evaluate the potential virulence focusing on 6 known pathogenic genera; *Campylobacter*, *Clostridium*, *Echerichia*, *Shigella*, *Listeria*, *Salmonella*
- Examine gene inventory changes in two common dietary transitions ordinarily taking place in cattle: the introduction of solid feed in young calves and the annual rotation between winter and summer diets in dairy cows.

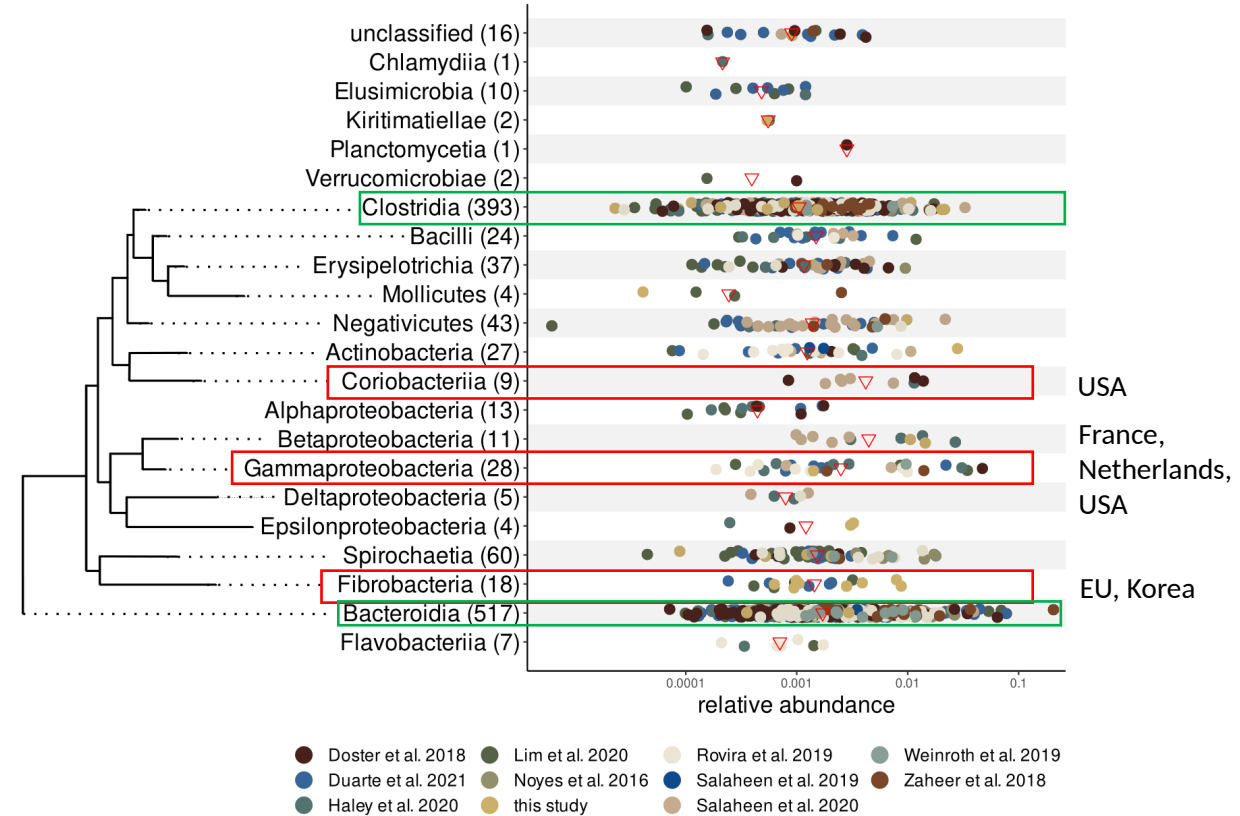
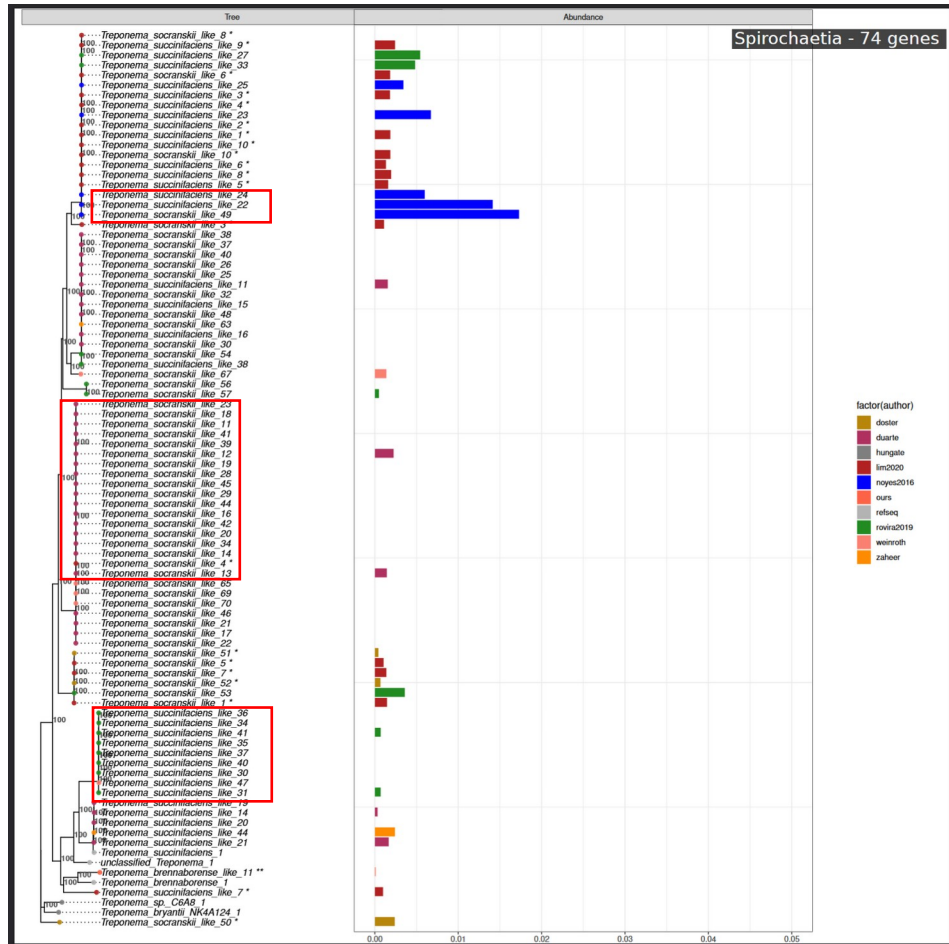
> Samples

- 436 Fecal Metagenomes (366 from previous studies)
- 11 studies (2016 -> 2021)
- 6 countries : Canada, France, Germany, Korea, Netherland, US (veal : 12 with liquid feed et 12 with solid feed)
- Controled dietary for the 70 french samples -> winter (indoors) : 22 with corn and grass silage, summer (outdoors) : 48 grazing + access to food supplement

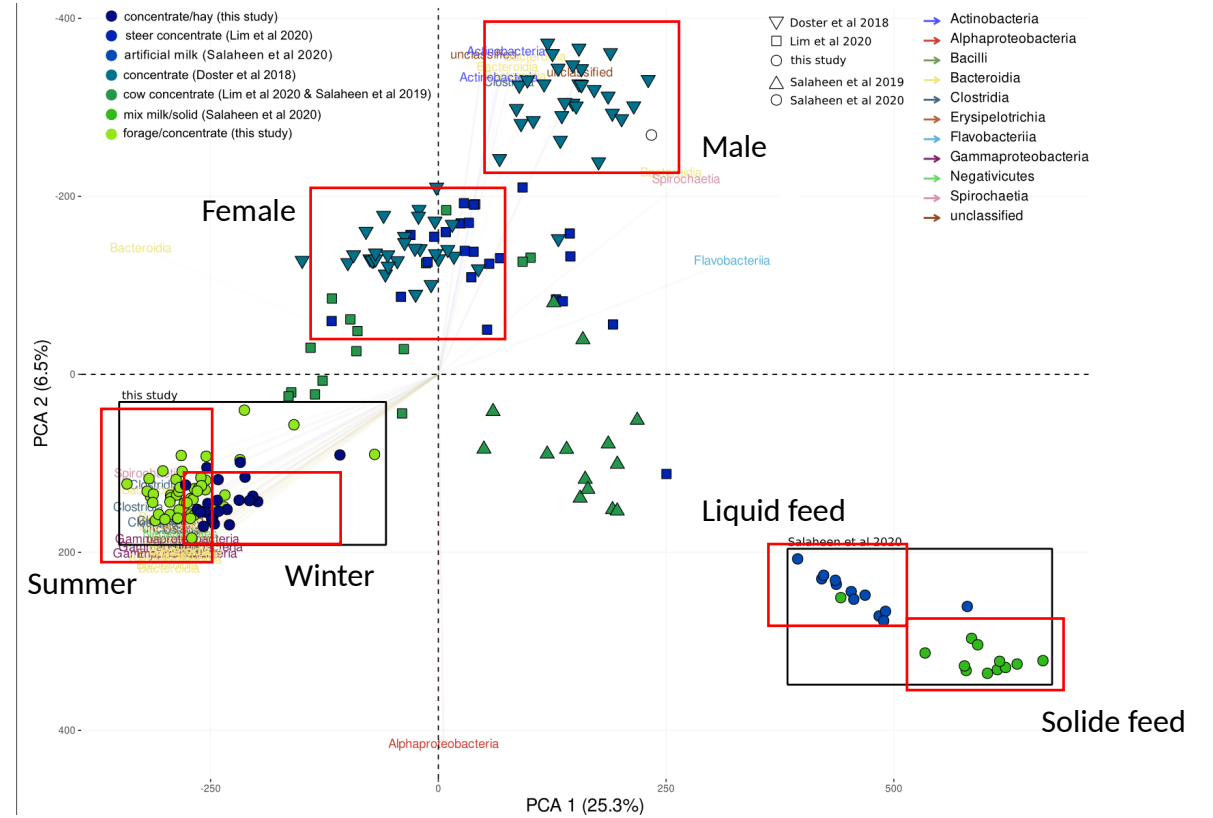
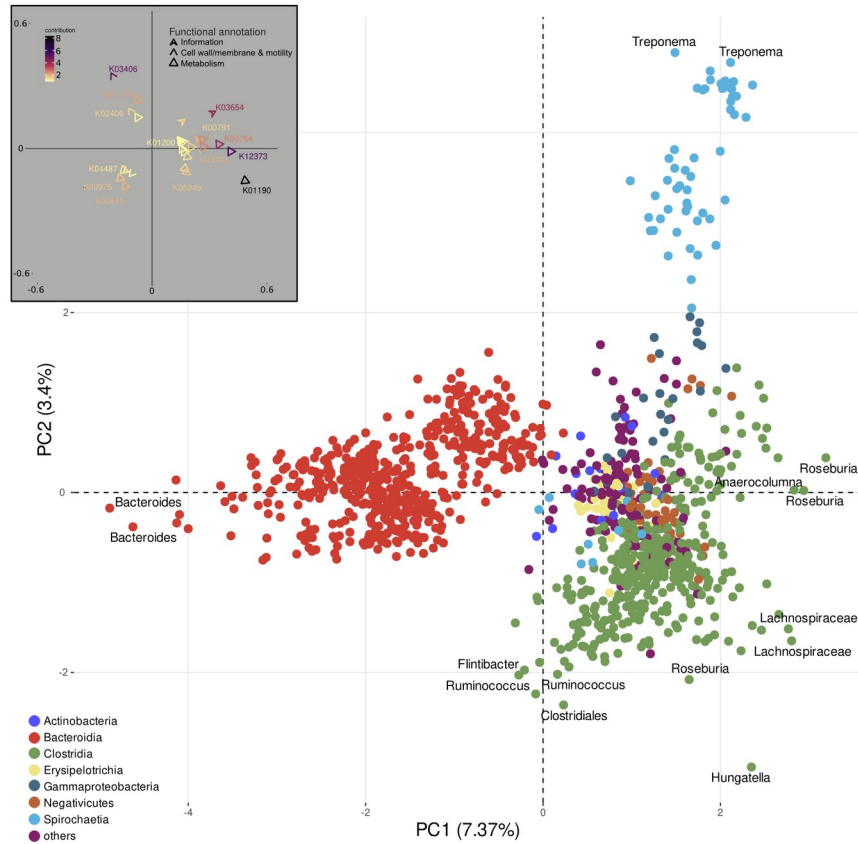
> Core MAGs



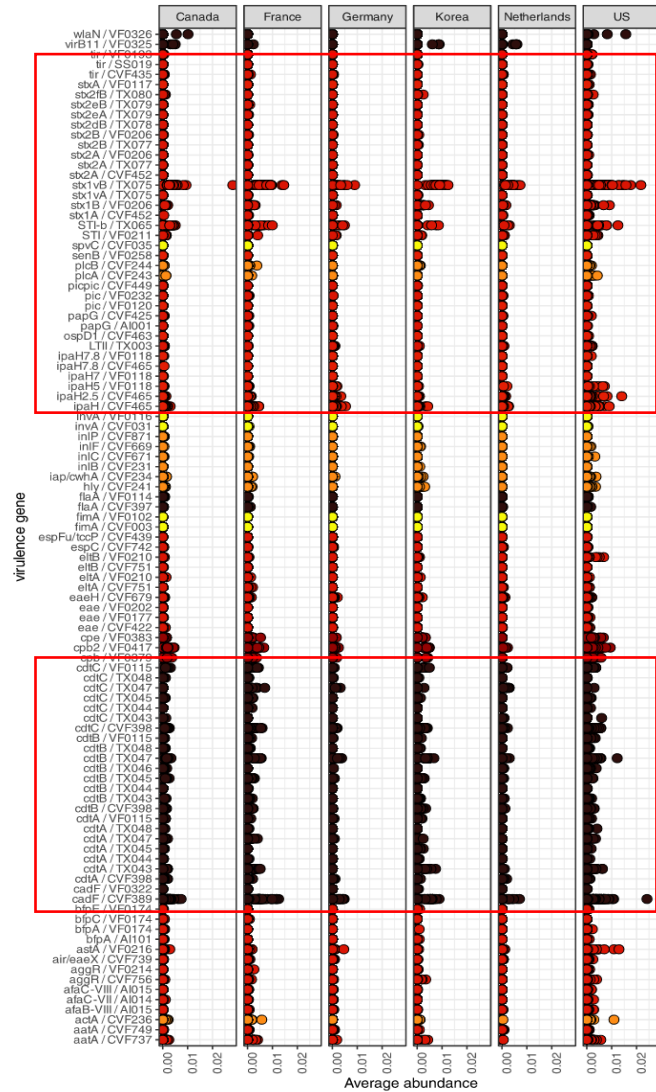
> The phylogenetic relationship of MAGs



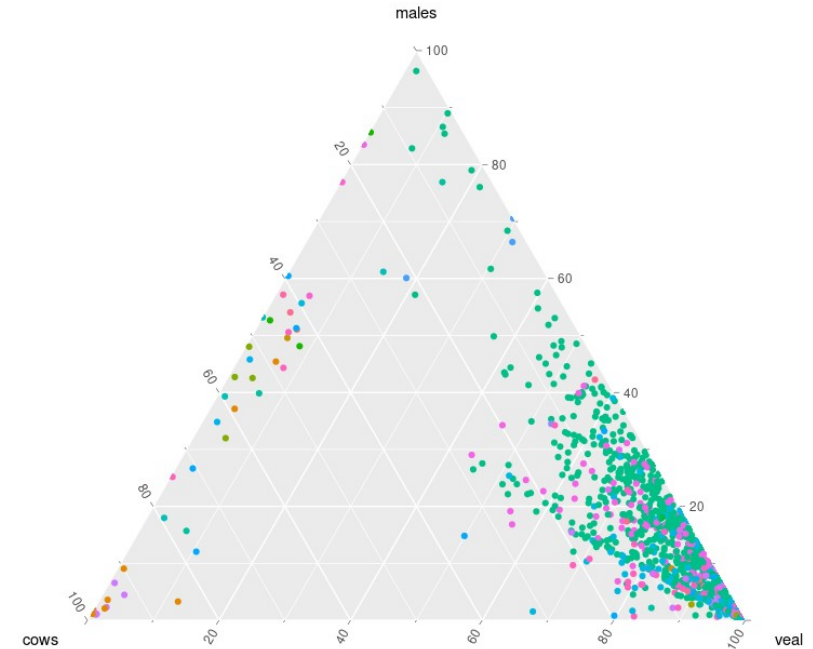
➤ Functionnal annotation and specific genes



> pathoMAGs occurrence



- genus
- Campylobacter
 - Clostridium
 - Escherichia
 - Shigella
 - Listeria
 - Salmonella



- genus
- Acine
 - Aerom
 - Bacte
 - Barto
 - Borde
 - Burkh
 - Campy
 - Citro
 - Clost
 - Dicke
 - Enter
 - Esche
 - Franc
 - Haemo
 - Helic
 - Klebs
 - Legio
 - Mycob
 - Mycop
 - Neiss
 - Pecto
 - Pseud
 - Salmo
 - Shige
 - Staph
 - Strep
 - Vibri
 - Yersi



> Conclusion

- There is clearly a study ID effect who could explain the MAG clustering of several class (phylogeny)
- The generated catalog cover ~ 70 % of the intestinal bacterial symbionte : Feces are representative of the gut lumen but also of the proximate environment
- The diatry change and the season affect the microbiota composition and gene inventories (summer = more metabolic options; introduction to solid = = more metabolic options)

- We are grateful to the Mesocentre Clermont Auvergne University and Aubi platform