

Characterization of the small human intestinal microbiome using an innovative medical device

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INTRODUCTION:

- The gut microbiome (microbial community with distinct physio-chemical properties in a given habitat) → **major role in maintaining health**.
- Stratification** through the gastrointestinal tract (micro-organisms and metabolites) (Figure 1).
- Dysbiosis = unbalanced microbiome → linked to some cancers, inflammatory, metabolic and neurological diseases...
- Current methods for the study of the human intestinal microbiome: **not representative** of the entire gut microbiome.
 - Faecal analysis: common but do not fully represent the intestinal microbiome (only large bowel).
 - Endoscopy and colonoscopy: expensive, invasive and complex to implement on a large scale. Could introduce a contamination bias during collection².

To overcome these issues, PELICAN HEALTH develops a cutting-edge **ingestible device**, able to perform **multi-sampling** in the **small intestine** (SI) to perform **multi-omics analysis** (Figure 2).

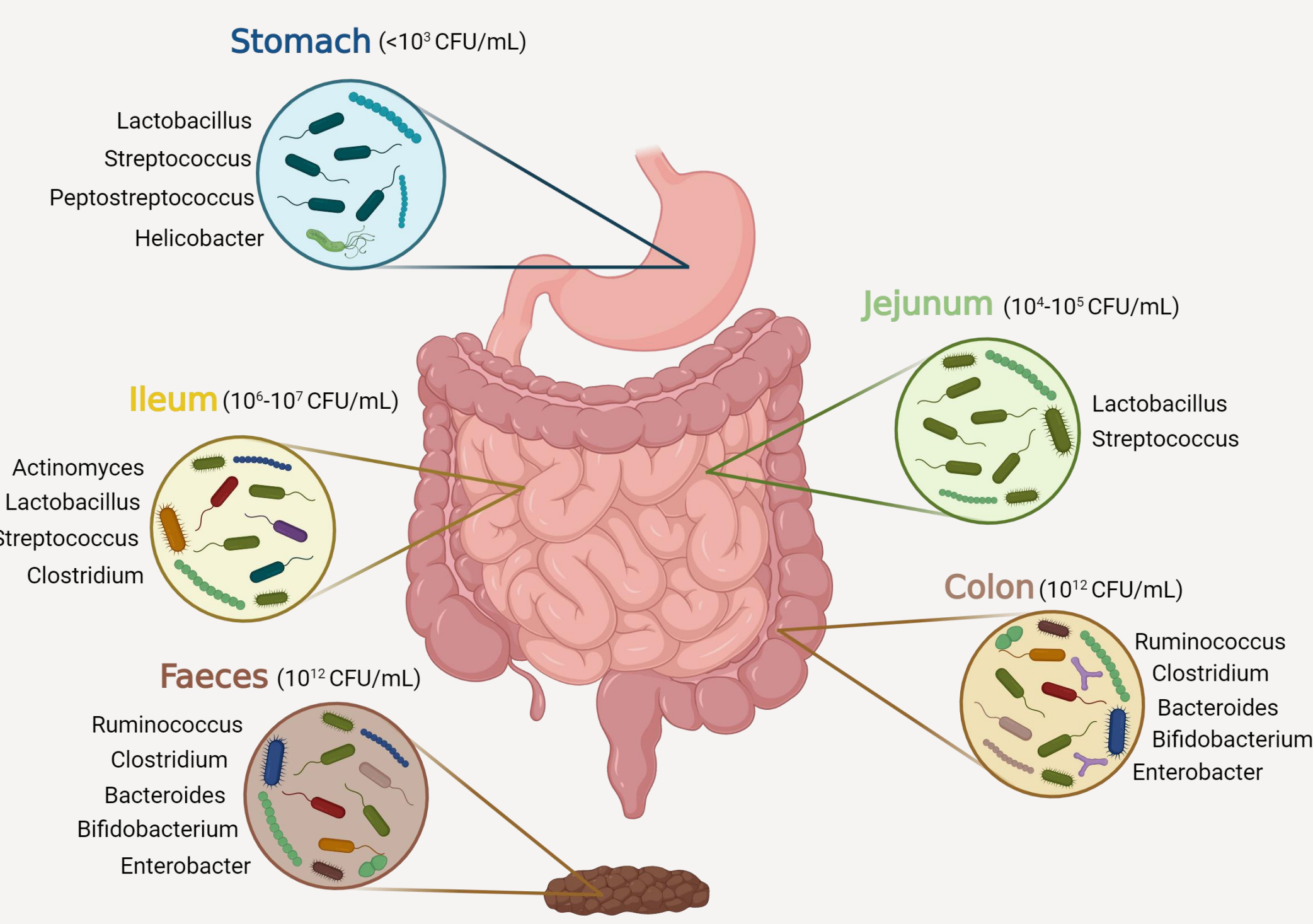


Figure 1: Microbial diversity and concentration in the human digestive tract^{3,4}



Figure 2: Structure and use of Pelican Sampler medical devices

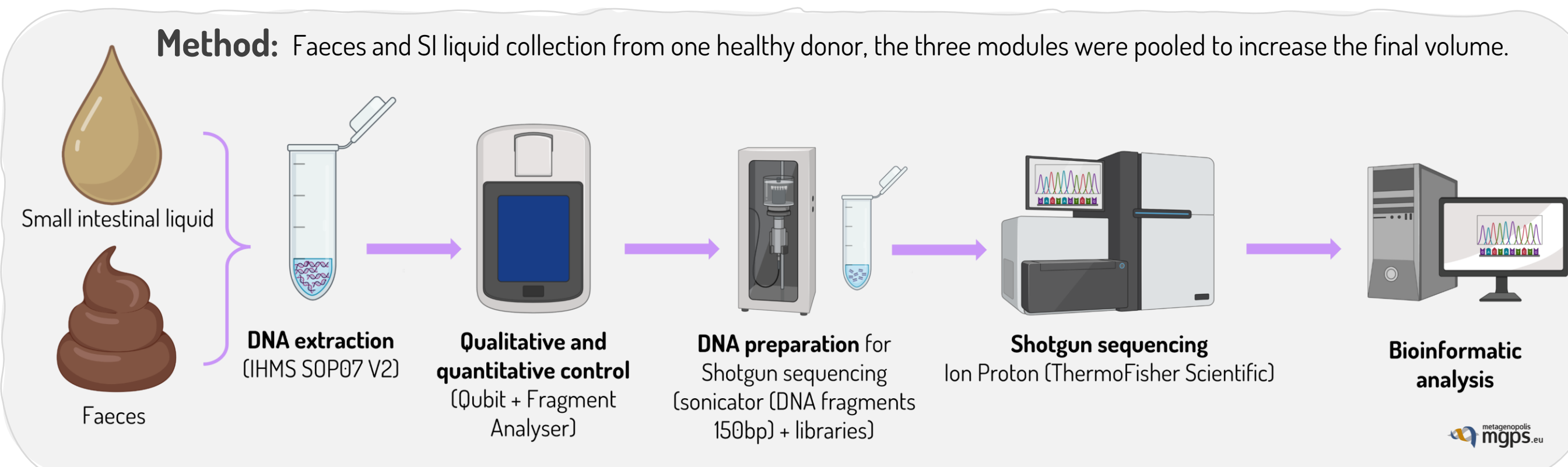


Figure 3: Bacterial species depending on the collection site.

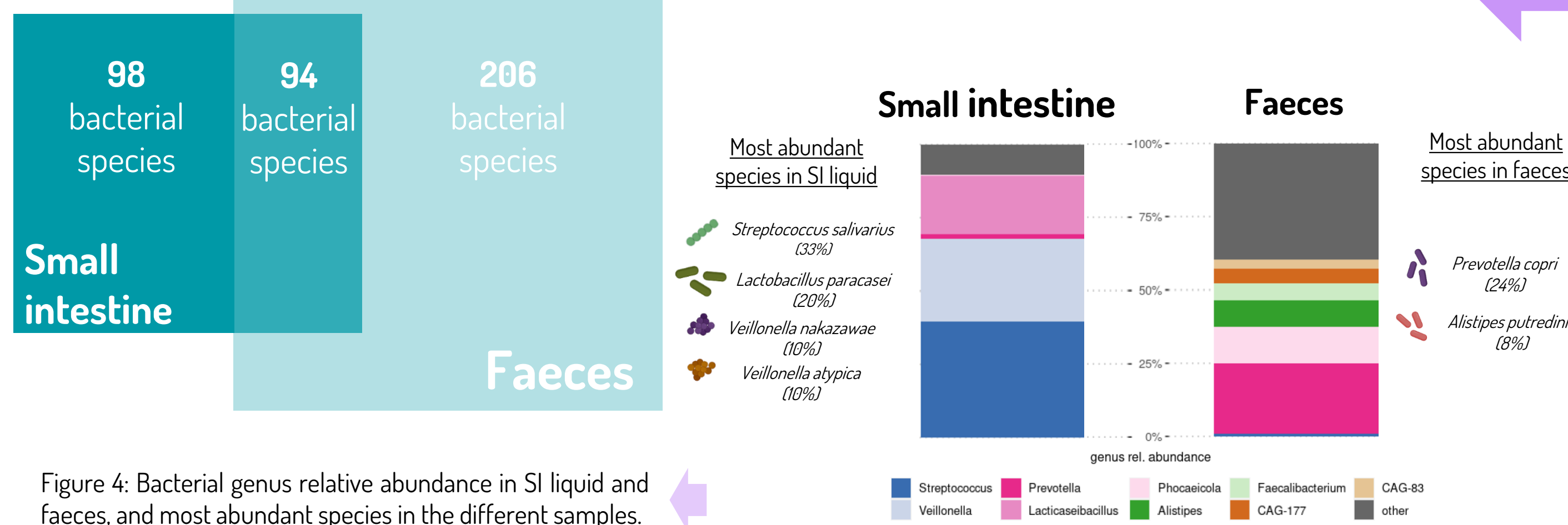


Figure 4: Bacterial genus relative abundance in SI liquid and faeces, and most abundant species in the different samples.

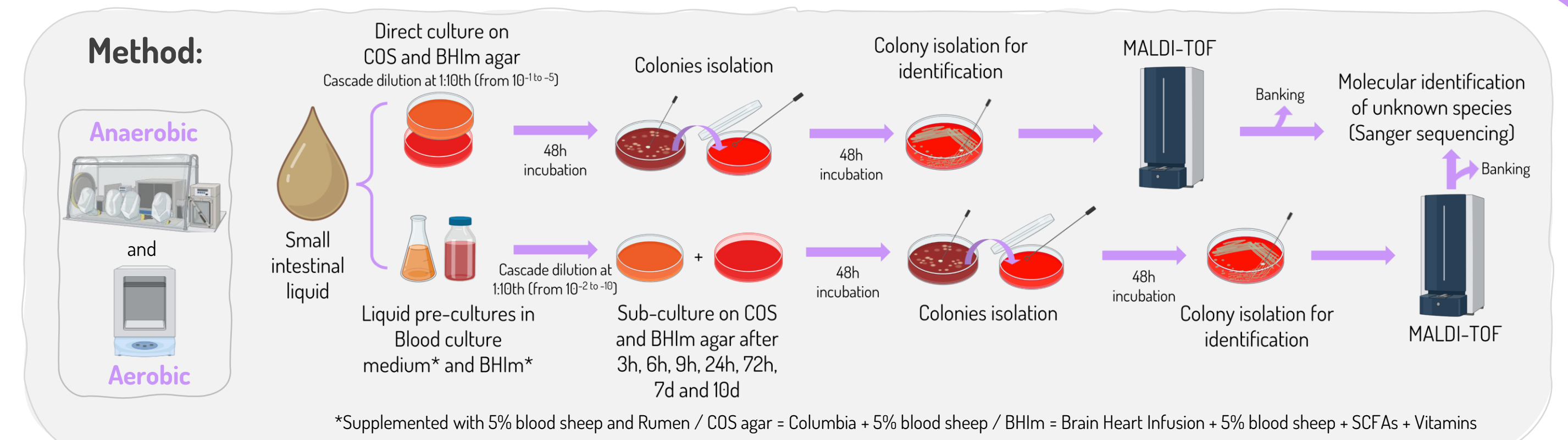


Figure 5: Percentage of identify species by culturomics depending on their oxygen tolerance.

Figure 6: Total bacterial phyla and genus identified by MALDI-TOF or 16S rRNA sequencing in SI liquid.

Phyla	Genus
Bacillota (28 species)	Massilioclostridium, Veillonella, Streptococcus, Intestinibacter, Flavonifractor, Mitsuokella, Actinomyces, Adlercreutzia, Tractidigestivbacter
Bacteroidota (9 species)	Bacteroides, Parabacteroides, Prevotella, Gaponibacter
Actinomycetota (9 species)	Bifidobacterium, Lancefieldella, Collinsella, Actinomyces
Pseudomonadota (3 species)	Sutterella, Escherichia
	Enterococcus, Staphylococcus, Dorea, Lachnoclostridium, Clostridium, Lactocaseibacillus, Blautia, Faecalitalea, Veillonella dispar, Dorea phocaensis, Actinomyces odontolyticus, Adlercreutzia equofaciens, Collinsella aerofaciens, Escherichia coli, Enterococcus faecalis, Lachnoclostridium edwardsi, Streptococcus vestibularis, Staphylococcus pasteurii, Enorma timonensis, Tractidigestivbacter scatoligenes

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Figure 6: Total bacterial phyla and genus identified by MALDI-TOF or 16S rRNA sequencing in SI liquid.

METAGENOMICS

CULTUROMICS

METABOLOMICS

Method: Faeces and SI liquid were collected from one healthy donor at two time points (June 2022 and February 2023). Four SI samples were analyzed and their three corresponding stools.

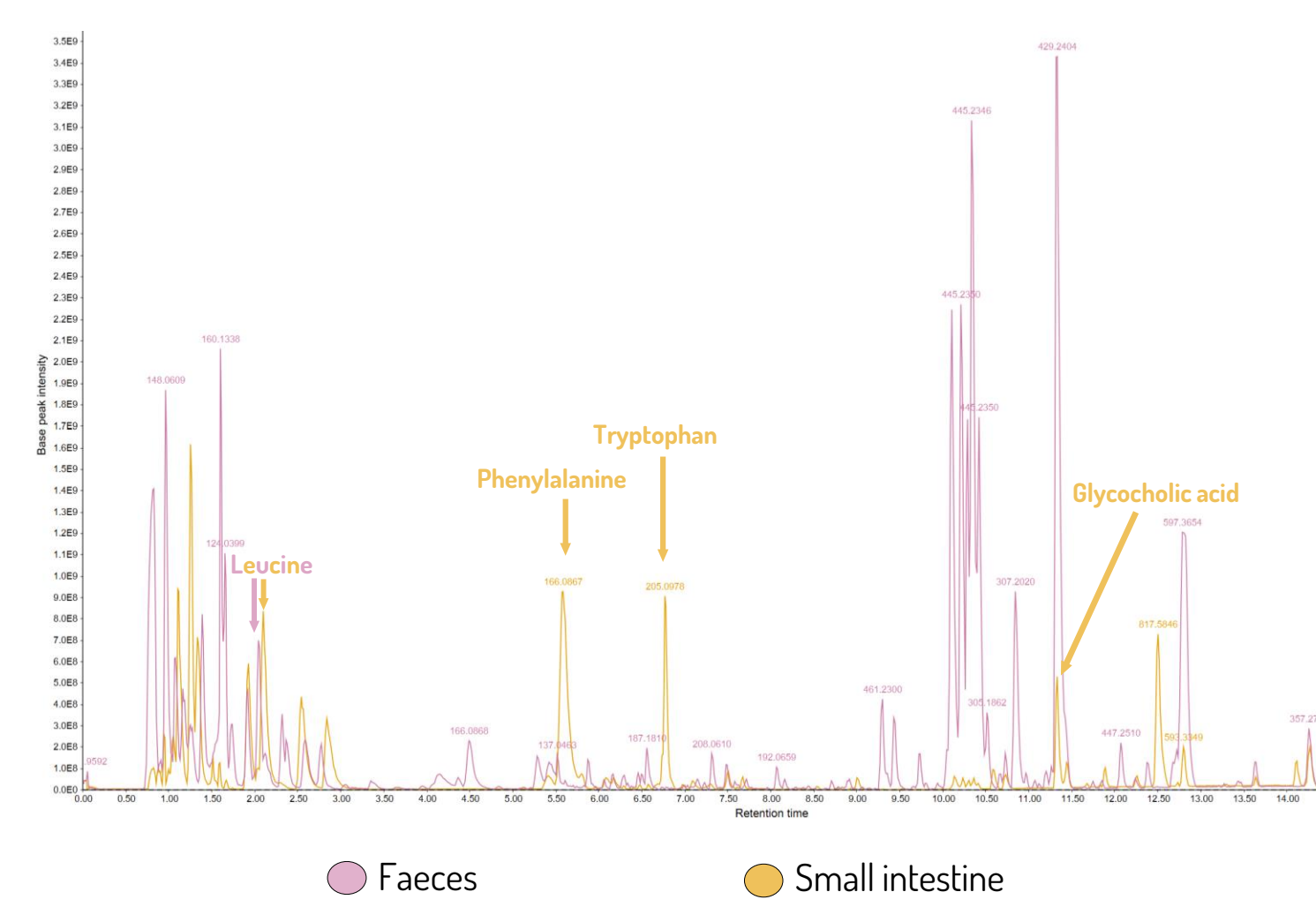
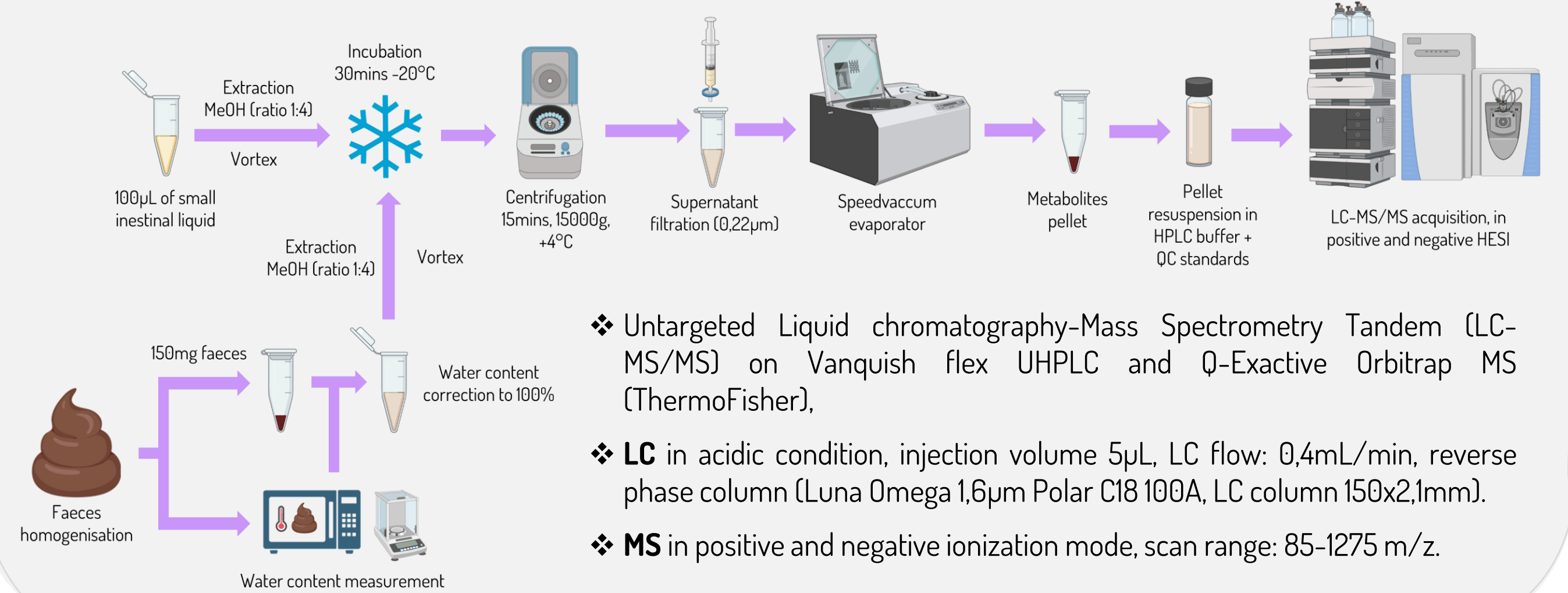


Figure 8: Chromatograms of SI and faecal metabolome using untargeted LC-MS/MS (HESI positive).

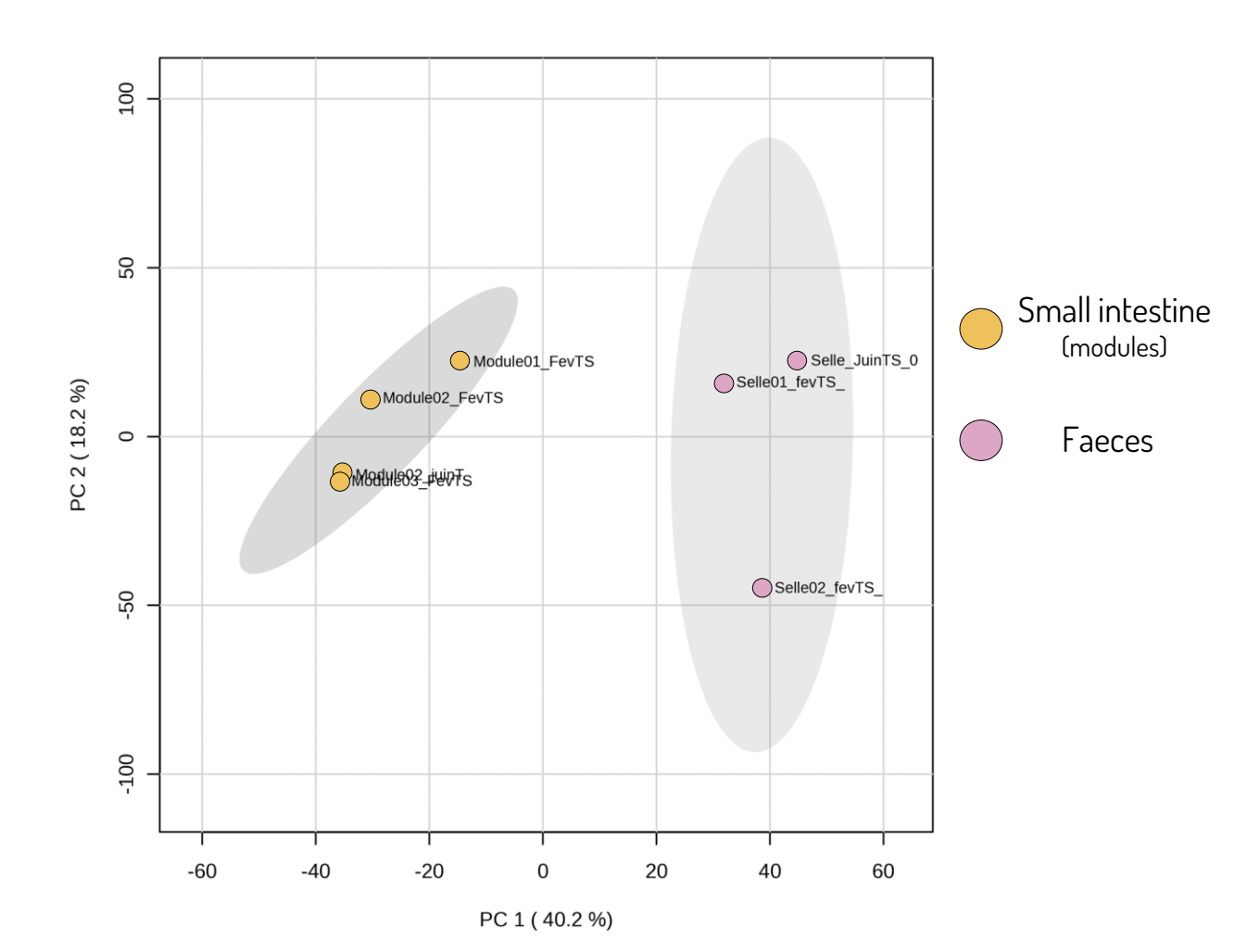


Figure 9: Principal Component Analysis (PCA) of SI liquids and faeces metabolomes from one healthy human donor at two different time points (June 2022 and February 2023).

CONCLUSION:

- The quality and quantity of the collected SI liquid by the MD enabled multi-omics analysis.
- The human SI microbiome differs drastically from the fecal microbiome.
- Ninety-eight bacterial species were specific to the SI microbiome (shotgun sequencing). Culturomics allowed to isolate 49 bacterial species (mostly strictly anaerobic). These two omics are complementary as they don't allow the same detection of species.
- We detected specific metabolites such as glycocholic acid (primary conjugated bile acid) in SI samples.
- Ongoing clinical trial (NCT05477069) on 15 healthy volunteers to demonstrate the MD's safety and the functional potential of the SI microbiome.

The SI microbiome study shows a great potential to revolutionize precision medicine.

References:

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