

Sample Stability 16S and metagenomics analysis in OC-Sensor sample bottles

From cataloguing to functional analyses of the gut microbiome in large-scale (mega-scale) prospective studies

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FIT for Screening Working Group
WEO CRC Screening Committee Meeting
Chicago, May 5, 2017

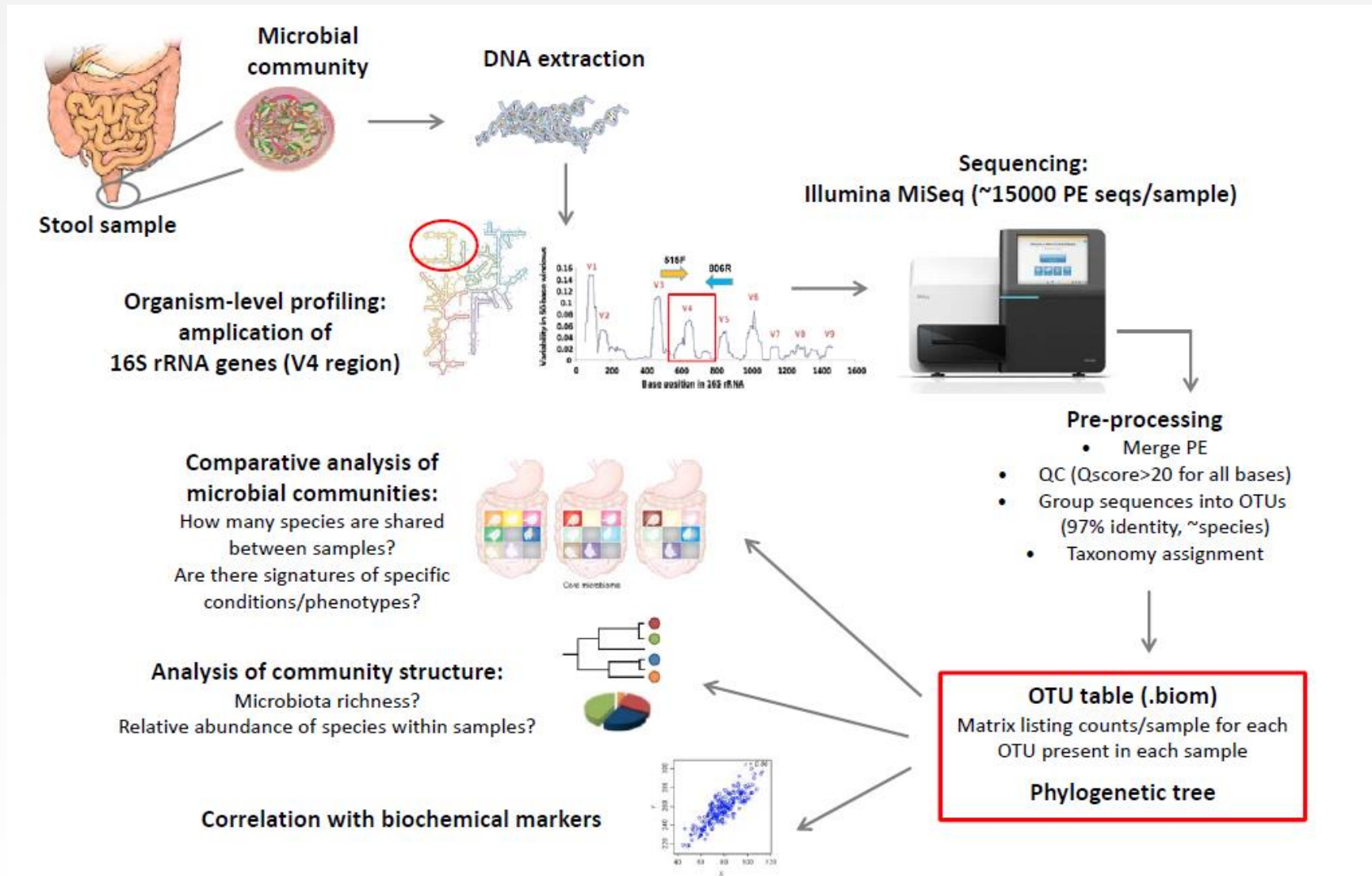


Possible conflicts of interest

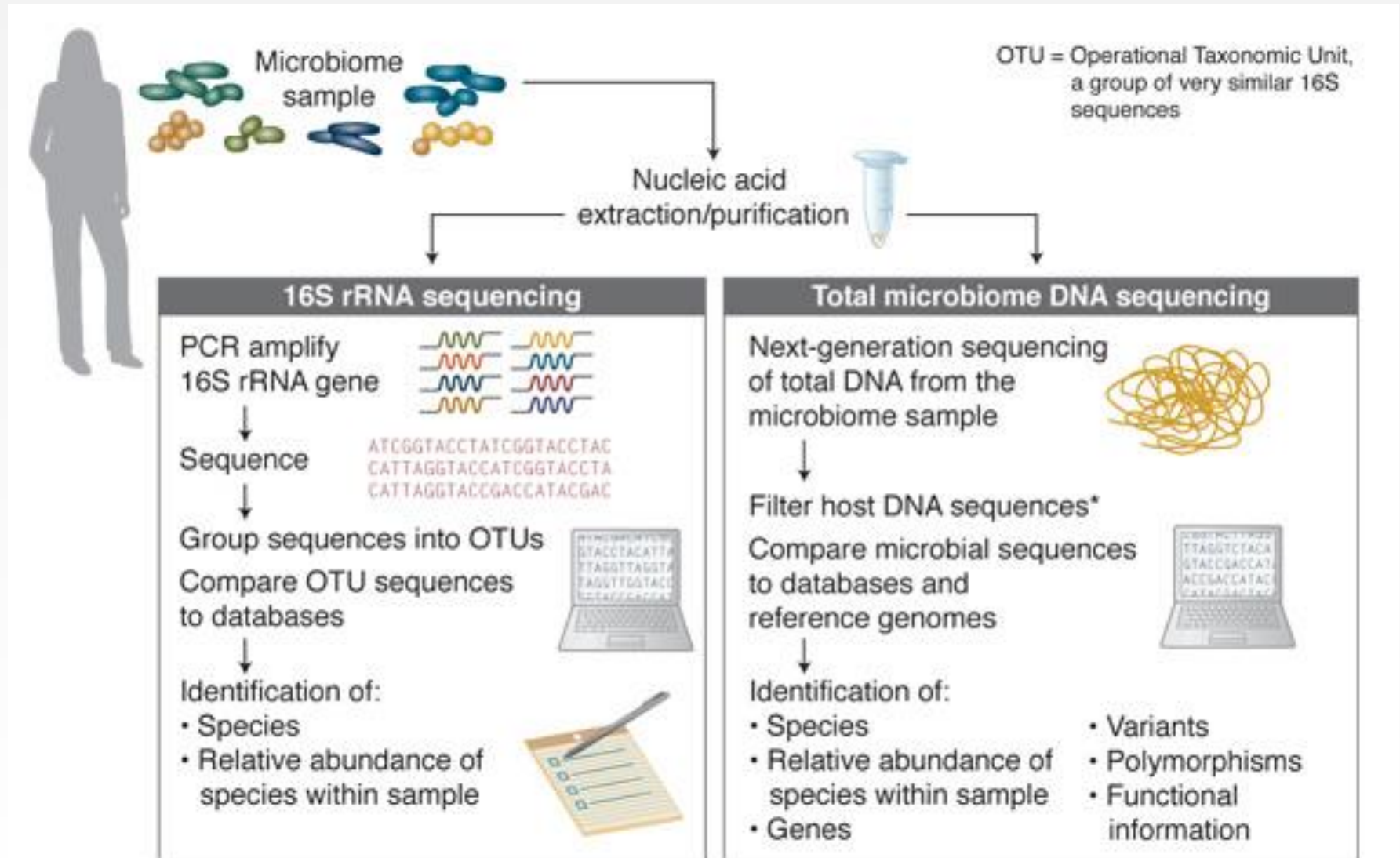
- *Eiken Chemical Co* – has supported screening studies of the involved groups with reagents



Profiling of 16S rRNA genes in fecal communities



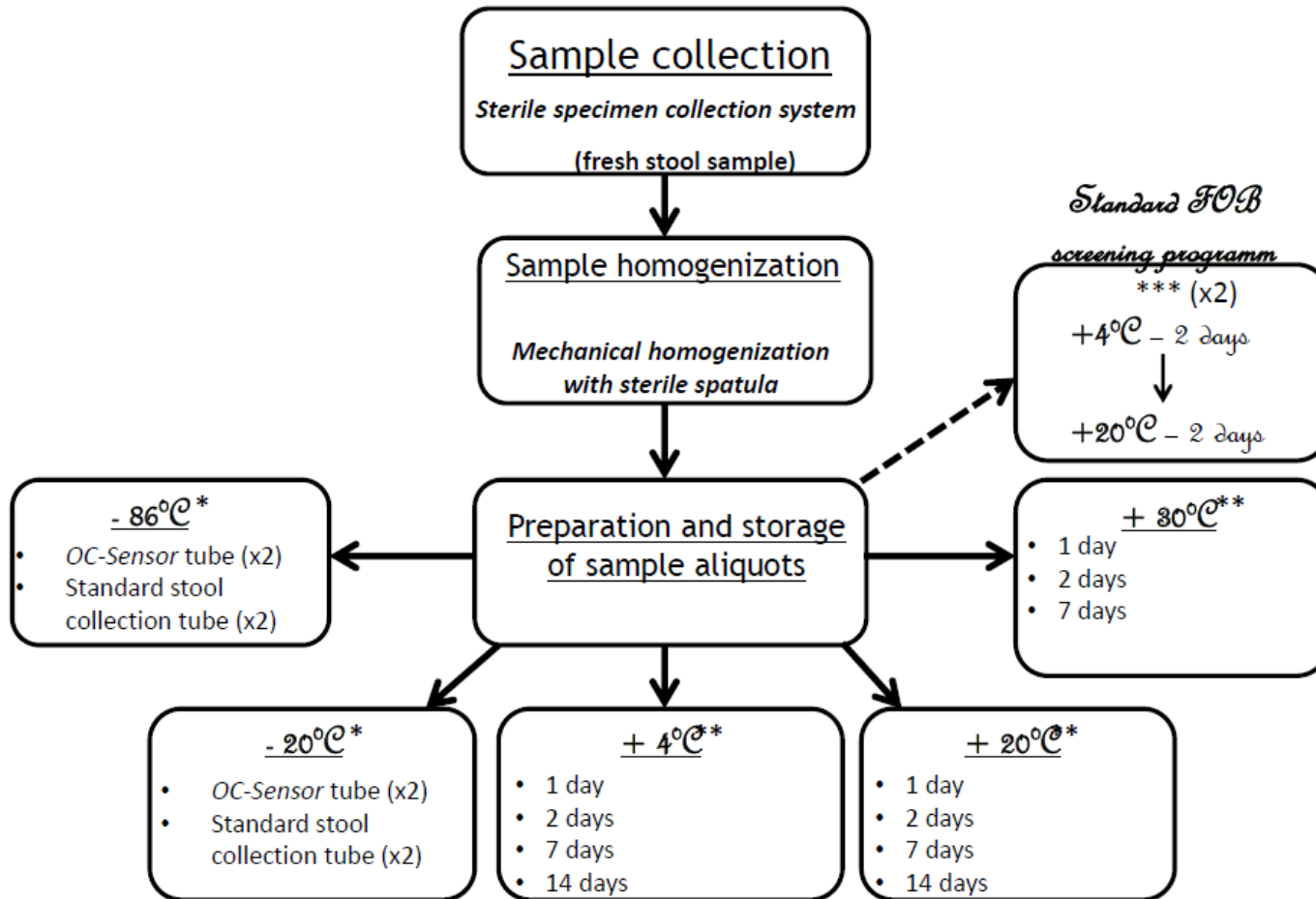
Metagenomics vs 16S rRNA in microbiome analysis



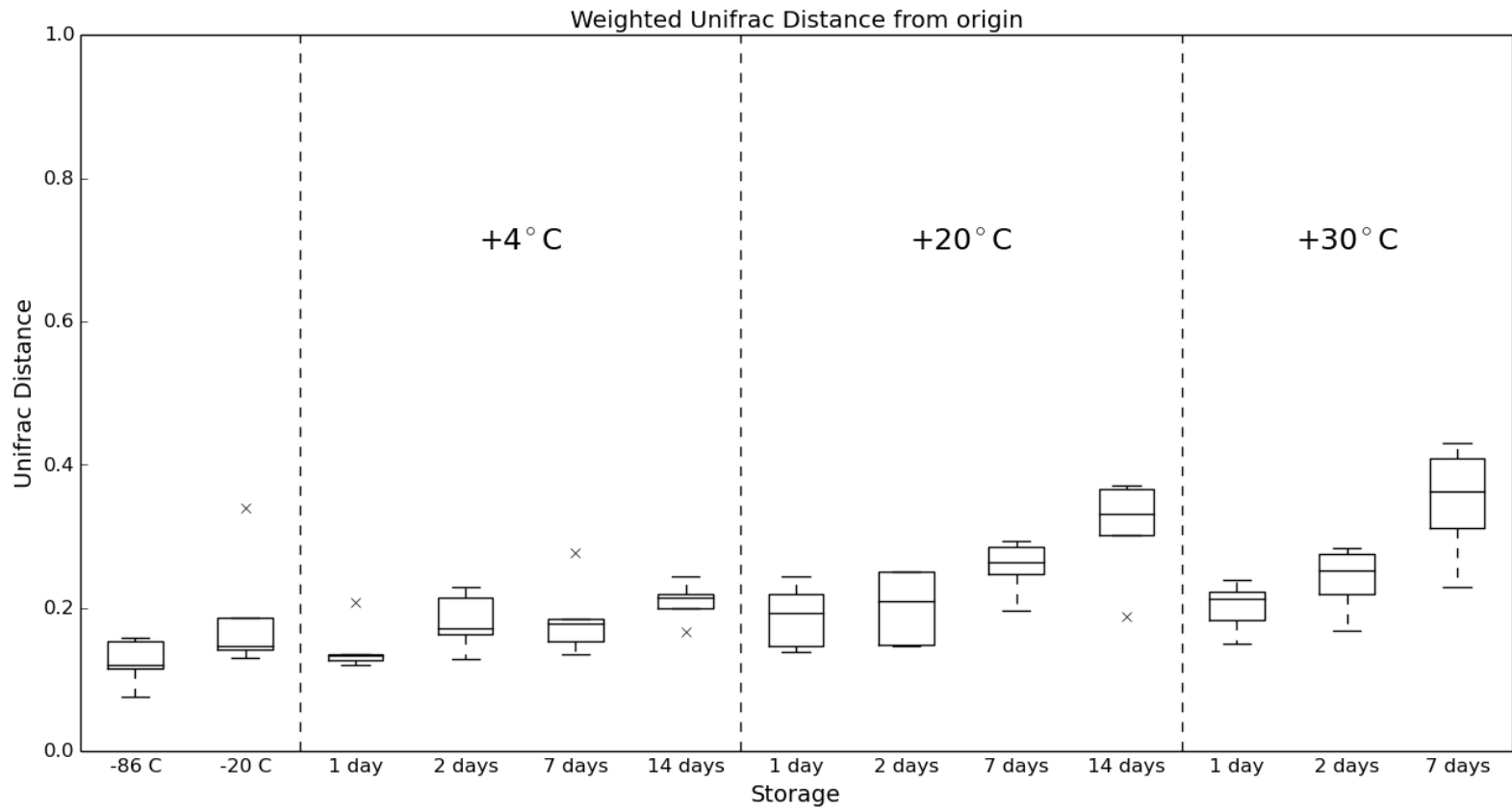
FIT buffer for microbiota

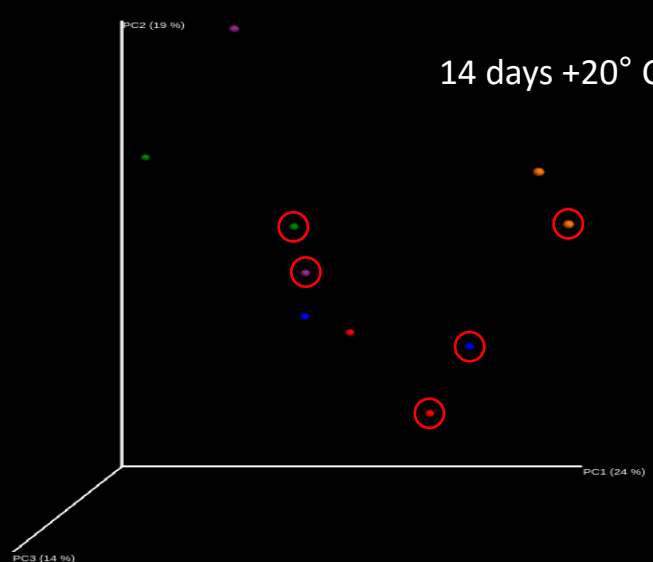
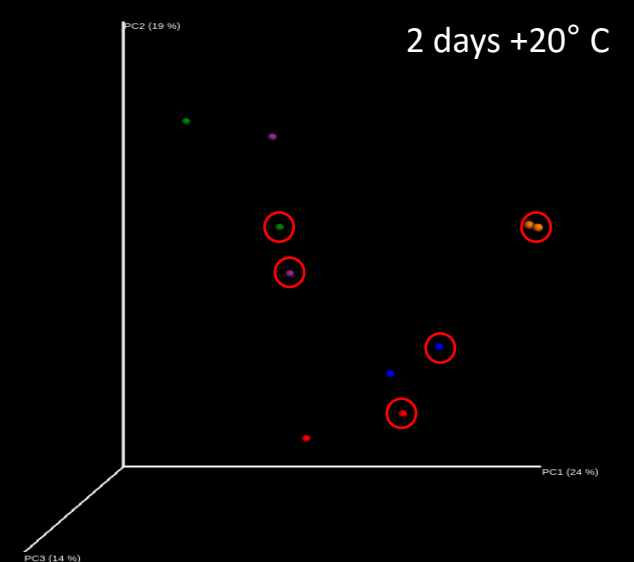
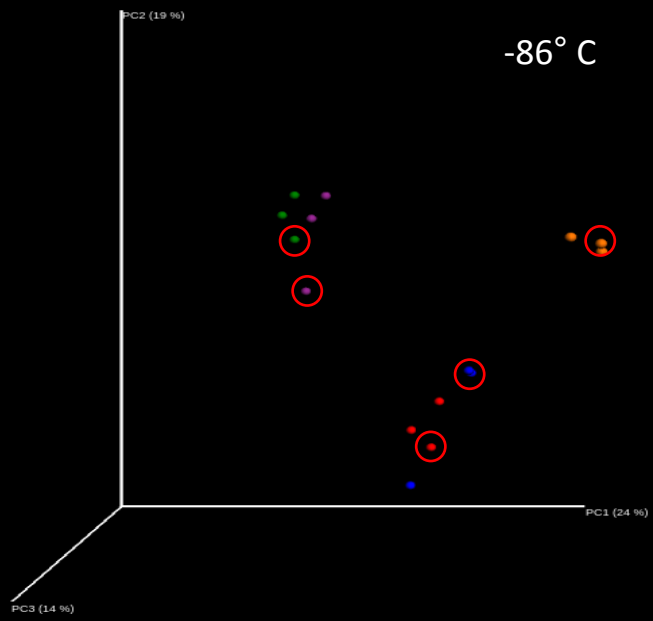
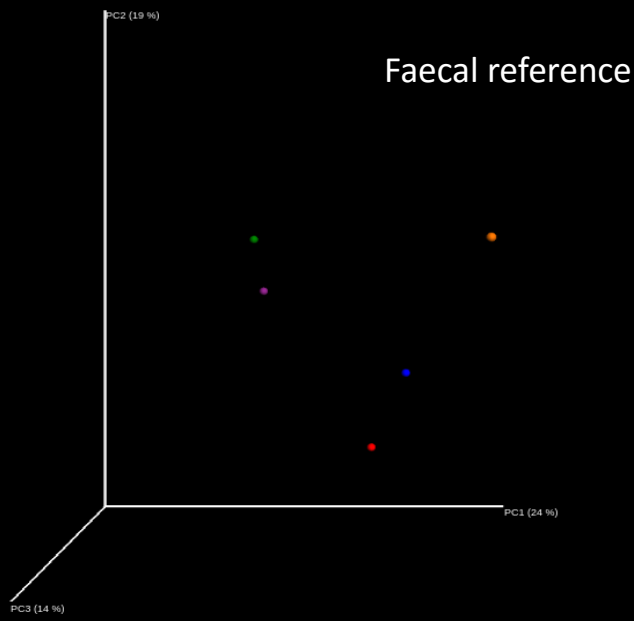


The design



16S rRNA





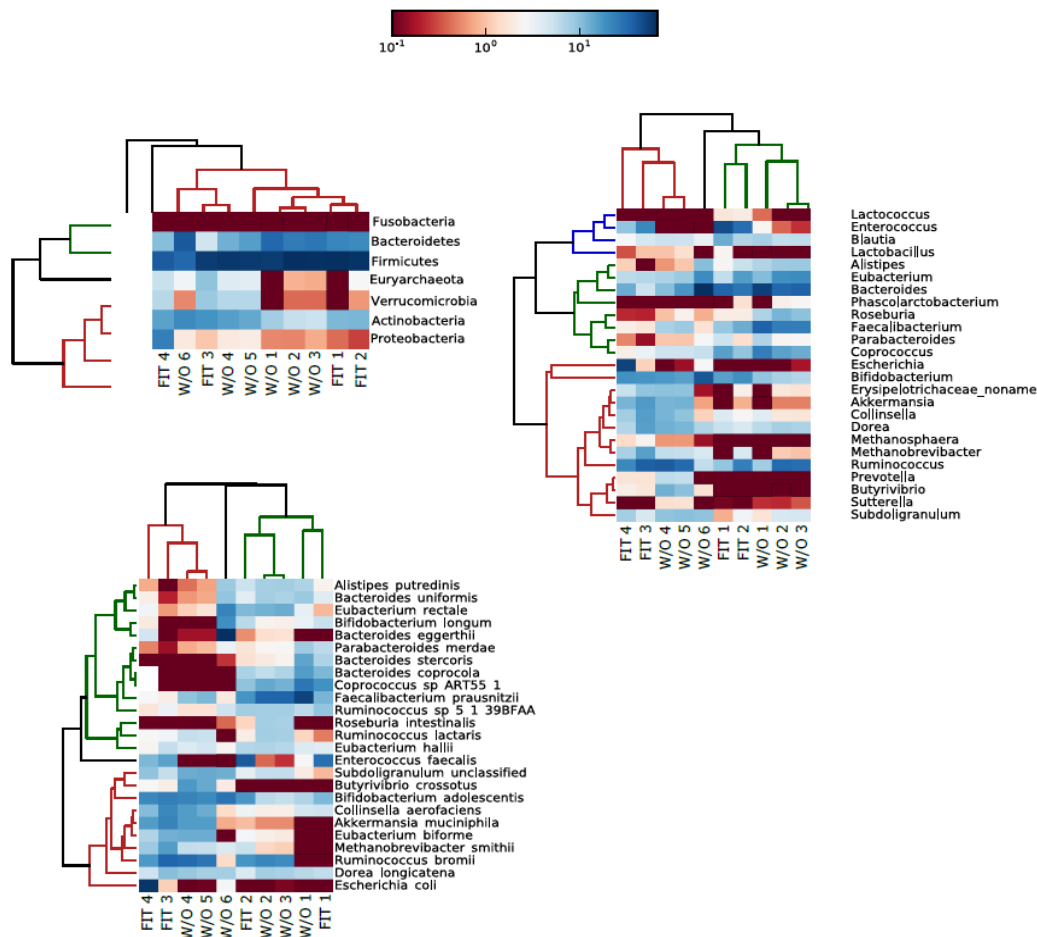
Parallel

Parallel

Parallel

Parallel

The metagenomics analysis on phyla (A), Genus (B) and species (C) level

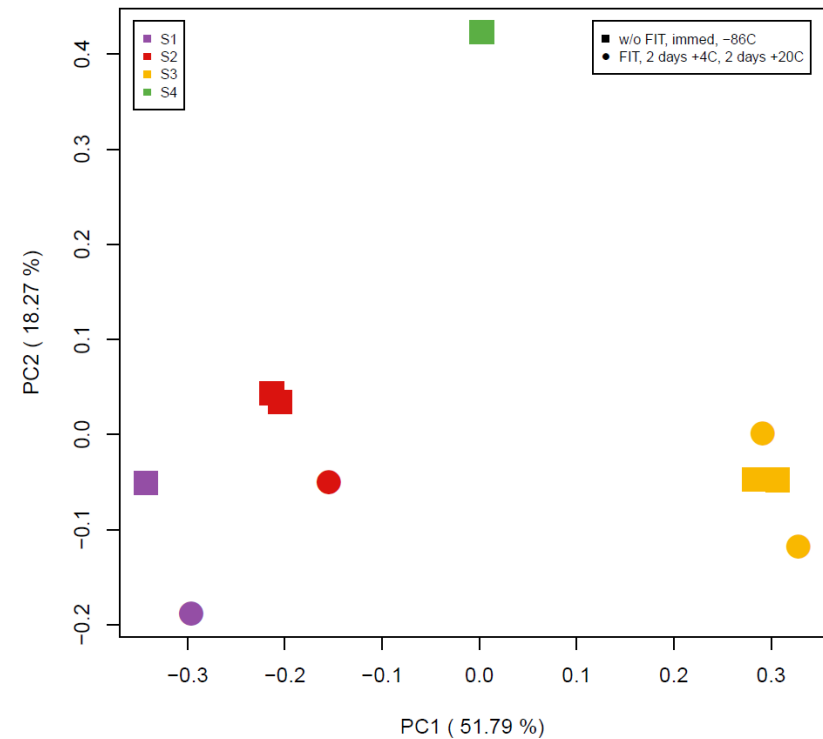
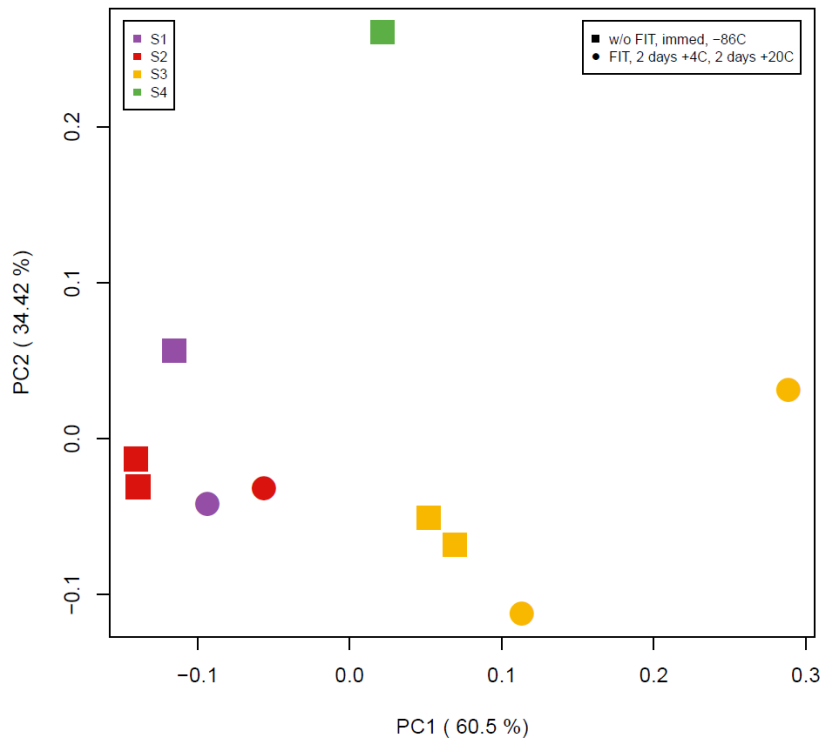


Consistency of the samples' composition in three different levels between:

- FIT: 2 days +4C, 2 days +20C and
- w/o: FIT, immediate -86C



Relative abundances at the phyla (A) and species (B) level



Bray-Curtis distance matrix analysis



Conclusions

1. Sample storage in OC-Sensor sample bottles may be used for faecal microbiome analysis either by 16S rRNA or metagenomics approaches
2. Samples are stable under standard colorectal screening program collection, storage and transportation conditions
3. This provides new possibilities for large-scale (mega-scale) prospective studies



Acknowledgements

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 - *Influence of Eradication of H.pylori on Gastrointestinal Tract Microbiome and Development of Screening Method for Detection of Genes Encoding Extended Spectrum Beta-Lactamases from Faecal Samples*

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