Multiunit *In vitro* Colon Model (MICODE) to study the effect on gut microbiota of foods for specific categories of consumers

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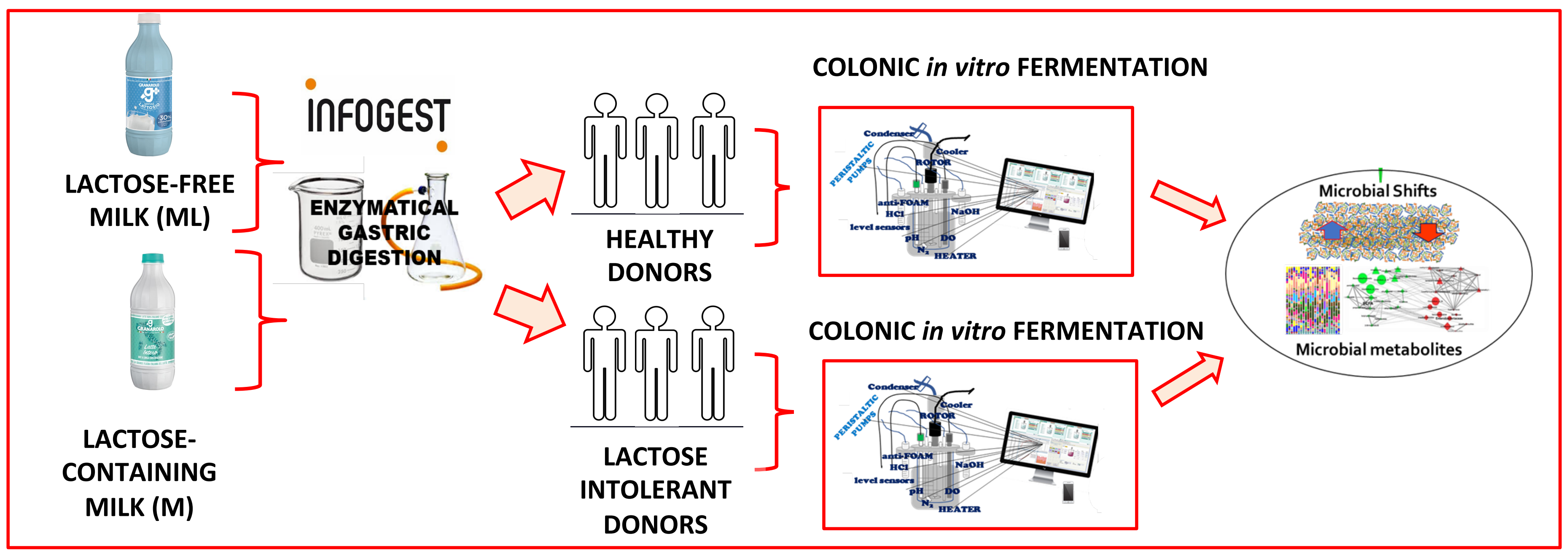
The first activities of the doctoral thesis project are repainted. Taking into consideration the new definition of “prebiotics” extending that concept to other compounds than polysaccharides (Gibson et al., 2017), an *in vitro* colonic fermentation model was developed to evaluate the effects on the human gut microbiota resulting from the consumption of food for specific categories of consumers. In particular, the effect on the gut microbiota of lactose-free milk (ML) was investigated by microbial shift (by qPCR and MiSeq 16S-RNA) and their metabolites (SPME GC-MS).

METHODS

- Gastro-duodenal digestion following Infogest protocol
- Colonic fermentation with **MICODE** set as a batch culture, mimicking the proximal colon
- Three fecal donors

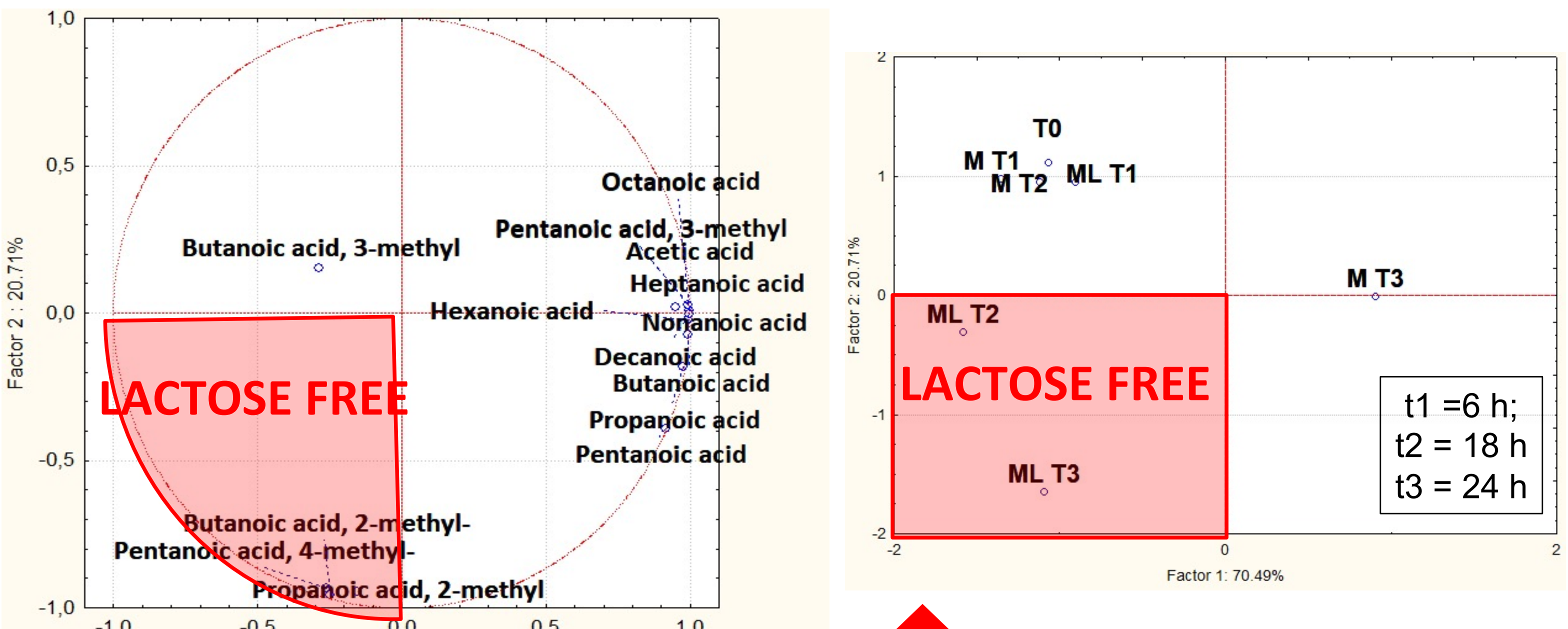


Conceptual and analytical outputs

MICROBIOTA		METABOLITES		INDICATORS
Eubacteria	+	*Acetate*	=	BIODIVERSITY
Bacteroidetes		*Propionate*		DYSBIOSIS
Proteobacteria		*Butyrate*		BIFIDOGENIC ACTIVITY
Firmicutes		*Iso-Butyrate*		PREBIOTIC SCORE
Enterobacteriaceae		*Iso-Valerate*		BENEFICIAL COMPOUNDS VOCs
Lactobacillales		*Hexanoic acid*		*TERPENES*
Faecalibacterium		*Heptanoic acid*		SCFAs
Escherichia coli		*ALCOHOLS*		MCFAs
Bifidobacteria		*ACIDS*		Antioxidant PUFAs
Bacteroides/Prevotella		*ALDEHYDES*		*BCFAs (protein ferm'n)*
Akkermansia		*KETONES*		TMAO / NH_3 / Phenol
Prevotella		*ESTERS*		Lipid oxidation
Clostridium group IV		*AMINES*		Enterotypes
Collinsella		*Indole/skatole*		Endotoxemia
Oscillospira		*trp catabolites*		

RESULTS
HEALTHY DONORS

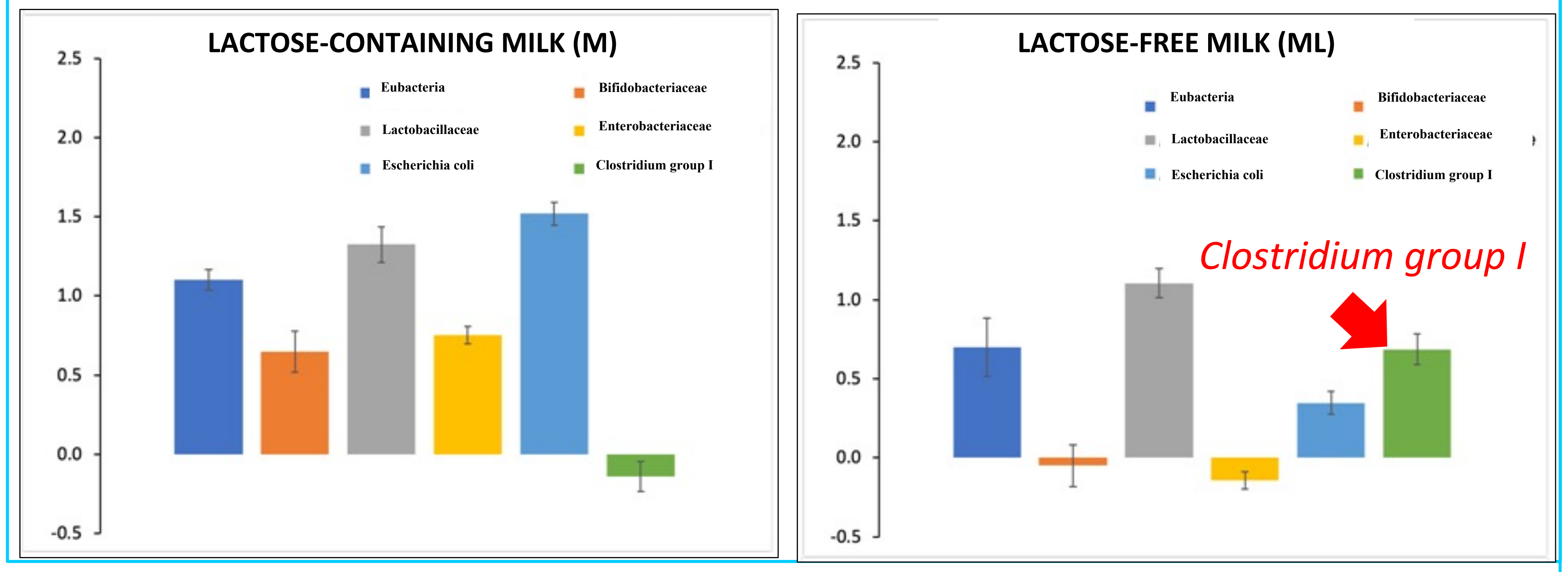
Volatile compounds (VOCs)



BCFA in lactose-free milk

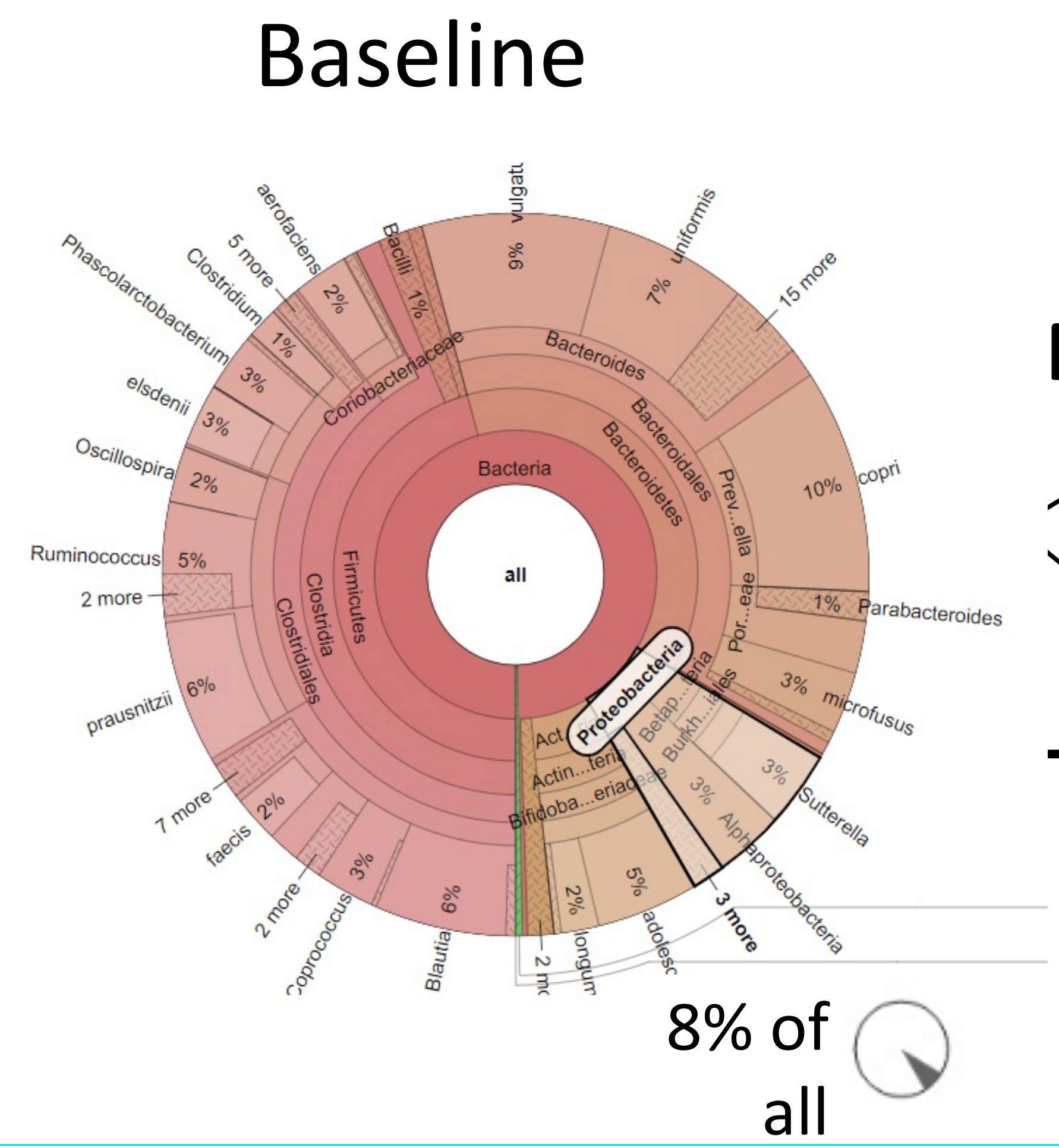
Microbial shifts by qPCR

qPCR shifts (24 h) in Log_{10} cells/ml



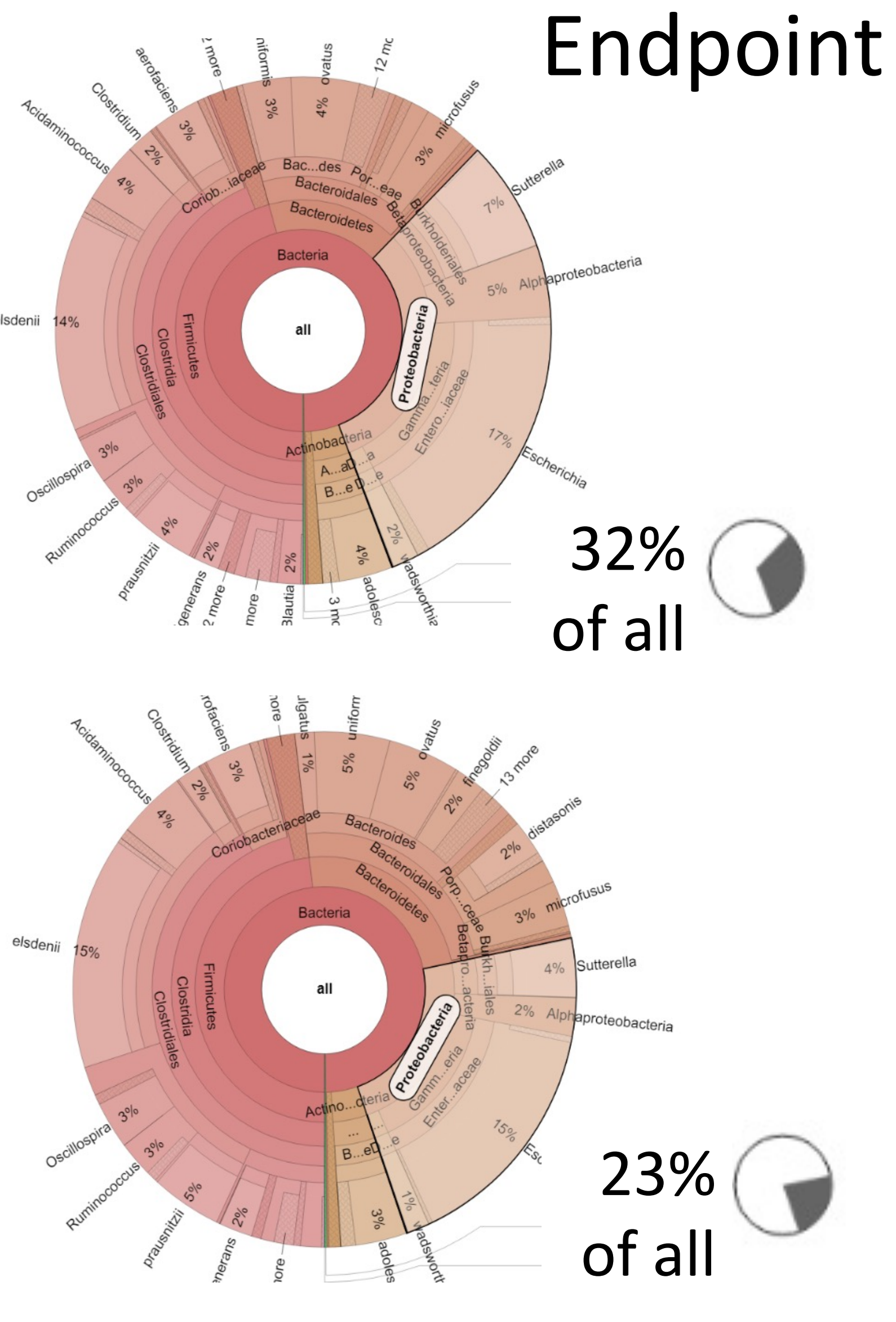
MiSeq of microbiota

Proteobacteria

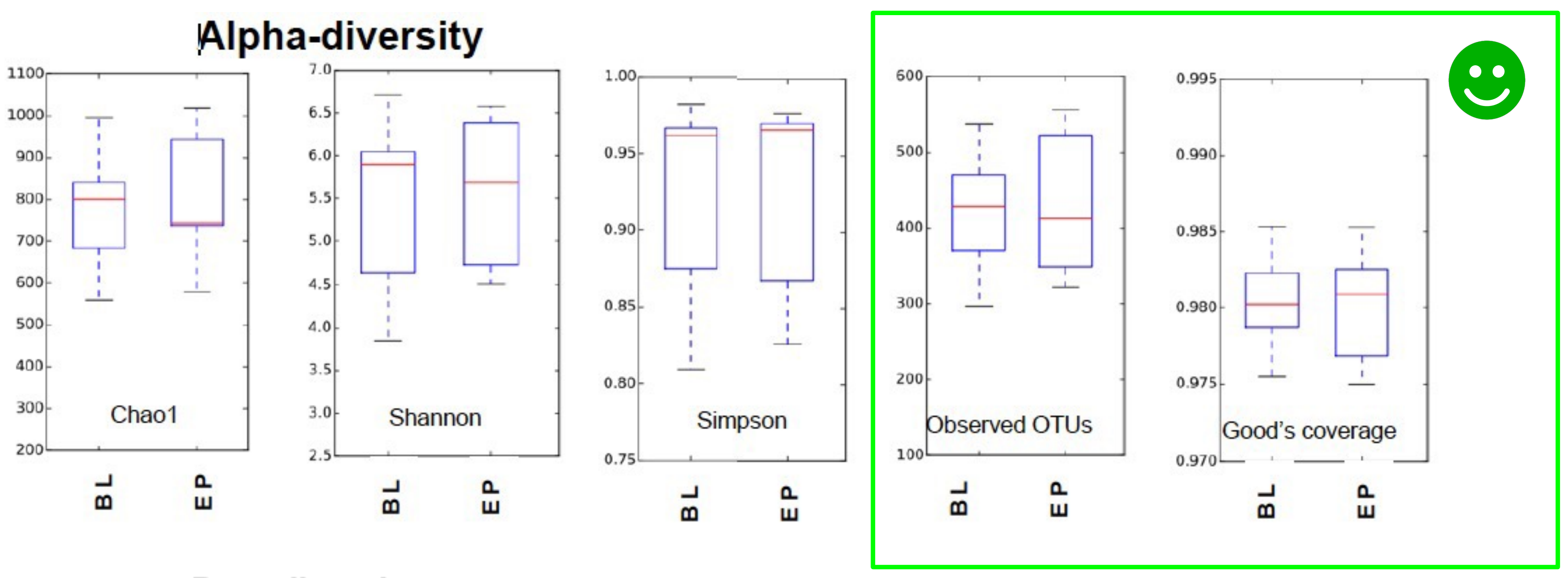


ML

+ M

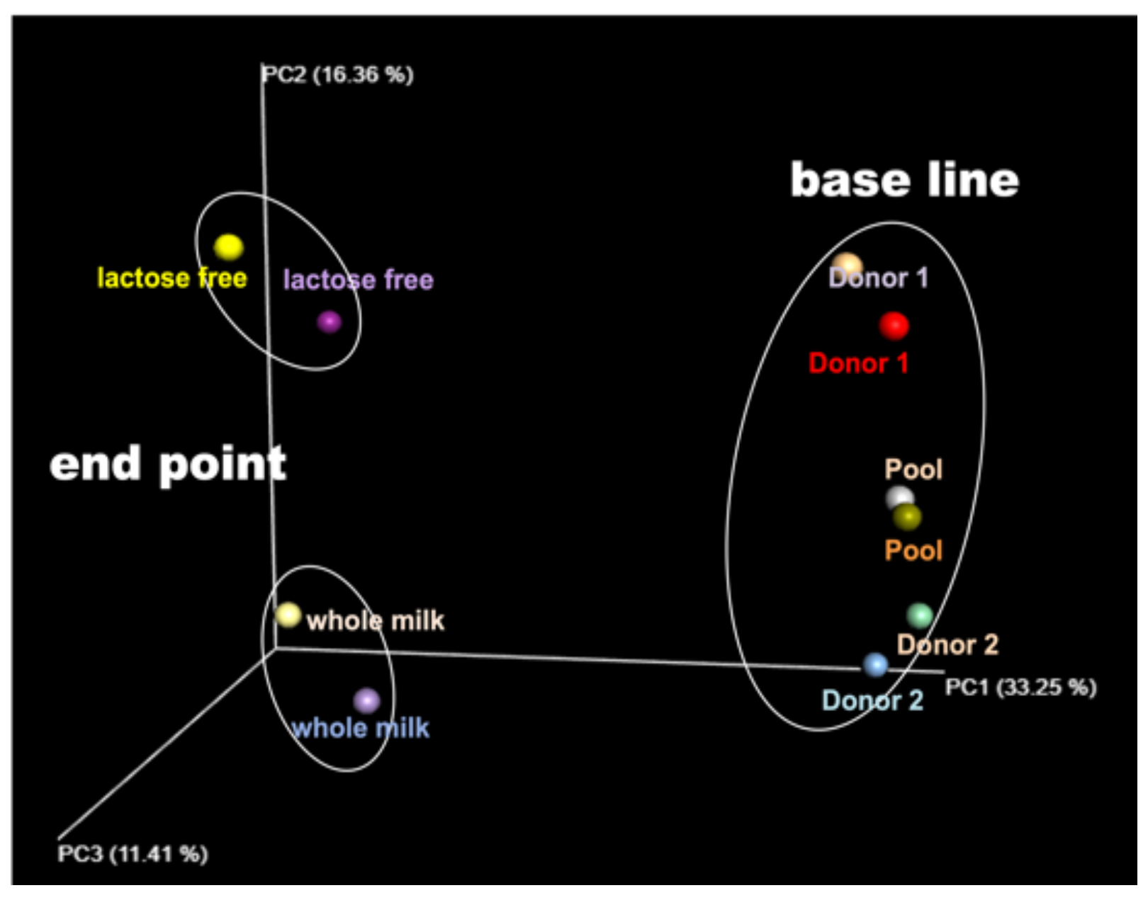


ML causes an **increase** in ***Proteobacteria*** greater than that of **M**



Beta-diversity

Bray-Curtis

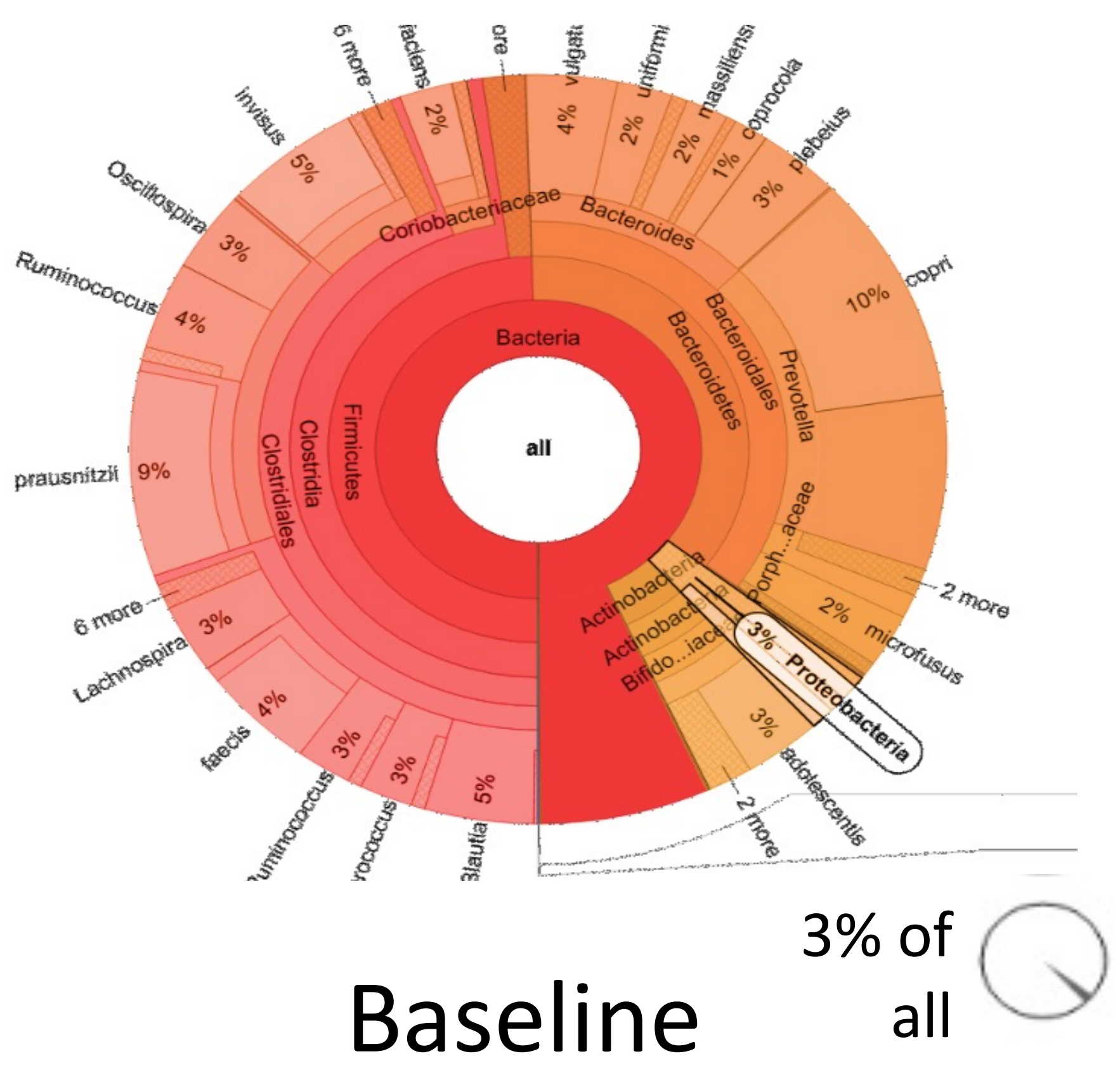


400-500 OTUs over the experyment

Rarity index similar over the experyment

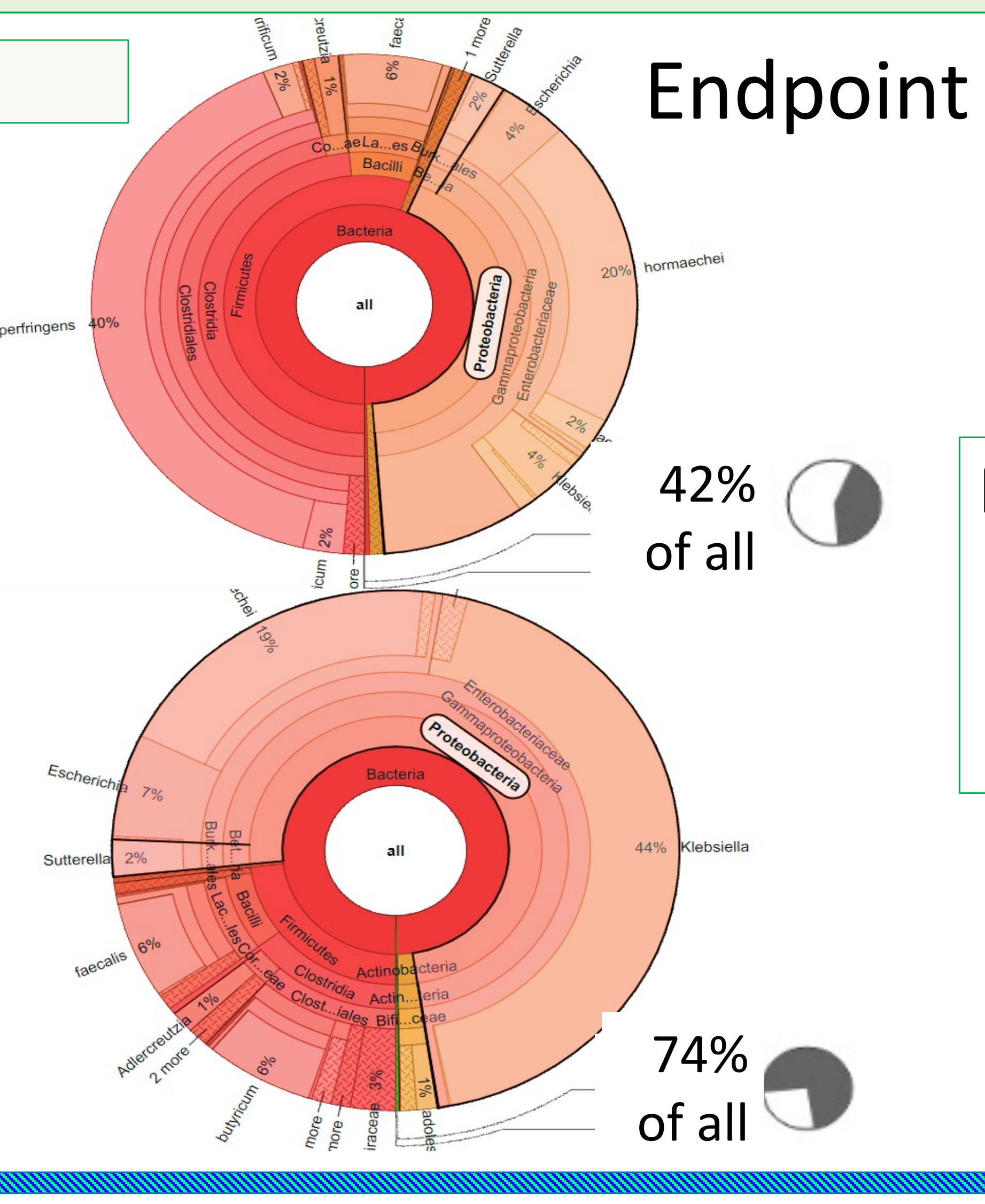
RESULTS
LACTOSE INTOLERANT DONORS

Proteobacteria



+ ML

+ M



M causes an **increase in *Proteobacteria*** almost double that observed with **ML**

Conclusion

MICODE has been shown to be a robust *in vitro* model evaluated by several parameters, such as the number of observed OTUs and rare species. The results show a negative impact of lactose-free milk on the intestinal microflora of healthy subjects, while in lactose-intolerant subjects this effect occurs with non-delactosed milk.