Supplementary Materials

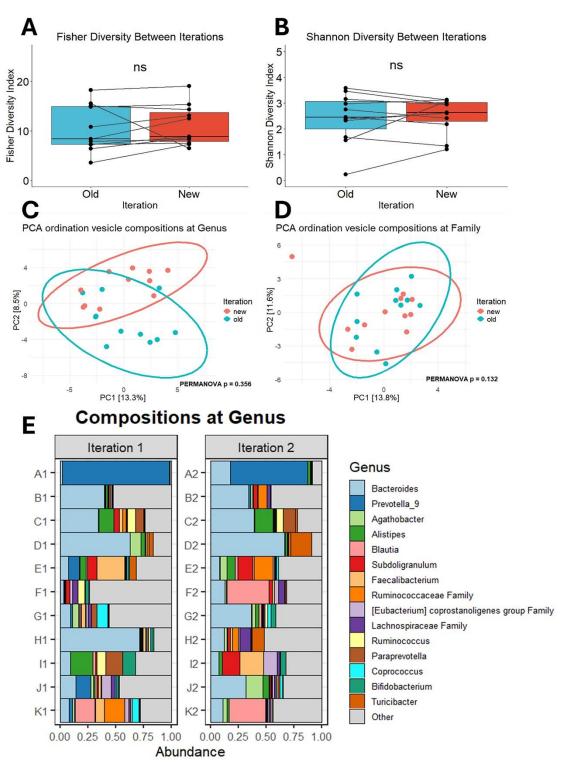
Assessment of the reproducibility of bacterial membrane vesicle isolation and characterization

Jari Verbunt^{1,2}, Johan Jocken², Emanuel Canfora², David Barnett¹, Ellen E. Blaak², Paul Savelkoul¹, Frank Stassen¹

¹Department of Medical Microbiology, Infectious Diseases & Infection Prevention, School of Nutrition and Translational Research in Metabolism (NUTRIM), Maastricht University Medical Center+, Maastricht 6202 AZ, The Netherlands. ²Department of Human Biology, School of Nutrition and Translational Research in

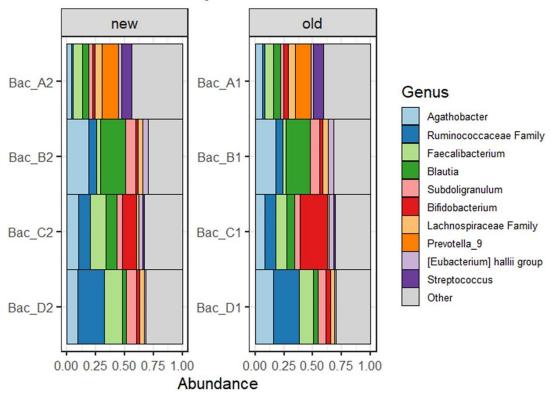
Metabolism (NUTRIM), Maastricht University Medical Center+, Maastricht 6202 AZ, The Netherlands.

Correspondence to: Dr. Frank Stassen, Department of Medical Microbiology, Infectious Diseases & Infection Prevention, School of Nutrition and Translational Research in Metabolism (NUTRIM), Maastricht University Medical Center+, Maastricht 6202 AZ, The Netherlands. E-mail: F.Stassen@maastrichtuniversity.nl



Supplementary Figure 1. Comparison of bMV compositions between iterations. (A) Fisher's alpha diversity at the family taxonomy level. Data are presented as means ± SEM; (B) Principal component analysis ordination biplot of CLR-transformed features at the taxonomic genus level. 95% confidence ellipses are drawn per iteration; (C) Bar charts showing the proportional abundance of detected taxa from vesicle DNA at the genus level between iterations. NS: Not significant.

Bacterial compositions at Genus



Supplementary Figure 2. Bar charts showing the proportional abundance of detected taxa from bacterial DNA at the genus level between iterations.