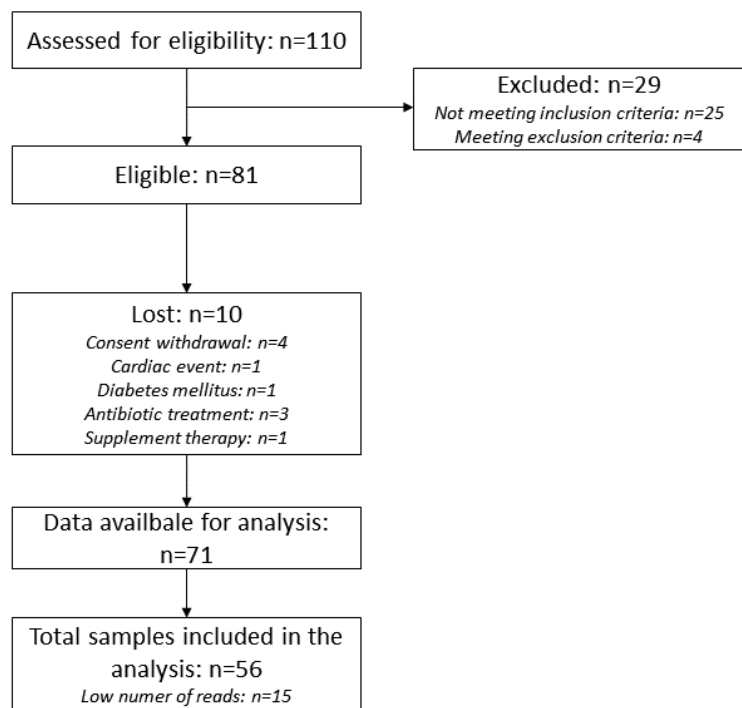


Supplementary data

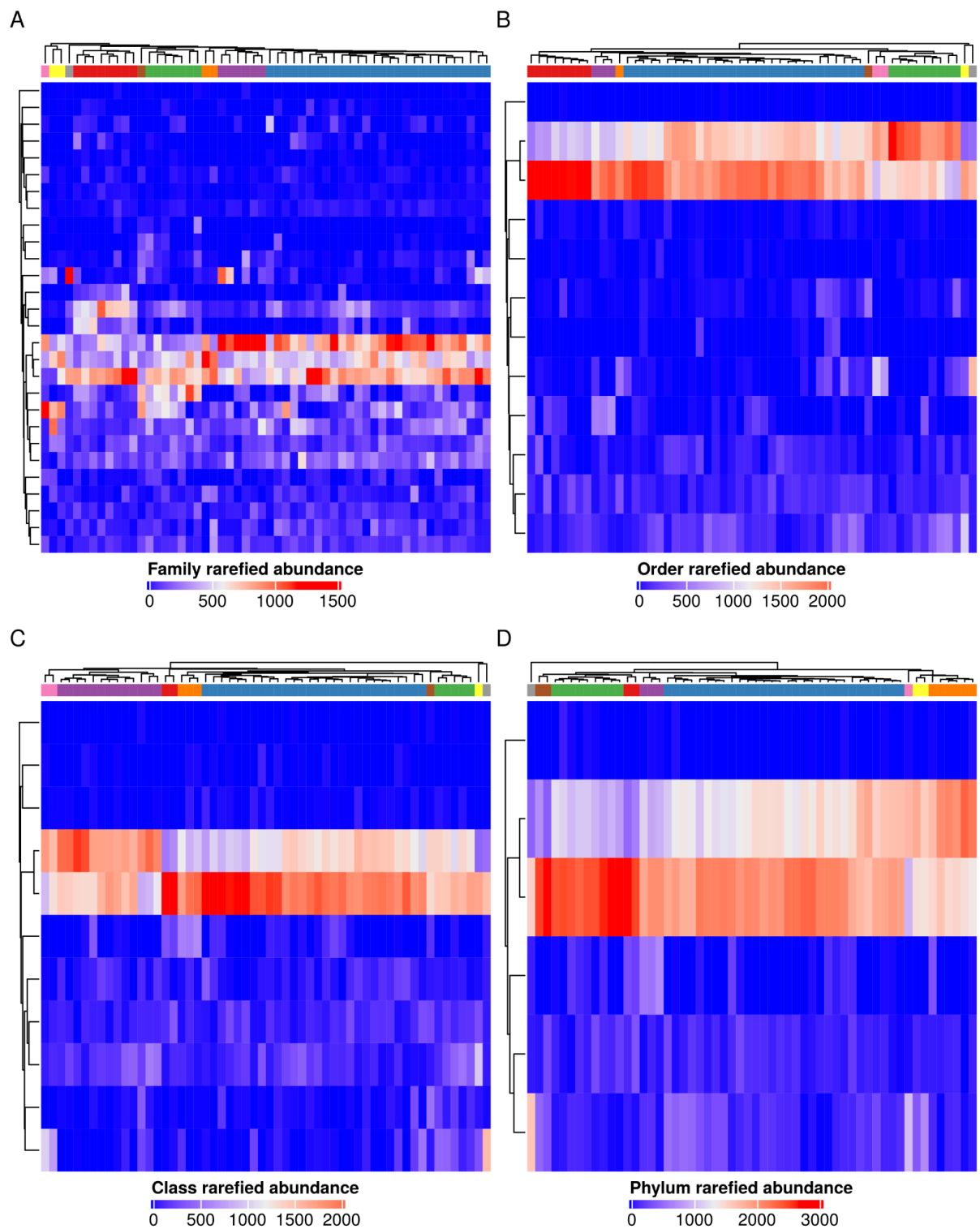
Analysis of correlations between gut microbiota, stool short chain fatty acids, calprotectine, and anthropometric, physiological and biochemical parameters in postmenopausal women with obesity: A cross-sectional study

Igor Łoniewski, Monika Szulińska, Mariusz Kaczmarczyk, Konrad Podsiadło, Daniel Styburski, Karolina Skonieczna-Żydecka, Paweł Bogdański

Supplementary Figure 1. Flow chart of the study population

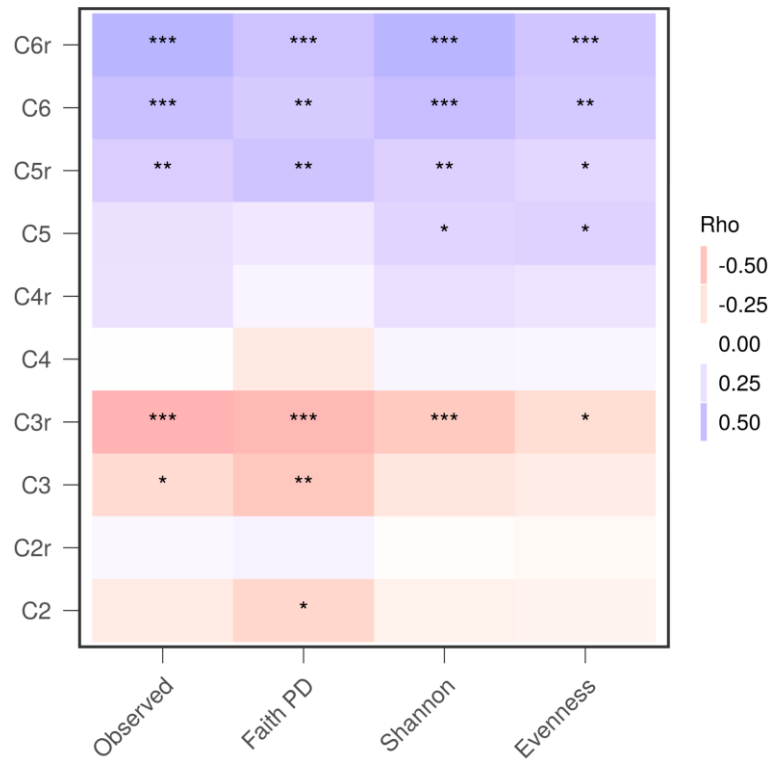


Supplementary Figure 2. Heatmaps of the rarefied abundance at different taxonomic levels



Columns (samples) and rows (taxa) were subjected to average linkage method and genus-level Bray-Curtis distance hierarchical clustering, top annotation - color bars reflect identified clusters

Supplementary Figure 3. Alpha-diversity correlation with SCFAs



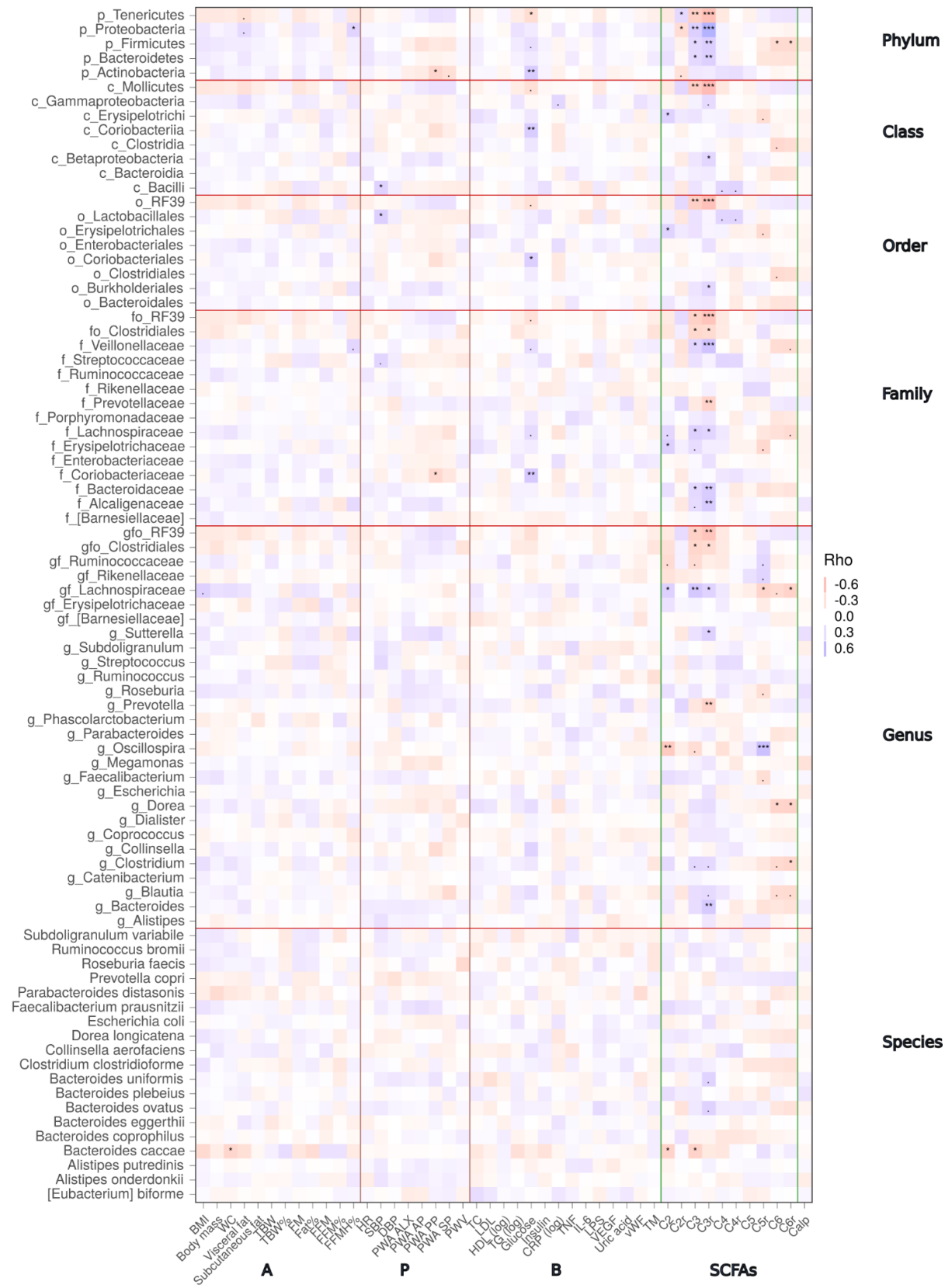
Mapping from p-value ranges to symbols: 0 - 0.001 '***', 0.001 - 0.01 '**', 0.01 - 0.05 '*', 0.05 - 0.1 '.', 0.1 - 1.0 No symbol; C2r - the ratio of acetic acid to all analyzed SCFAs, C3r - The ratio of propionic acid to all analyzed SCFAs, C4r - the ratio of butyric acid to all analyzed SCFAs, C5r - The ratio of valeric acid to all analyzed SCFAs, C6r - The ratio of hexanoic acid to all analyzed SCFAs.

Supplementary Table 1. db-RDA models summary

Model	Taxon	Variance explained - full model*	Simplified model - explanatory variables	Simplified model (R2)	Simplified model (adjusted R2)
Anthropometric	Genus	Constrained 0.06; Unconstrained 0.94 P_{ANOVA}=0.202	NULL	NULL	NULL
	Family	Constrained 0.07; Unconstrained 0.93 P_{ANOVA}=0.189	NULL	NULL	NULL
	Order	Constrained 0.05; Unconstrained 0.95 P_{ANOVA}=0.522	NULL	NULL	NULL
	Class	Constrained 0.05; Unconstrained 0.95 P_{ANOVA}=0.510	NULL	NULL	NULL
	Phylum	Constrained 0.06; Unconstrained 0.94 P_{ANOVA}=0.368	NULL	NULL	NULL
	MetaCyc	Constrained 0.12; Unconstrained 0.88 P_{ANOVA}=0.003	Visceral, WC	0.09381904	0.05962354
Physiological	Genus	Constrained 0.15; Unconstrained 0.85 P_{ANOVA}=0.511	NULL	NULL	NULL
	Family	Constrained 0.14; Unconstrained 0.86 P_{ANOVA}=0.598	NULL	NULL	NULL
	Order	Constrained 0.15; Unconstrained 0.85 P_{ANOVA}=0.465	NULL	NULL	NULL
	Class	Constrained 0.14; Unconstrained 0.86 P_{ANOVA}=0.507	NULL	NULL	NULL
	Phylum	Constrained 0.15 Unconstrained 0.85 P_{ANOVA}=0.453	PWA AP	0.06529508	0.04765914
	MetaCyc	Constrained 0.11; Unconstrained 0.89 P_{ANOVA}=0.959	NULL	NULL	NULL
Biochemical	Genus	Constrained 0.31; Unconstrained 0.69 P_{ANOVA}=0.145	Glucose	0.04262094	0.02308259
	Family	Constrained 0.32; Unconstrained 0.68 P_{ANOVA}=0.112	Glucose	0.06366385	0.04455495
	Order	Constrained 0.32; Unconstrained 0.68 P_{ANOVA}=0.137	NULL	NULL	NULL
	Class	Constrained 0.33; Unconstrained 0.67 P_{ANOVA}=0.107	NULL	NULL	NULL
	Phylum	Constrained 0.28; Unconstrained 0.72 P_{ANOVA}=0.453	NULL	NULL	NULL
	MetaCyc	Constrained 0.32; Unconstrained 0.68 P_{ANOVA}=0.140	Insulin	0.05522586	0.03594476

P_{ANOVA} Monte Carlo permutation test (number of permutations 999); variance inflation factor < 10 to avoid co-linearity issues: WC, subcutaneous, visceral from A group, all from the P group, all from the B group)

Supplementary Figure 4. Correlations between bacterial taxa and anthropometric, physiological and biochemical parameters



Spearman correlation of the bacterial abundance at the species, genus, family, order, class and phylum levels (separated by horizontal red lines) with anthropometric (A), physiological (P), biochemical (B) parameters (separated by vertical brown lines), short chain fatty acids (SCFAs) and calprotectin (separated by green line). Mapping from FDR adjusted P values ranges to symbols: 0 - 0.001 '****', 0.001 - 0.01 '***', 0.01 - 0.05 '**', 0.05 - 0.1 '.', 0.1 - 1.0 no symbol, Rho - Spearman correlation coefficient; C2r - the ratio of acetic acid to all analyzed SCFAs, C3r - The ratio of propionic acid to all analyzed SCFAs, C4r - the ratio of butyric acid to all analyzed SCFAs, C5r - The ratio of valeric acid to all analyzed SCFAs, C6r - The ratio of hexanoic acid to all analyzed SCFAs.

ratio of propionic acid to all analyzed SCFAs, C4r - the ratio of butyric acid to all analyzed SCFAs, C5r - The ratio of valeric acid to all analyzed SCFAs, C6r - The ratio of hexanoic acid to all analyzed SCFAs.

Supplementary Table 2. Phylum relative abundance

	This study ¹ (n=56)	BMI-NORMAL (n=1,293)	BMI-HIGH (n=875)
Actinobacteria	3.06%	1.09%	0.91%
Bacteroidetes	36.1%	27.8%	30.1%
Cyanobacteria	0.13%	0.14%	0.14%
Firmicutes	52.7%	34.2%	33.2%
Fusobacteria	0.016%	0.51%	0.23%
Proteobacteria	5.82%	32.8%	32.9%
Tenericutes	2.08%	0.80%	0.50%

BMI-NORMAL, BMI-HIGH > 0.1%; this study >0.1%, 1 - Time0

Class

This study vs BMI-HIGH: 997.4, p<0.0001

This study vs BMI-NORMAL: 691.4, p<0.0001

BMI-HIGH vs BMI-NORMAL: 203.0, p<0.0001

Order

This study vs BMI-HIGH: 994.3, p<0.0001

This study vs BMI-NORMAL: 647.8, p<0.001

BMI-HIGH vs BMI-NORMAL: -26.9, p=1

Family

This study vs BMI-HIGH: 2098.7, p<0.0001

This study vs BMI-NORMAL: 1509.3, p<0.0001

BMI-HIGH vs BMI-NORMAL: -222.9, p=1

Genus

This study vs BMI-HIGH: 2615.9, p<0.0001

This study vs BMI-NORMAL: 2031.9, p<0.0001

BMI-HIGH vs BMI-NORMAL: -1343, p<0.0001

