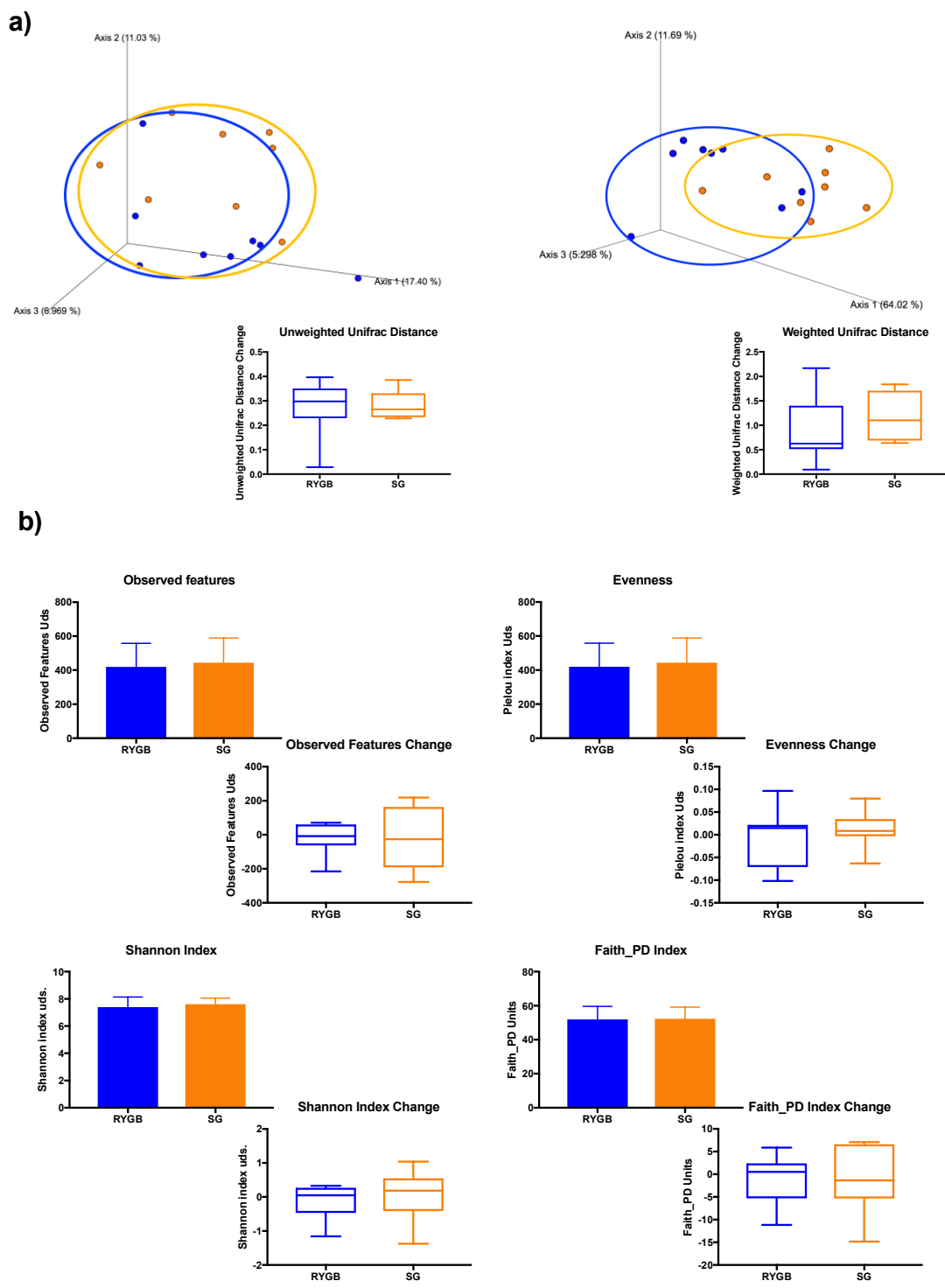


**Supplementary Table S1.** List of the pathways.

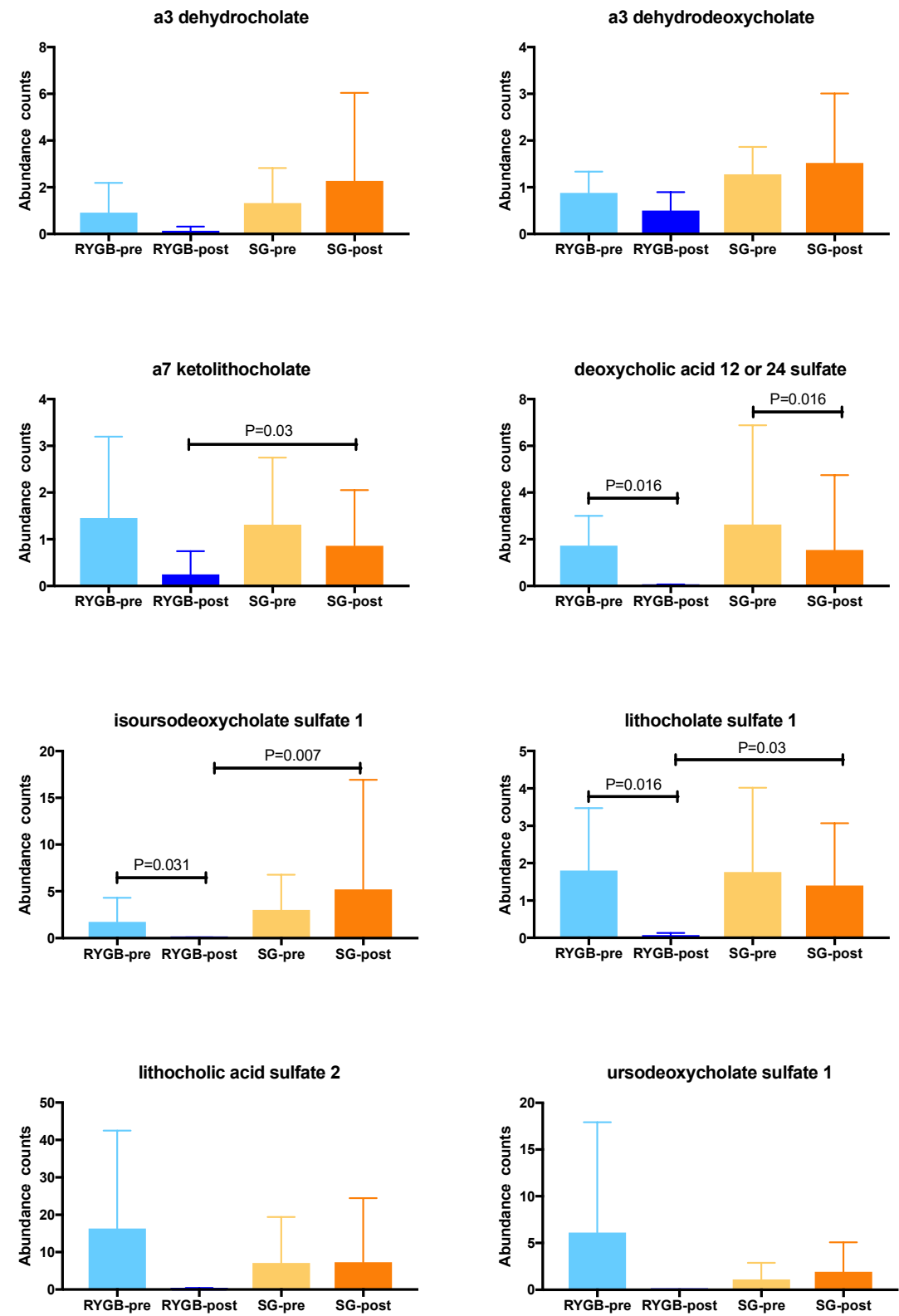
BioCyc Pathway ID	Pathway
<b>ARG+POLYAMINE-SYN</b>	superpathway of arginine and polyamine biosynthesis
<b>POLYAMINSYN3-PWY</b>	superpathway of polyamine biosynthesis II
<b>POLYAMSYN-PWY</b>	superpathway of polyamine biosynthesis I
<b>P101-PWY</b>	ectoine biosynthesis
<b>BRANCHED-CHAIN-AA-SYN-PWY</b>	superpathway of branched chain amino acid biosynthesis
<b>SER-GLYSYN-PWY</b>	superpathway of L-serine and glycine biosynthesis I
<b>PWY0-1061</b>	superpathway of L-alanine biosynthesis
<b>HSERMETANA-PWY</b>	L-methionine biosynthesis III
<b>PWY-6629</b>	superpathway of L-tryptophan biosynthesis
<b>CALVIN-PWY</b>	Calvin-Benson-Bassham cycle
<b>GLUCONEO-PWY</b>	gluconeogenesis I
<b>PWY0-1241</b>	ADP-L-glycero-&beta;
<b>PWY-5659</b>	GDP-mannose biosynthesis
<b>PEPTIDOGLYCANSYN-PWY</b>	peptidoglycan biosynthesis I (meso-diaminopimelate containing)
<b>PWY-6385</b>	peptidoglycan biosynthesis III (mycobacteria)
<b>PWY-6386</b>	UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
<b>PWY-6387</b>	UDP-N-acetylmuramoyl-pentapeptide biosynthesis I
<b>PWY0-1338</b>	polymyxin resistance
<b>KDO-NAGLIPASYN-PWY</b>	superpathway of (Kdo) <sub>2</sub> -lipid A biosynthesis
<b>PYRIDNUCSAL-PWY</b>	NAD salvage pathway I (PNC VI cycle)
<b>PWY-5862</b>	superpathway of demethylmenaquinol-9 biosynthesis
<b>PWY-5850</b>	superpathway of menaquinol-6 biosynthesis
<b>PWY-5896</b>	superpathway of menaquinol-10 biosynthesis
<b>PWY-5855</b>	ubiquinol-7 biosynthesis (early decarboxylation)
<b>PWY-5856</b>	ubiquinol-9 biosynthesis (early decarboxylation)
<b>PWY-5857</b>	ubiquinol-10 biosynthesis (early decarboxylation)
<b>PWY-6708</b>	ubiquinol-8 biosynthesis (early decarboxylation)
<b>UBISYN-PWY</b>	superpathway of ubiquinol-8 biosynthesis (early decarboxylation)
<b>LPSSYN-PWY</b>	superpathway of lipopolysaccharide biosynthesis
<b>PWY-7094</b>	fatty acid salvage
<b>PPGPPMET-PWY</b>	ppGpp metabolism
<b>PWY-6277</b>	superpathway of 5-aminoimidazole ribonucleotide biosynthesis
<b>PWY-6121</b>	5-aminoimidazole ribonucleotide biosynthesis I
<b>PWY-6122</b>	5-aminoimidazole ribonucleotide biosynthesis II

<b>PWY-7222</b>	guanosine deoxyribonucleotides de novo biosynthesis II
<b>PWY-7221</b>	guanosine ribonucleotides de novo biosynthesis
<b>PWY-7208</b>	superpathway of pyrimidine nucleobases salvage
<b>PWY-5121</b>	superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)
<b>PWY-7398</b>	coumarins biosynthesis (engineered)
<b>ENTBACSYN-PWY</b>	enterobactin biosynthesis
<b>PWY-7560</b>	methylerythritol phosphate pathway II
<b>PWY-5188</b>	tetrapyrrole biosynthesis I (from glutamate)
<b>PWY-5189</b>	tetrapyrrole biosynthesis II (from glycine)
<b>AST-PWY</b>	L-arginine degradation II (AST pathway)
<b>TYRFUMCAT-PWY</b>	L-tyrosine degradation I
<b>VALDEG-PWY</b>	L-valine degradation I
<b>CODH-PWY</b>	reductive acetyl coenzyme A pathway I (homoacetogenic bacteria)
<b>P23-PWY</b>	reductive TCA cycle I
<b>GLUCOSE1PMETAB-PWY</b>	glucose and glucose-1-phosphate degradation
<b>PWY-621</b>	sucrose degradation III (sucrose invertase)
<b>PWY-5747</b>	2-methylcitrate cycle II
<b>PWY0-42</b>	2-methylcitrate cycle I
<b>SULFATE-CYS-PWY</b>	superpathway of sulfate assimilation and cysteine biosynthesis
<b>SO4ASSIM-PWY</b>	assimilatory sulfate reduction I
<b>GLYCOCAT-PWY</b>	glycogen degradation I
<b>PWY-7446</b>	sulfoquinovose degradation I
<b>ANAGLYCOLYSIS-PWY</b>	glycolysis III (from glucose)
<b>GLYCOLYSIS</b>	glycolysis I (from glucose 6-phosphate)
<b>PWY-5484</b>	glycolysis II (from fructose 6-phosphate)
<b>NONOXIPENT-PWY</b>	pentose phosphate pathway (non-oxidative branch) I
<b>ECASYN-PWY</b>	enterobacterial common antigen biosynthesis
<b>TRNA-CHARGING-PWY</b>	tRNA charging
<b>PWY0-781</b>	aspartate superpathway

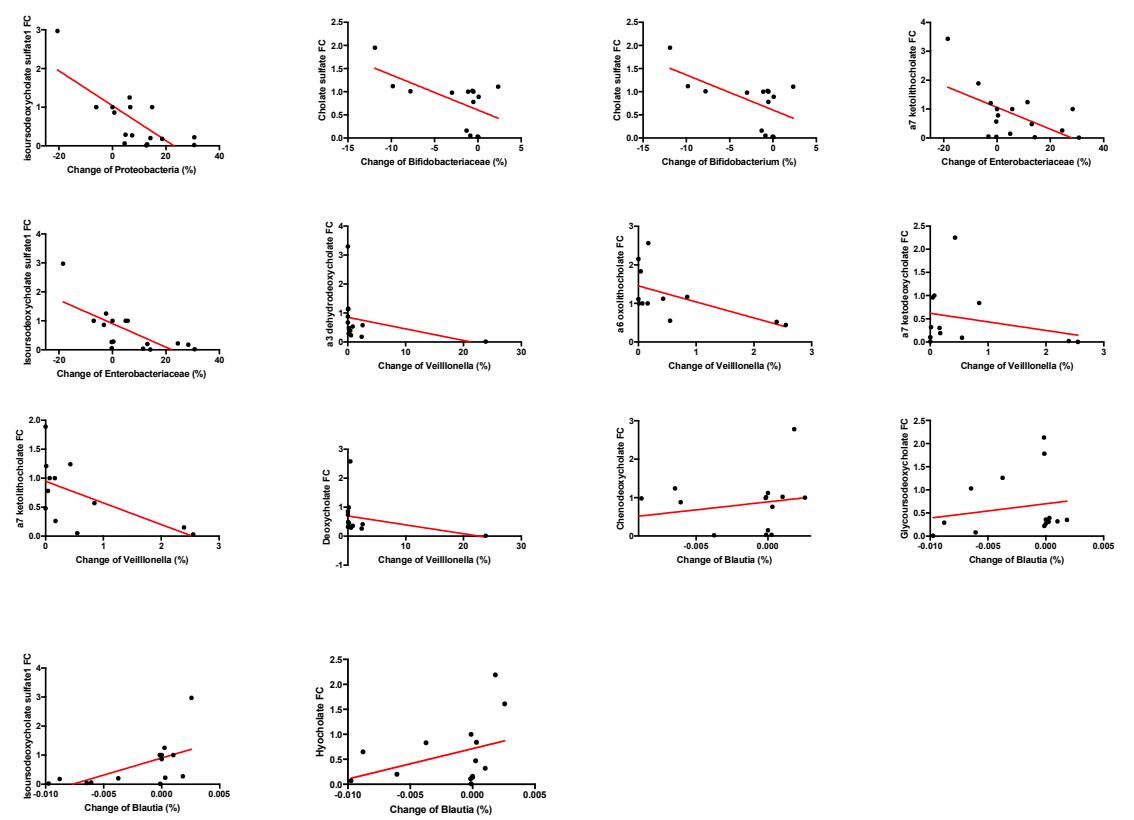
**Supplementary Figure S1.** Gut microbiota diversity measurements. a) Beta diversity: Unweighted and Weighted Unifrac distances. b) Alpha diversity indexes. It is presented the values at final point (histograms) and changes in values between final and baseline time-points (box and whiskers plots). RYGB is shown in blue; SG is shown in orange.



**Supplementary Figure S2.** Bar graphs of the bile acids fold changes in the two bariatric surgery procedures studies that resulted statistically significant between procedures ( $P<0.05$ ) or at least with a statistical tendency ( $P<0.10$ ).



**Supplementary Figure S3.** Scatterplots of Spearman correlations between changes in bacteria relative abundance and fold change (FC) of the secondary bile acids statistically significant ( $P < 0.05$ ).



**Supplementary Figure S4.** Scatterplots of the Spearman correlations between changes in anthropometric and biochemical variables with the fold-changes (FC) in secondary bile acids statistically significant ( $P < 0.05$ ).

