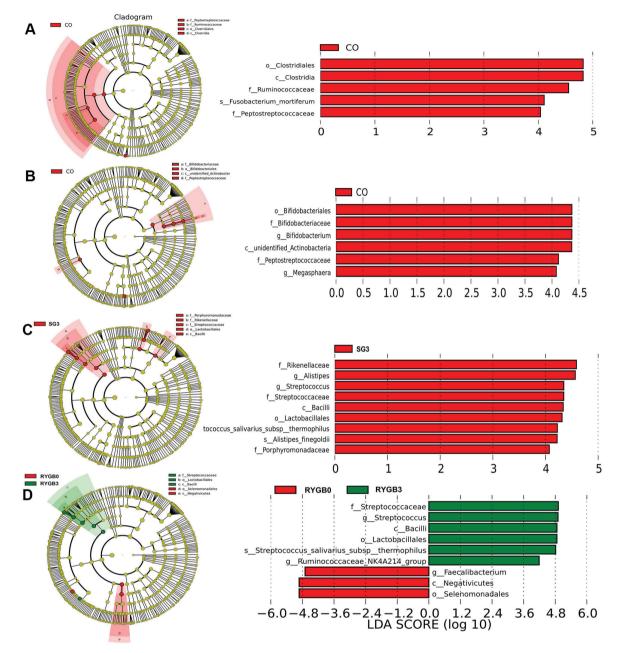
Figure S1. Species with statistically significant differences between groups. (A) CO vs. SG0; (B) CO vs. RYGB0; (C) SG0 vs. SG3; (D) RYGB0 vs. RYGB3. The left part in each separate figure displays the LEfSe-derived phylogenetic tree. The right part in each separate figure presents the LDA score of enriched species (LDA >4). The colors of the bars indicate the relative abundance. The detailed statistical method used in LEfSe software (version 1.0) was the Kruskal-Wallis test. LEfSe, linear discriminant analysis effect size; CO, control group; SG, sleeve gastrectomy; RYGB, Roux-en-Y gastric bypass; SG0/3, group prior to/3 months after SG.



0.2 0 BMI \* -0.2 -0.4 Glu GHb BRC1 Armatimonadetes FBP Parcubacteria Bacteroidetes Firmicutes Actinobacteria Spirochaetes Fusobacteria Saccharibacteria Chloroflexi Acidobacteria Gemmatimonadetes Planctomycetes Elusimicrobia Hydrogenedentes Fibrobacteres Thaumarchaeota Omnitrophica Synergistetes Thermomicrobia Deferribacteres Latescibacteria Deinococcus. Thermus Lentisphaerae Euryarchaeota Proteobacteria Cyanobacteria Verrucomicrobia Tenericutes Nitrospirae TM6\_.Dependentiae

Figure S2. Spearman correlation between the abundance of species and the BMI, GHb and Glu at the phylum level. Blue represents a negative correlation and red represents a positive correlation. The depth of the colors represents correlation coefficients. \*P<0.05. BMI, body mass index; GHb, glycosylated hemoglobin; Glu, blood glucose.

0.4 0.2 BMI 0 -0.2 -0.4 Glu GHb Bacilli SCG Synergistia Rubrobacteria Bacteroidia Negativicutes Gammaproteobacteria Clostridia unidentified\_Actinobacteria Betaproteobacteria Alphaproteobacteria Coriobacteriia Flavobacteriia Melainabacteria Erysipelotrichia Verrucomicrobiae unidentified\_Spirochaetes Fusobacteriia Mollicutes unidentified\_Saccharibacteria Deltaproteobacteria Epsilonproteobacteria Chloroplast Ktedonobacteria Sphingobacteriia Thermoleophilia unidentified\_Gemmatimonadetes Acidimicrobiia Planctomycetacia Subgroup\_2 Cytophagia unidentified\_Elusimicrobia Nitrospira Fibrobacteria unidentified\_Thermomicrobia

Figure S3. Spearman correlation between the abundance of species and the BMI, GHb and Glu at the class level. Blue represents a negative correlation and red represents a positive correlation. The depth of the colors represents correlation coefficients. \*P<0.05. BMI, body mass index; GHb, glycosylated hemoglobin; Glu, blood glucose.

0.4 0.2 BMI 0 -0.2 -0.4 Glu GHb Bacteroidales Burkholderiales Spirochaetales Pseudomonadales Xanthomonadales unidentified\_Chloroplast Alteromonadales Ferrovales Actinomycetales Selenomonadales Enterobacteriales Clostridiales Bifidobacteriales Coriobacteriales Flavobacteriales Gastranaerophilales Erysipelotrichales Rhizobiales Rhodobacterales Corynebacteriales Fusobacteriales Oceanospirillales Bacillales Pasteurellales Mollicutes\_RF9 unidentified\_Saccharibacteria Desulfovibrionales Campylobacterales Cellvibrionales Chromatiales Halanaerobiales Caulobacterales Aeromonadales Lactobacillales Verrucomicrobiales

Figure S4. Spearman correlation between the abundance of species and the BMI, GHb and Glu at the order level. Blue represents a negative correlation and red represents a positive correlation. The depth of the colors represents correlation coefficients. \*P<0.05. BMI, body mass index; GHb, glycosylated hemoglobin; Glu, blood glucose.

0.4 0.2 BMI 0 -0.2 -0.4 \* \* Glu \* \* GHb Ruminococcaceae Peptostreptococcaceae Streptococcaceae Coriobacteriaceae Spirochaetaceae Enterococcaceae Oxalobacteraceae Campylobacteraceae Xanthomonadaceae Prevotellaceae Veillonellaceae Bacteroidaceae Enterobacteriaceae Bifidobacteriaceae Rikenellaceae Lachnospiraceae Lactobacillaceae Alcaligenaceae Porphyromonadaceae Flavobacteriaceae Acidaminococcaceae Bacteroidales\_S24.7\_group Erysipelotrichaceae Phyllobacteriaceae Verrucomicrobiaceae Rhodobacteraceae Leuconostocaceae Nocardiaceae Corynebacteriaceae Fusobacteriaceae Oceanospirillaceae Planococcaceae Pasteurellaceae unidentified\_Saccharibacteria Desulfovibrionaceae

Figure S5. Spearman correlation between the abundance of species and the BMI, GHb and Glu at the family level. Blue represents a negative correlation and red represents a positive correlation. The depth of the colors represents correlation coefficients. \*P<0.05. BMI, body mass index; GHb, glycosylated hemoglobin; Glu, blood glucose.

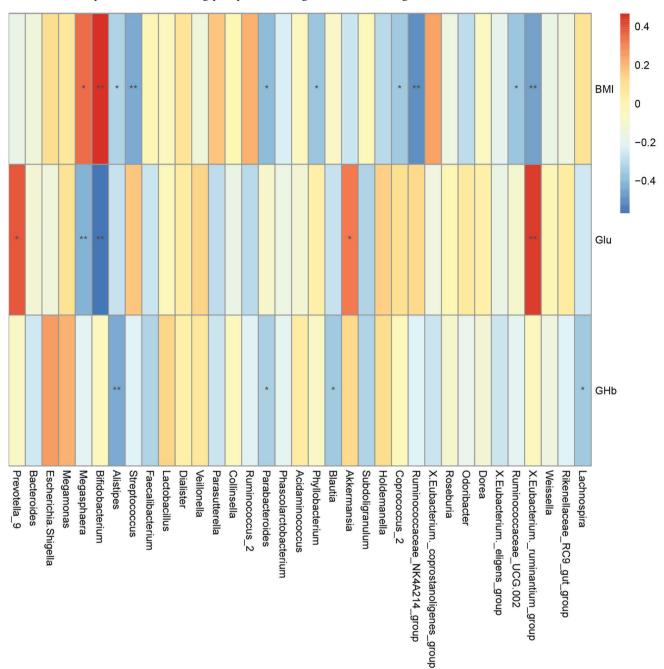


Figure S6. Spearman correlation between the abundance of species and the BMI, GHb and Glu at the genus level. Blue represents a negative correlation and red represents a positive correlation. The depth of the colors represents correlation coefficients. \*P<0.05. BMI, body mass index; GHb, glycosylated hemoglobin; Glu, blood glucose.

0.3 0.2 0.1 BMI 0 -0.1 -0.2 -0.3 -0.4 Glu GHb Escherichia\_coli Bacteroides\_ovatus Bacteroides\_coprocola Dorea\_longicatena Rhodococcus\_erythropolis Ruminococcus\_sp\_5\_1\_39BFAA Bacteroides\_caccae Fusobacterium\_mortiferum Fusobacterium\_varium Blautia\_obeum Lactobacillus\_iners Parabacteroides\_distasonis Bacteroides\_nordii Megasphaera\_elsdenii Streptococcus\_salivarius\_subsp\_thermophilus Bacteroides\_plebeius Alistipes\_finegoldii Bacteroides\_stercoris Lactobacillus\_mucosae Bacteroides\_vulgatus Parabacteroides\_merdae Bacteroides\_massiliensis Bacteroides\_dorei Akkermansia\_muciniphila Bacteroides\_fragilis Roseburia\_intestinalis Weissella\_confusa Bacteroides\_coprophilus Bacteroides\_uniformis bacterium\_OL.1 Prevotella\_copri Bacteroides\_cellulosilyticus Megasphaera\_cerevisiae Parabacteroides\_goldsteinii Bacteroides\_eggerthii

Figure S7. Spearman correlation between the abundance of species and the BMI, GHb and Glu at the species level. Blue represents a negative correlation and red represents a positive correlation. The depth of the colors represents correlation coefficients. \*P<0.05. BMI, body mass index; GHb, glycosylated hemoglobin; Glu, blood glucose.