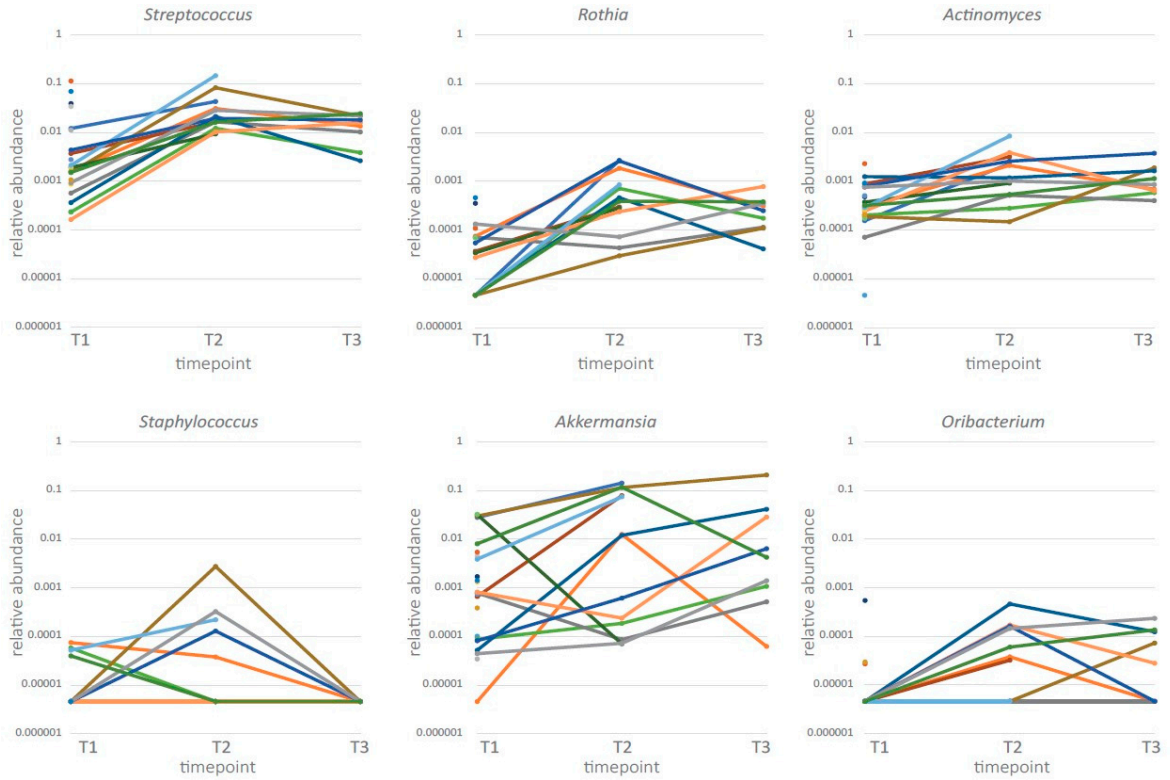**Supplemental Figure S1**. The fecal Firmicutes/Bacteroidetes (F/B) ratio in healthy individuals (HC), individuals pre-SG (T1), individuals post-SG two months (T2) and six months (T3) post-GS. Data are presented as boxplots displaying medians with interquartile ranges. ** indicates p<0.0001

Supplemental Figure S2. Relative abundances of specific taxa at specified time points (pre-SG (T1), two (T2) and six (T3) months post-SG). Horizontal axis: "timepoint", vertical axis: "relative abundance".

versus   T3   (6   months   post-SG).
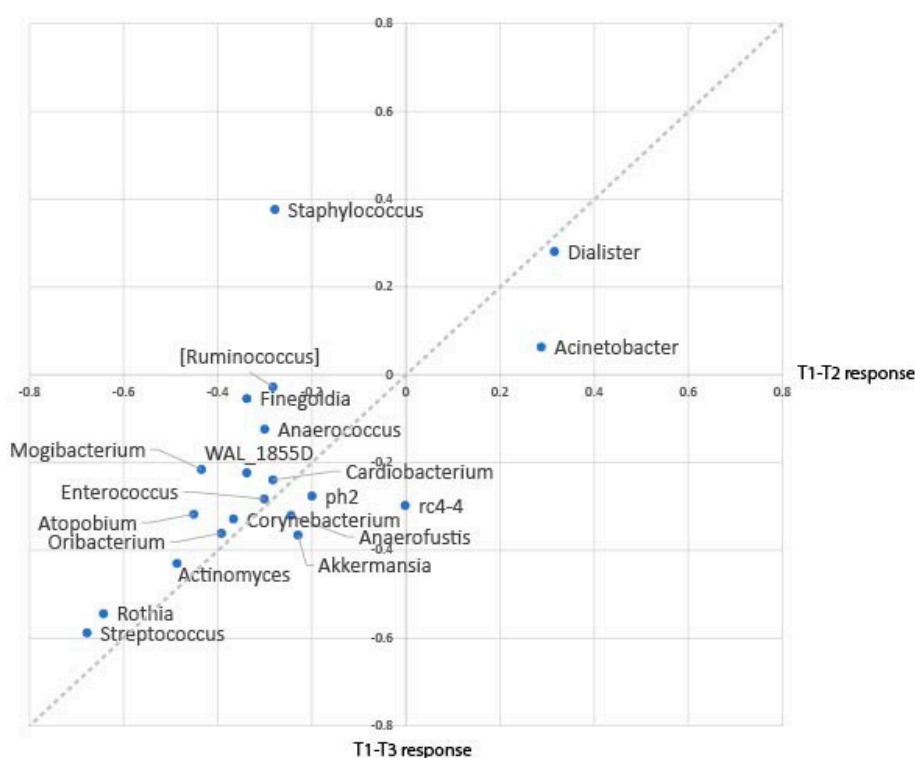
Supplemental Figure S3. Scatterplot based on the coordinates of the most important taxa according to the RDAs comparing samples T1 (pre-SG) versus T2 (2 months post-SG) and RDAs comparing samples T1 (pre-SG)

Supplemental Table S1. Taxa that contributed most to the separation between healthy individuals (HC) and obese individuals pre-SG (T1) according to their importance scores.

Taxa important for HC vs T1	importance score
Odoribacter	0.7567
Bacteroides	0.7068
[Eubacterium]	0.6681
Sutterella	0.6581
Lachnospira	0.6467
Butyricimonas	0.6310
Actinomyces	0.6228
Dorea	0.6014
[Ruminococcus]	0.5914
Parabacteroides	0.5664
Blautia	0.5059
Peptococcus	0.3183
Anaerostipes	0.3045
Paraprevotella	0.2640
Bulleidia	0.2634
Mitsuokella	0.2115
Catenibacterium	0.1597
Desulfovibrio	0.1356

[Prevotella]	0.0412
Prevotella	0.0235

Supplemental Table S2. Taxa that contributed most to the separation between obese individuals pre-SG (T1), two months (T2) and six months (T3) post-SG according to their importance scores.

Taxa important for T1 vs T2 vs T3	importance score
Streptococcus	0.8789
Rothia	0.6062
Oribacterium	0.5109
Actinomyces	0.4825
Corynebacterium	0.3900
Atopobium	0.3757
Dialister	0.3535
Mogibacterium	0.3439
Lactococcus	0.3305
Akkermansia	0.3239
[Ruminococcus]	0.3101
Finegoldia	0.2277
Selenomonas	0.2121
Staphylococcus	0.1754
Brevibacterium	0.1513
Campylobacter	0.1500
Bacillus	0.1467
Desulfomonile	0.1448
ph2	0.1426
LCP-26	0.1387

Supplemental Table S3. Taxa that contributed most to the separation between obese individuals pre-SG (T1) and obese individuals two months (T2) post-SG.

Taxa important for T1 vs T2	importance score
Streptococcus	0.6780
Rothia	0.6427
Actinomyces	0.4866
Atopobium	0.4513
Mogibacterium	0.4347
Oribacterium	0.3923
Corynebacterium	0.3667
WAL_1855D	0.3384
Finegoldia	0.3382
Dialister	0.3156
Enterococcus	0.3013
Anaerococcus	0.3004
Acinetobacter	0.2875
[Ruminococcus]	0.2830
Cardiobacterium	0.2828

Staphylococcus	0.2786
Fusobacterium	0.2750
Varibaculum	0.2697
Campylobacter	0.2670
Porphyromonas	0.2604

Supplemental Table S4. Taxa that contributed most to the separation between obese individuals pre-SG (T1) and obese individuals six months (T3) post-SG.

Taxa important for T1 vs T3	importance score
Streptococcus	0.5878
Rothia	0.5444
Actinomyces	0.4298
Staphylococcus	0.3768
Akkermansia	0.3652
Oribacterium	0.3610
Brevibacterium	0.3434
Corynebacterium	0.3286
Anaerofustis	0.3205
Atopobium	0.3178
rc4-4	0.2976
Enterococcus	0.2828
Dialister	0.2811
ph2	0.2760
Campylobacter	0,2683
Peptostreptococcus	0.2594
Lactococcus	0.2571
Bacillus	0.2554
Pseudoramibacter_Eubacterium	0.2412

Supplemental Table S5. Confounder analysis of patient characteristics by means of RDA.

Variable tested	Study group	Explained variation (%)	P-value
Diabetes	T1	3.2	0.84
Metformin	T1	5.4	0.20
Metformin	T2	8.3	0.46
Metformin	T3	15.4	0.19
Gender	HC	2.9	0.78
Gender	T1	4.0	0.52
Smoking	T1	8.3	0.57
Antidepressants	T1	6.0	0.98
PPI	T1	4.1	0.54

Supplemental Table S6. Associations between host markers and the microbiota composition as examined by CCA.

Variable tested	Study group	Explained variation (%)	P-value
Calprotectin	HC	6.2	0.05
Calprotectin	T1	4.8	0.29
Calprotectin	T2	6.9	0.84
Calprotectin	T3	15.0	0.17
hsCRP	HC	3.0	0.63
hsCRP	T1	9.7	0.002
hsCRP	T2	9.2	0.27
hsCRP	T3	13.9	0.26
L/R ratio	HC	3.6	0.56
L/R ratio	T1	4.2	0.47
L/R ratio	T2	9.4	0.40
L/R ratio	T3	15.5	0.10
protein content	HC	4.2	0.31
protein content	T1	4.6	0.37
protein content	T2	11.2	0.24
protein content	T3	14.7	0.26
Hba1c	T1	4.9	0.62
Hba1c	T2	11.7	0.22
Hba1c	T3	18.0	0.07
S/E ratio	HC	1.4	0.31
S/E ratio	T1	3.3	0.89
S/E ratio	T2	6.2	0.92
S/E ratio	T3	13.1	0.36
sucrose	HC	3.7	0.51
sucrose	T1	4.5	0.48
sucrose	T2	9.9	0.17
sucrose	T3	11.5	0.68

Supplemental Table S7. Pearson correlation coefficients (R) between changes in the three most strongly affected taxa by SG and markers of glycemic control, inflammatory and intestinal permeability.

Variable	Streptococcus			Actinomytes			Rothia		
	R	p	FDR	R	p	FDR	R	p	FDR
hba1c ΔT1-ΔT2	0.796	0.010	0.225	-0.154	0.693	0.846	-0.560	0.117	0.642
hba1c ΔT1-ΔT3	0.526	0.180	0.692	-0.520	0.186	0.692	0.307	0.460	0.764
CRP ΔT1-ΔT2	0,314	0.300	0.705	0.021	0.946	0.968	-0.152	0.620	0.801
CRPc ΔT1-ΔT3	0.384	0.308	0.713	-0.532	0.141	0.687	0.474	0.198	0.692
calprotectin ΔT1-ΔT2	0.176	0.565	0.801	0.240	0.429	0.738	0.409	0.166	0.692
calprotectin ΔT1-ΔT3	0.417	0.264	0.692	-0.429	0.249	0.692	0.654	0.056	0.434
sucrose ΔT1-ΔT2	0.158	0.625	0.720	-0.343	0.276	0.434	-0.584	0.046	0.738
sucrose ΔT1-ΔT3	0.629	0.070	0.801	-0.669	0.049	0.692	0.303	0.428	0.434
SE ΔT1-ΔT2	0.183	0.549	0.801	0.091	0.767	0.855	-0.112	0.717	0.852

SE ΔT1-ΔT3	0.007	0.986	0.986	0.298	0.436	0.738	-0.109	0.779	0.855
LR ΔT1-ΔT2	0.285	0.369	0.738	0.354	0.260	0.692	0.161	0.617	0,801
LR ΔT1-ΔT3	-0.318	0.405	0.738	0.236	0.541	0.801	-0.112	0.774	0.855
BMI ΔT1-ΔT2	0.376	0.229	0.801	0.161	0.617	0.924	-0.297	0.349	0.801
BMI ΔT1-ΔT3	0.214	0.580	0.692	0.069	0.861	0.801	-0.220	0.569	0.732