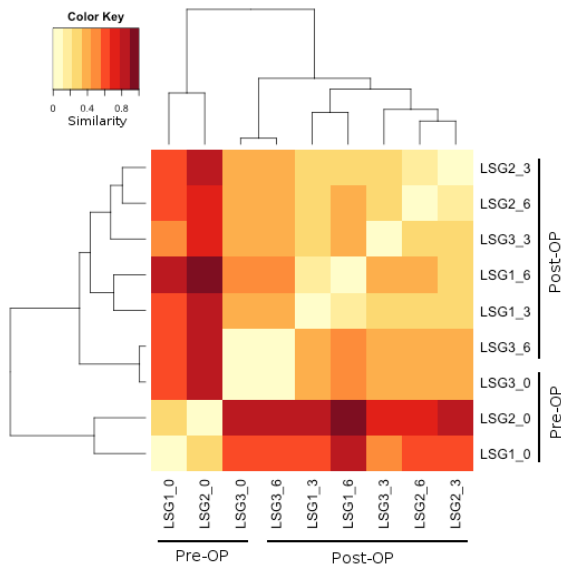


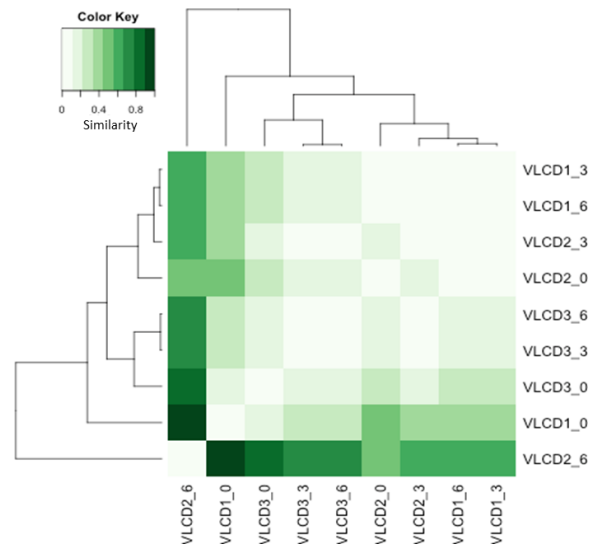
Supporting information 1: Figures

SI-Figure 1: Dissimilarity- and cluster analysis of the phylogenetic trees in the course of weight loss therapy for obesity derived from sequencing of the intestinal microbiome. (A) (red): Laparoscopic sleeve gastrectomy (subject numbers LSG 1-3), (B) (green): Very low calorie diet (subject numbers VLCD 1-3). The color code of the heatmap corresponds to values of the normalized Euclidian distances of the phylogenetic trees.

(A) LSG

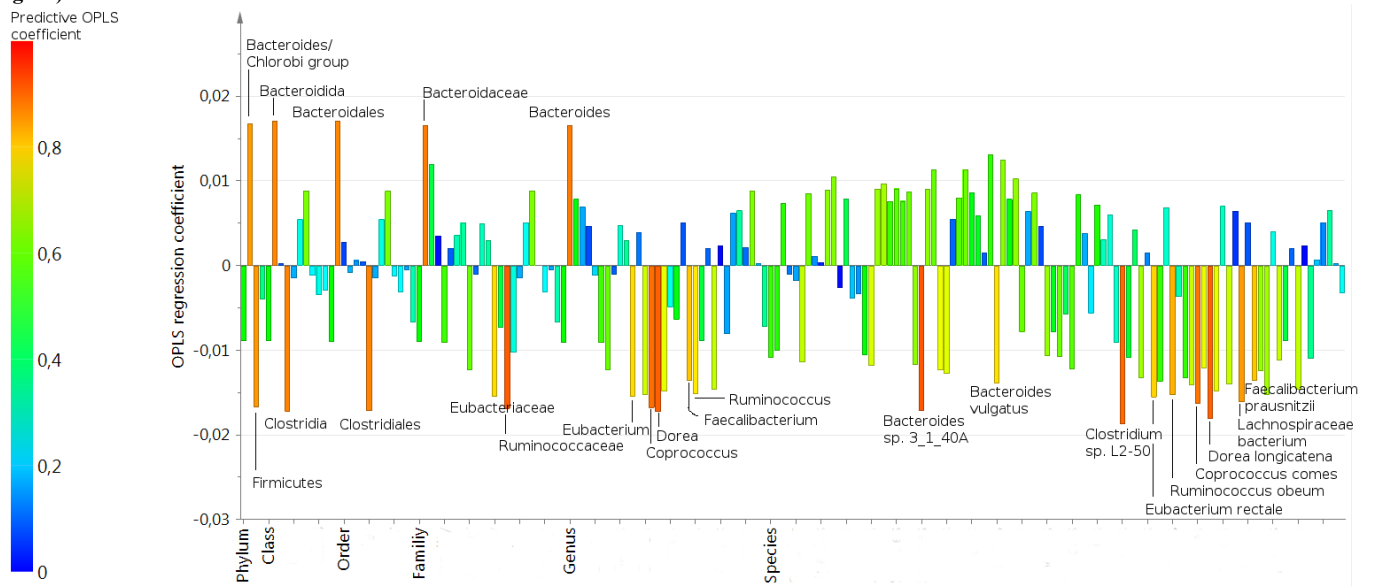


(B) VLCD



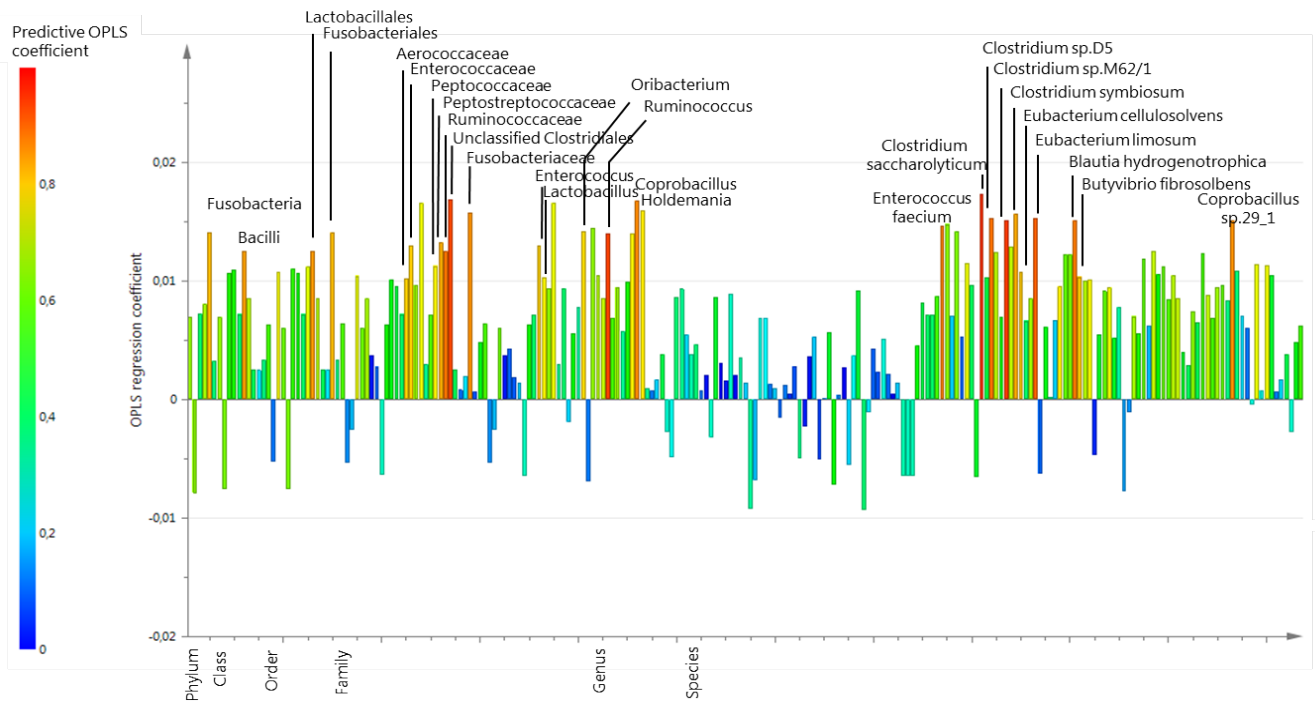
SI-Figure 2: OPLS-DA coefficient plots for identification of pre- to post-interventional gut microbial changes on all taxonomic levels during *Laparoscopic sleeve gastrectomy (LSG; SDC-Fig. 2a)* and *Very low calorie diet (VLCD; SDC-Fig. 2b)*. Labeled are bacterial groups with predictive OPLS coefficient $p(\text{corr}) > 0.75$ and < -0.75 , respectively, as indicated by the color code shown on the left.

Fig. 2a) LSG



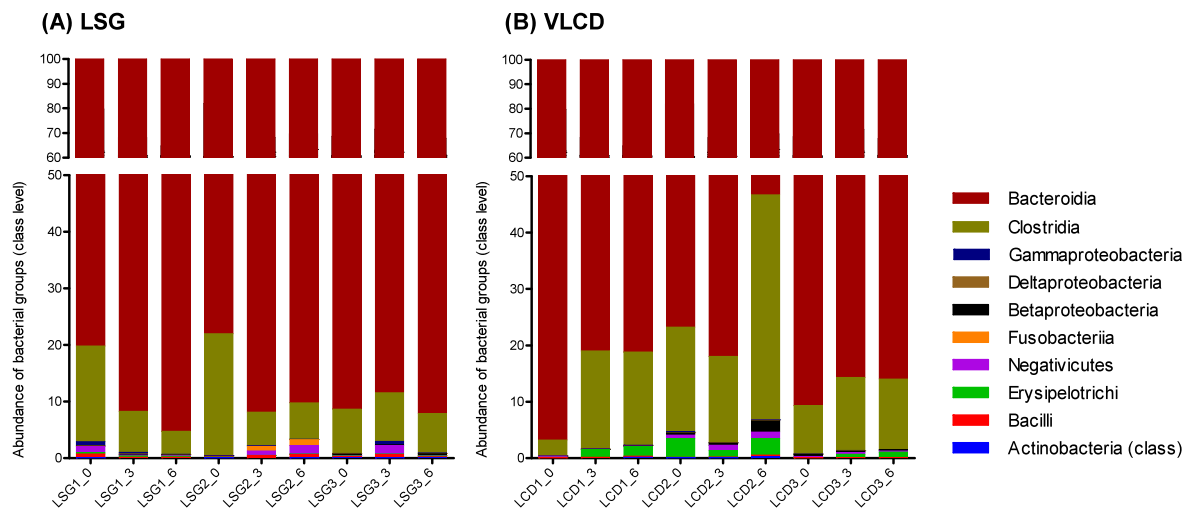
Model statistics: $Q^2=0.337$, $R^2X=0.265$

Fig. 2b) VLCD

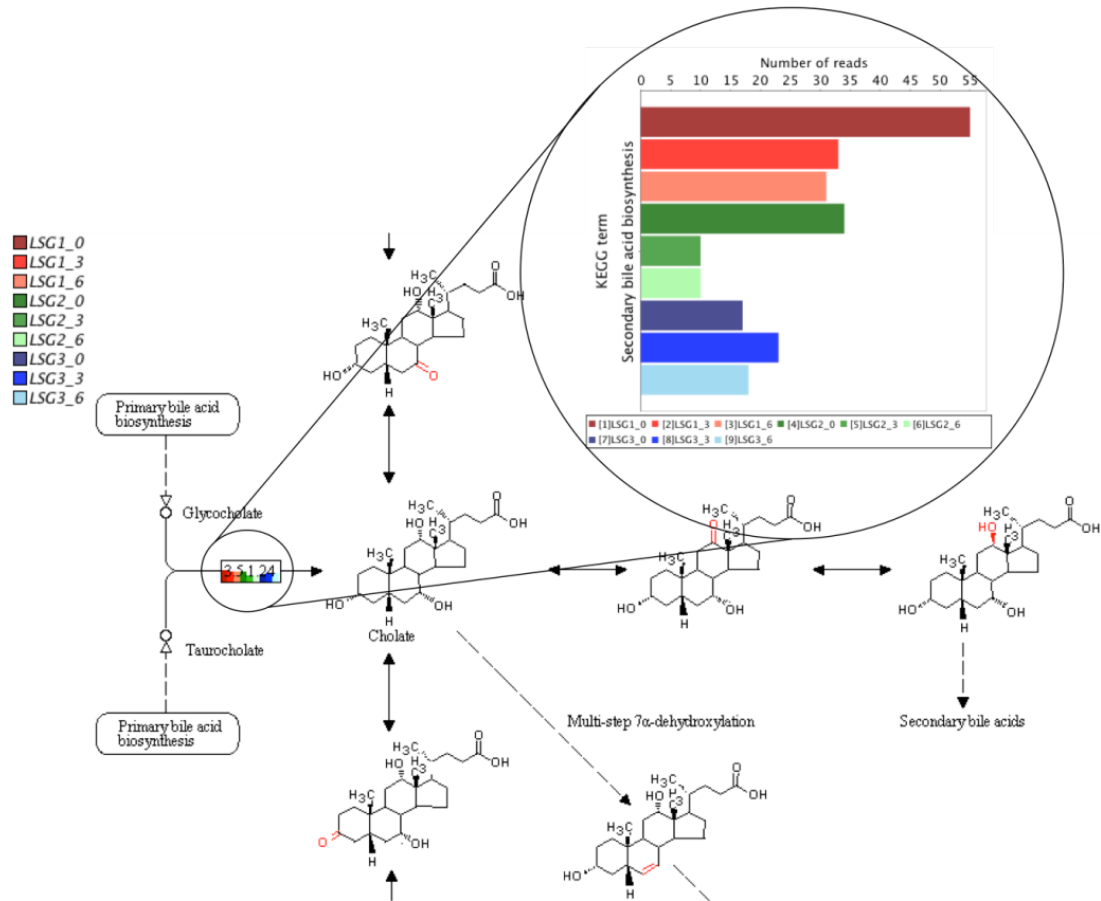


Model statistics: $Q^2=0.56$, $R^2X=0.216$

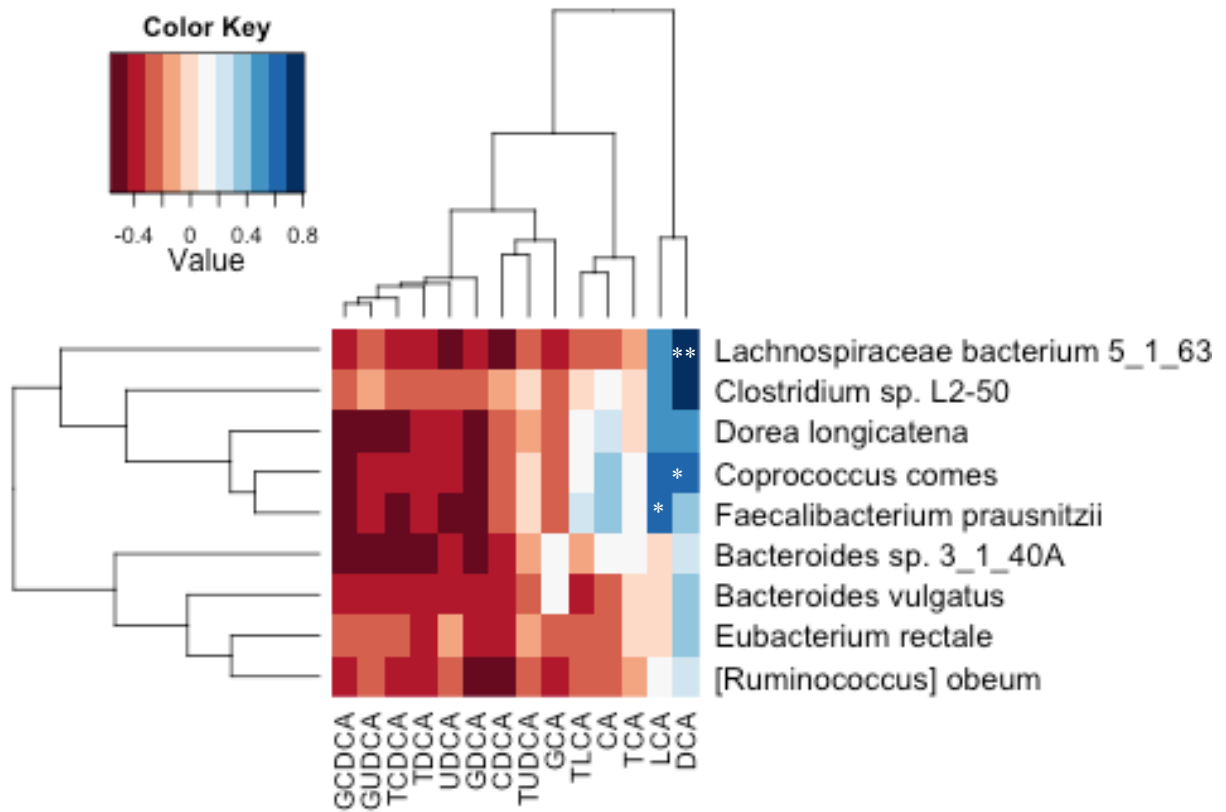
SI-Figure 3: Abundance of bacterial groups at the class level in 6 obese subjects undergoing weight loss therapy obtained by next-generation sequencing (SOLiD shotgun sequencing) during a period of 6 months (timepoints 0, 3, and 6 months): (A) *Laparoscopic sleeve gastrectomy* (subject numbers: LSG 1-3) and (B) *Very low calorie diet* (subject numbers: VLCD 1-3).



SI-Figure 4: KEGG analysis of the microbial metabolic capacity for primary and secondary bile acid synthesis after intervention with **laparoscopic sleeve gastrectomy** (*subject numbers LSG 1-3, timepoints 0, 3, and 6 months*). Only a section of the biosynthesis pathway is shown.



SI-Figure 5 Correlation and cluster analysis of fecal bile acids with intestinal microbes, which changed following laparoscopic sleeve gastrectomy. Stars indicate significant correlations (* $p < 0.05$, ** $p < 0.01$). LCA, DCA: Secondary bile acids.



Supporting information 2: Tables

SI-Table 1: Alterations of the intestinal microbiota on different taxonomic levels following a) laparoscopic sleeve gastrectomy and b) Very low calorie diet-induced weight loss in obese subjects

Taxonomic level	Bacteria category	Predictive coefficient ^a	P value ^b	Reads (normalized) Month 0	Reads (normalized) Month 3	Reads (normalized) Month 6
a) Laparoscopic sleeve gastrectomy (LSG)						
Phylum	<i>Bacteroidetes/Chlorobi group</i>	0.8478	0.1667	77128.3 ± 5700.4	85069 ± 2011.1	86482.7 ± 2382.6
	<i>Firmicutes</i>	-0.8501	0.0952	15858.0 ± 5434.9	8488.7 ± 2025.2	6784.7 ± 2027.3
Class	<i>Bacteroidia</i>	0.8679	0.1667	75474.0 ± 5478.8	83494.7 ± 2170.1	84630.3 ± 1998.5
	<i>Clostridia</i>	-0.8725	0.0476*	14014.0 ± 5215.9	6572.3 ± 1196.3	5333.0 ± 1415.7
Order	<i>Bacteroidales</i>	0.8679	0.1667	75474.0 ± 5478.8	83494.7 ± 2170.1	84630.3 ± 1998.5
	<i>Clostridiales</i>	-0.8721	0.0476*	13978.0 ± 5212.3	6669.0 ± 1196.1	5320.3 ± 1412.0
Family	<i>Bacteroidaceae</i>	0.8790	0.1667	64302.0 ± 3587.6	69971.0 ± 2504.2	70006.3 ± 1345.0
	<i>Eubacteriaceae</i>	-0.7842	0.1667	5075.7 ± 3959.9	259.0 ± 178.3	652.0 ± 412.8
	<i>Ruminococcaceae</i>	-0.0908	0.0476*	1386.3 ± 448.0	605.0 ± 322.7	539.7 ± 319.0
Genus	<i>Bacteroides</i>	-0.8790	0.1667	64302.0 ± 3587.6	69971.0 ± 2504.2	70006.3 ± 1345.0
	<i>Eubacterium</i>	-0.8784	0.1667	5072.3 ± 3957.9	257.7 ± 178.8	650.7 ± 412.3
	<i>Coprococcus</i>^s	-0.8902	0.0238*	397.0 ± 135.2	116.3 ± 107.3	154.7 ± 120.3
	<i>Dorea</i>	-0.9061	0.0238*	180.0 ± 28.3	72.7 ± 66.9	72.3 ± 49.7
	<i>Faecalibacterium</i>	-0.8053	0.2619	380.7 ± 48.7	163.3 ± 194.3	167.3 ± 196.7
	<i>Ruminococcus</i>	-0.7700	0.0476*	914.7 ± 506.3	357.7 ± 80.6	307.3 ± 140.7
Species	<i>Bacteroides sp.3_1_40A</i>	-0.9155	0.0238*	304.3 ± 59.7	142.3 ± 68.5	150.0 ± 88.8
	<i>Bacteroides vulgatus</i>	-0.7785	0.0952	4731.7 ± 2283.9	1913.7 ± 1788.5	1814.0 ± 1481.3
	<i>Clostridium sp. L2-50</i>^s	-0.8967	0.0269*	50.3 ± 10.4	18.3 ± 7.2	27.7 ± 7.4
	<i>Eubacterium rectale</i>	-0.7927	0.1667	4370.0 ± 3501.9	103.7 ± 119.4	383.7 ± 486.8
	<i>Ruminococcus obeum</i>	-0.8239	0.0476*	143.0 ± 81.1	53.3 ± 36.5	33.0 ± 8.5
	<i>Coprococcus comes</i>	-0.8842	0.0952	269.7 ± 61.0	78.3 ± 79.1	124.3 ± 111.2
	<i>Dorea longicatena</i>	-0.9053	0.0238*	132.0 ± 17.1	43.7 ± 38.5	53.0 ± 42.6
	<i>Lachnospiraceae bacterium 5_1_63FAA</i>	-0.8476	0.1667	65.3 ± 40.5	14.3 ± 11.4	11.3 ± 4.7
	<i>Faecalibacterium prausnitzii</i>	-0.8053	0.2619	380.7 ± 48.7	163.3 ± 194.3	167.3 ± 196.7

Taxonomic level	Bacteria category	Predictive coefficient ^a	P value ^b	Reads (normalized) Month 0	Reads (normalized) Month 3	Reads (normalized) Month 6
b) Very low calorie diet (VLCD)						
Phylum	<i>Fusobacteria</i> [§]	0.8155	0.0476*	39.0 ± 46.2	97.7 ± 20.5	107.0 ± 16.7
Class	<i>Bacilli</i> [§]	0.8429	0.0238*	609.3 ± 319.8	1519.0 ± 375.4	2400.7 ± 1150.7
Order	<i>Lactobacillales</i> [§]	0.8479	0.0238*	485.7 ± 210.1	1257.3 ± 385.7	1966.7 ± 954.6
	<i>Fusobacteriales</i> [§]	0.8155	0.0476*	39.0 ± 46.2	97.7 ± 20.5	107.0 ± 16.7
Family	<i>Aerococcaceae</i>	0.7963	0.2619	46.0 ± 68.7	100.7 ± 10.5	183.3 ± 105.6
	<i>Enterococcaceae</i> [§]	0.7954	0.0238*	85.7 ± 74.2	348.7 ± 162.4	482.7 ± 256.8
	<i>Peptococcaceae</i>	0.7586	0.2619	27.3 ± 33.0	67.0 ± 15.1	90.0 ± 52.0
	<i>Peptostreptococcaceae</i> [§]	0.8301	0.0238*	92.7 ± 94.0	263.3 ± 10.6	471.7 ± 174.8
	<i>Ruminococcaceae</i> [§]	0.8842	0.0238*	9498.7 ± 8154.5	28360.0 ± 7046.3	52656.3 ± 24157.4
	<i>UnclassifiedRum Clostridiales</i>	0.9275	0.0238*	1262.0 ± 446.0	3158.0 ± 172.6	3179.3 ± 706.3
	<i>Fusobacteriaceae</i> [§]	0.8557	0.0238*	31.0 ± 33.2	90.0 ± 14.1	95.3 ± 9.6
Genus	<i>Enterococcus</i> [§]	0.7940	0.0238*	85.7 ± 74.2	347.3 ± 163.7	482.7 ± 256.8
	<i>Lactobacillus</i> [§]	0.7583	0.0476*	27.3 ± 32.3	83.0 ± 19.9	204.0 ± 131.5
	<i>Oribacterium</i>	0.7832	0.0238*	36.7 ± 36.5	131.3 ± 58.0	141.3 ± 45.7
	<i>Ruminococcus</i>	0.9321	0.0476*	6951.3 ± 6549.9	20517 ± 6500.0	34982.3 ± 8870.5
	<i>Coprobacillus</i>	0.8627	0.0238*	107.7 ± 98.7	711.0 ± 110.1	800.7 ± 251.9
	<i>Holdemania</i>	0.7672	0.0238*	48.7 ± 42.3	406.0 ± 154.9	357.7 ± 101.2
Species	<i>Enterococcus faecium</i>	0.8705	0.0238*	49.3 ± 45.0	215.3 ± 113.8	265.7 ± 69.8
	<i>Clostridium saccharolyticum</i> [§]	0.9435	0.0238*	160.3 ± 49.0	554.7 ± 130.5	591.3 ± 56.0
	<i>Clostridium sp. D5</i>	0.8852	0.0238*	79.0 ± 68.7	521.3 ± 233.8	594.3 ± 206.2
	<i>Clostridium sp. M62/1</i>	0.9416	0.0238*	348.3 ± 315.2	909.7 ± 160.6	1033.7 ± 232.1
	<i>Clostridium symbiosum</i>	0.8330	0.0238*	299.7 ± 147.7	1690.3 ± 798.0	1685.7 ± 327.8
	<i>Eubacterium cellulosolvens</i> [§]	0.7998	0.0952	36.0 ± 35.5	120.3 ± 80.1	224.0 ± 141.2
	<i>Eubacterium limosum</i>	0.9025	0.0238*	24.0 ± 25.6	105.0 ± 38.0	103.0 ± 28.1
	<i>Blautia hydrogenotrophica</i>	0.8775	0.0238*	96.7 ± 55.2	293.7 ± 30.6	294.7 ± 124.6
	<i>Butyrivibrio fibrisolvens</i>	0.8039	0.1667	35.0 ± 39.0	73.0 ± 38.0	131.7 ± 66.2
	<i>Coprobacillus sp. 29_1</i>	0.8558	0.0238*	94.0 ± 83.8	509.3 ± 113.2	663.7 ± 289.9

Shown are coefficients > 0.75 and < -0.75; ^a derived from OPLS-DA models (LSG: Q²=0.337, R²X=0.265, VLCD: Q²=0.56, R²X=0.216) with class discrimination pre (Month 0) to post (Month 3 and 6 combined) intervention; ^b Mann-Whitney-U Test comparing pre- to post-intervention; [§] (bold) significant changes (p=0.0278) for time course (Friedman test)