

Table S1. Sequences, OTUs and OPUs. “Nr OPUs filtered” excluded identical values (i.e. zeros) across all samples and features that appear in only one sample. M: control mucosa samples, A: experimental anastomosis samples.

Sample	Nr total sequences	Nr OTUs	Nr OPUs	Nr OPUs filtered
M1	15387	132	44	12
M2	10213	47	15	12
M3	10659	149	75	67
M4	5943	65	37	37
M5	15444	171	83	72
M6	15606	142	56	49
M7	9237	132	75	64
M8	26448	564	13	12
M9	20689	379	1	1
M10	15960	224	40	34
M11	15328	346	18	11
M12	10774	66	9	8
total	171688	1569	210	124
Mean	14307	201	39	32
SD	5513	154	28	26
A1	12066	118	49	49
A2	12960	96	42	40
A3	11426	122	63	55
A4	12375	68	39	37
A5	16833	156	44	39
A6	13402	138	57	54
A7	16777	155	48	47
A8	18107	338	140	108
A9	17998	157	43	40
A10	14334	170	50	46
A11	12944	110	45	43
A12	18723	110	21	21
total	177945	1090	213	151
Mean	14829	145	53	48
SD	2668	68	29	21
TOTAL	349633	2484	317	169

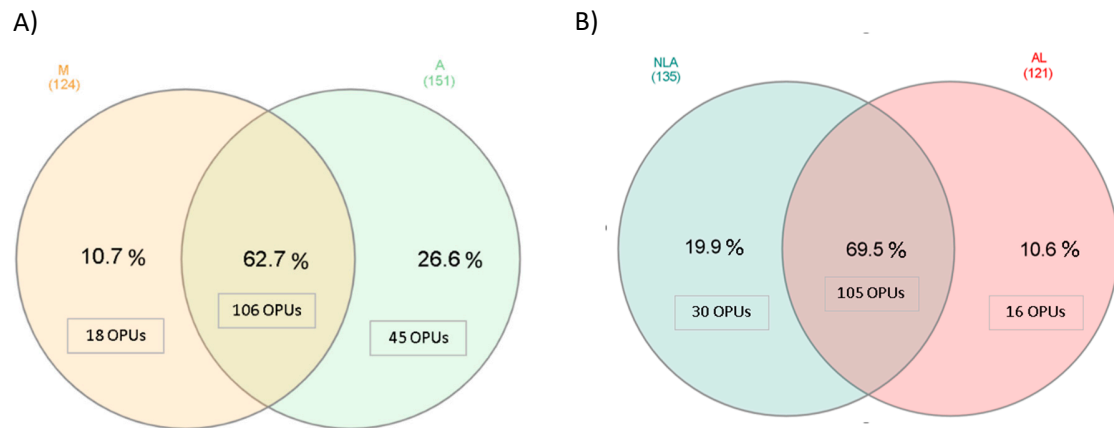


Figure S1. Venn diagram of OPUs obtained. These graphics were made after discarding OPUs with identical values in all samples, as well as OPUs present in only one sample. M: control mucosa group, A: experimental anastomosis group, NLA: non-leak anastomosis, AL: anastomotic leak.

Table S2. Alpha diversity indices. M: control mucosa samples, A: experimental anastomosis samples.

Sample	Chao-1	Dominance-D index	Shannon–Weiner index	Evenness
M1	44	0.07	3.01	0.46
M2	15	0.34	1.69	0.36
M3	75	0.09	3.07	0.29
M4	37	0.11	2.70	0.40
M5	83	0.06	3.38	0.36
M6	56	0.15	2.75	0.28
M7	75	0.09	3.06	0.29
M8	13	0.98	0.09	0.08
M9	1	1.00	0.00	1.00
M10	40	0.65	0.95	0.06
M11	18	0.81	0.58	0.10
M12	9	0.62	0.77	0.24
Mean	39	0.41	1.84	0.33
SD	28	0.37	1.29	0.25
A1	49	0.15	2.55	0.26
A2	42	0.10	2.73	0.37
A3	63	0.21	2.38	0.17
A4	39	0.18	2.41	0.29
A5	44	0.65	1.05	0.06
A6	57	0.10	2.81	0.29
A7	48	0.41	1.66	0.11
A8	140	0.04	3.79	0.32
A9	43	0.27	1.56	0.11
A10	50	0.47	1.35	0.08
A11	45	0.19	2.18	0.20
A12	21	0.21	1.90	0.32
Mean	53	0.25	2.20	0.21
SD	29	0.18	0.75	0.11

Table S3. Heat tree data of taxonomic differences between A and M. Result from comparison between microbial communities of Figure 3. Statistically, Wilcoxon Rank Sum test $p < 0.05$. M: control, A: anastomosis. “p”=phylum, “c”=class, “o”=order, “f”=family, “g”=genus, “s”=species.

tax_rank	tax_name	G1	G2	log2_median_ratio	median_diff	mean_diff	wilcox_p_value
p	Fusobacteriata	A	M	Inf	0.0056537	0.016737	0.000964
p	Campylobacterota	A	M	-6.775942901	-0.4878357	-0.491993	0.003407
p	Firmicutes	A	M	1.042100162	0.2089626	0.226212	0.020489
p	Proteobacteria	A	M	1.471870751	0.1571441	0.132335	0.026197
c	Fusobacteriia	A	M	Inf	0.0056537	0.016737	0.000964
c	Campylobacteriia	A	M	-6.775942901	-0.4878357	-0.491993	0.003407
c	Bacilli	A	M	3.15323081	0.2624777	0.191711	0.017271
c	Gammaproteobacteria	A	M	1.462988704	0.1556358	0.136881	0.022459
c	Negativicutes	A	M	3.116655648	0.0477196	0.039915	0.039536
o	Fusobacteriales	A	M	Inf	0.0056537	0.016737	0.000964
o	Rhodospirillales	A	M	Inf	0.0005718	0.004350	0.001084
o	Staphylococcales	A	M	Inf	0.1879922	0.225497	0.001849
o	Campylobacterales	A	M	-6.775942901	-0.4878357	-0.491993	0.003407
o	Acidaminococcales	A	M	Inf	0.0146038	0.020108	0.003929
o	Enterobacterales	A	M	5.243994683	0.2377824	0.154125	0.005880
o	RF39	A	M	Inf	0.0006630	0.001313	0.030982
o	Xanthomonadales	A	M	0	0.0000000	-0.009254	0.036687
f	Gemellaceae	A	M	Inf	0.1879922	0.267173	0.000038
f	Pasteurellaceae	A	M	Inf	0.0806828	0.126894	0.000052
f	Fusobacteriaceae	A	M	Inf	0.0056537	0.016737	0.000964
f	Helicobacteraceae	A	M	-6.775942901	-0.4878357	-0.491993	0.003407
f	Acidaminococcaceae	A	M	Inf	0.0146038	0.020108	0.003929
f	Bacteroidales_1	A	M	Inf	0.0002320	0.001015	0.007054
f	Bacteroidaceae	A	M	5.618467188	0.1668760	0.154478	0.011654
f	Rikenellaceae	A	M	Inf	0.0013822	0.002167	0.013072
f	Carnobacteriaceae	A	M	Inf	0.0010055	0.005052	0.033976
f	Streptococcaceae	A	M	0	0.0000000	0.002554	0.036687
f	Staphylococcaceae	A	M	0	0.0000000	-0.041676	0.036687
f	Xanthomonadaceae	A	M	0	0.0000000	-0.009254	0.036687
f	Rhodospirillales_3	A	M	0	0.0000000	0.001035	0.036687
f	Rhodospirillales_4	A	M	0	0.0000000	0.002979	0.036687
f	RF39_5	A	M	0	0.0000000	0.000542	0.036687
f	RF39_6	A	M	0	0.0000000	0.000529	0.036687
g	Gemella	A	M	Inf	0.1879922	0.267173	0.000038
g	Rodentibacter	A	M	Inf	0.0806828	0.126894	0.000052
g	Fusobacterium	A	M	Inf	0.0056537	0.016737	0.000964
g	Helicobacter	A	M	-6.775942901	-0.4878357	-0.491993	0.003407
g	Phascolarctobacterium	A	M	Inf	0.0146038	0.020108	0.003929
g	Bacteroidales_1	A	M	Inf	0.0002320	0.001015	0.007054
g	Bacteroides	A	M	5.618467188	0.1668760	0.154478	0.011654
g	Prevotellaceae_1	A	M	0	0.0000000	0.001209	0.016473
g	Sphaerochaeta	A	M	0	0.0000000	0.000586	0.016473
g	UCG_008	A	M	0	0.0000000	0.000422	0.016473
g	Carnobacteriaceae_1	A	M	Inf	0.0010055	0.005052	0.033976
g	Facklamia	A	M	0	0.0000000	-0.027586	0.036687
g	Globicatella	A	M	0	0.0000000	0.002705	0.036687
g	Streptococcus	A	M	0	0.0000000	0.002554	0.036687
g	Jeitgalicoccus	A	M	0	0.0000000	-0.011633	0.036687
g	Xanthomonadaceae_1	A	M	0	0.0000000	-0.009254	0.036687
g	Rhodospirillales_3	A	M	0	0.0000000	0.001035	0.036687
g	Rhodospirillales_4	A	M	0	0.0000000	0.002979	0.036687
g	RF39_5	A	M	0	0.0000000	0.000542	0.036687
g	RF39_6	A	M	0	0.0000000	0.000529	0.036687
g	Johnsonella	A	M	0	0.0000000	0.000219	0.036687
s	Gemella_palaticanis	A	M	Inf	0.1879922	0.267173	0.000038
s	Rodentibacter_ratti	A	M	Inf	0.0276695	0.088834	0.000079
s	Bacteroides_sartorii	A	M	Inf	0.0489763	0.074472	0.000505
s	Fusobacterium_gastrusuis	A	M	Inf	0.0056537	0.016737	0.000964
s	Bacteroides_uniformis	A	M	Inf	0.0009443	0.006443	0.001084
s	Rodentibacter_4	A	M	Inf	0.0009632	0.012824	0.002856
s	Phascolarctobacterium_succinatutens	A	M	Inf	0.0146038	0.020108	0.003929
s	Bacteroidales_1	A	M	Inf	0.0002320	0.001015	0.007054
s	Rodentibacter_3	A	M	Inf	0.0002707	0.011388	0.007054
s	Prevotellaceae_1	A	M	0	0.0000000	0.001209	0.016473
s	Sphaerochaeta_1	A	M	0	0.0000000	0.000586	0.016473
s	Rodentibacter_6	A	M	0	0.0000000	0.005194	0.016473
s	UCG_008_1	A	M	0	0.0000000	0.000422	0.016473
s	Helicobacter_muridarum	A	M	0	-0.0116239	-0.098321	0.028503
s	Carnobacteriaceae_1	A	M	Inf	0.0010055	0.005052	0.033976
s	Facklamia_tabacinasalis	A	M	0	0.0000000	-0.027586	0.036687
s	Globicatella_1	A	M	0	0.0000000	0.002705	0.036687
s	Streptococcus_1	A	M	0	0.0000000	0.002554	0.036687
s	Jeitgalicoccus_nanhaiensis	A	M	0	0.0000000	-0.011633	0.036687
s	Allaprevotella_2	A	M	0	0.0000000	0.000370	0.036687
s	Escherichia_cali_4	A	M	0	0.0000000	0.001599	0.036687
s	Escherichia_Shipella_2	A	M	0	0.0000000	0.003043	0.036687
s	Rodentibacter_1	A	M	0	0.0000000	0.009411	0.036687
s	Xanthomonadaceae_1	A	M	0	0.0000000	-0.009254	0.036687
s	Rhodospirillales_3	A	M	0	0.0000000	0.001035	0.036687
s	Rhodospirillales_4	A	M	0	0.0000000	0.002979	0.036687
s	RF39_5	A	M	0	0.0000000	0.000542	0.036687
s	RF39_6	A	M	0	0.0000000	0.000529	0.036687
s	Johnsonella_1	A	M	0	0.0000000	0.000219	0.036687
s	Oribacterium_1	A	M	0	0.0000000	0.000514	0.036687
s	Rikenellaceae_RC9_gut_group_3	A	M	Inf	0.0005239	0.001617	0.040513
s	Helicobacter_1	A	M	0	-0.0208354	-0.311105	0.041607
s	Bacteroides_acidifaciens	A	M	Inf	0.0049116	0.007562	0.048481

Table S4. Data summary of LEfSe analysis between A and M. Data of taxonomic differences between A and M from Figure 5A. LEfSe/LDA score >2, and a raw P value cutoff of 0.05, Kruskal-Wallis test. M: control, A: anastomosis.

OPI	Species	P values	FDR	A	M	LDA score
OPI_138	<i>Gemella_palaticanis</i>	0.00003	0.005	2672200	0	6.1
OPI_334	<i>Rodentibacter_ratti</i>	0.00007	0.006	890820	2366	5.7
OPI_172	<i>Bacteroides_sartorii</i>	0.00045	0.025	829660	84909	5.6
OPI_48	<i>Phascolarctobacterium_succinatutens</i>	0.00357	0.085	207440	6341.7	5.0
OPI_325	<i>Fusobacterium_gastrosuis</i>	0.00086	0.032	174210	6810.9	4.9
OPI_338	<i>Rodentibacter_4</i>	0.00254	0.070	128390	0	4.8
OPI_337	<i>Rodentibacter_3</i>	0.00629	0.116	114050	0	4.8
OPI_335	<i>Rodentibacter_1</i>	0.03287	0.182	94320	0	4.7
OPI_167	<i>Bacteroides_acidifaciens</i>	0.04513	0.227	100350	24660	4.6
OPI_170	<i>Bacteroides_uniformis</i>	0.00096	0.032	64426	0	4.5
OPI_340	<i>Rodentibacter_6</i>	0.01473	0.182	52015	0	4.4
OPI_122	<i>Carnobacteriaceae_1</i>	0.03106	0.182	53878	3356.4	4.4
OPI_332	<i>Escherichia_Shigella_2</i>	0.03287	0.182	30448	0	4.2
OPI_358	<i>Rhodospirillales_4</i>	0.03287	0.182	29812	0	4.2
OPI_126	<i>Globicatella_1</i>	0.03287	0.182	27047	0	4.1
OPI_127	<i>Streptococcus_1</i>	0.03287	0.182	25539	0	4.1
OPI_314	<i>Rikenellaceae_RC9_gut_group_3</i>	0.03712	0.199	17960	1783.4	3.9
OPI_330	<i>Escherichia_coli_4</i>	0.03287	0.182	16006	0	3.9
OPI_157	<i>Prevotellaceae_1</i>	0.01473	0.182	12113	0	3.8
OPI_308	<i>Bacteroidales_1</i>	0.00629	0.116	10152	0	3.7
OPI_357	<i>Rhodospirillales_3</i>	0.03287	0.182	10349	0	3.7
OPI_323	<i>Sphaerochaeta_1</i>	0.01473	0.182	5860.9	0	3.5
OPI_383	<i>RF39_5</i>	0.03287	0.182	5424.5	0	3.4
OPI_384	<i>RF39_6</i>	0.03287	0.182	5294.2	0	3.4
OPI_94	<i>Oribacterium_1</i>	0.03287	0.182	5146.6	0	3.4
OPI_37	<i>UCG_008_1</i>	0.01473	0.182	4218.3	0	3.3
OPI_179	<i>Alloprevotella_2</i>	0.03287	0.182	3702	0	3.3
OPI_91	<i>Johnsonella_1</i>	0.03287	0.182	2186.2	0	3.0
OPI_353	<i>Xanthomonadaceae_1</i>	0.03287	0.182	0	97310	-4.7
OPI_137	<i>Jeotgalicoccus_nanhaiensis</i>	0.03287	0.182	0	123270	-4.8
OPI_125	<i>Facklamia_tabacinasalis</i>	0.03287	0.182	0	292480	-5.2
OPI_362	<i>Helicobacter_muridarum</i>	0.02634	0.182	25595	1011500	-5.7
OPI_361	<i>Helicobacter_1</i>	0.03870	0.201	71139	3195300	-6.2

Table S5. Correlation coefficients results between A and M. Correlation values in Figure 5B are shown. Taxon 1 correspond to species highlighted in Figure 5, with a LEfSe-LDA score >2 and a FDR-adjusted P value < 0.05. Taxon 2 correspond to species with LEfSe/LDA score >2, and a raw P value cutoff < 0.05, Kruskal-Wallis test.

Taxon 1	Taxon 2	Correlation	P Value
<i>Gemella_palaticanis</i>	<i>Rodentibacter_ratti</i>	0.8373	0.0099
<i>Gemella_palaticanis</i>	<i>Bacteroides_uniformis</i>	0.561	0.0198
<i>Gemella_palaticanis</i>	<i>Rodentibacter_4</i>	0.4474	0.0495
<i>Gemella_palaticanis</i>	<i>Phascolarctbacterium_succinatutens</i>	0.4079	0.0198
<i>Gemella_palaticanis</i>	<i>Jeotgalicoccus_nanhaiensis</i>	-0.4422	0.0198
<i>Gemella_palaticanis</i>	<i>Facklamia_tabacinasalis</i>	-0.4685	0.0297
<i>Gemella_palaticanis</i>	<i>Xanthomonadaceae_1</i>	-0.469	0.0297
<i>Gemella_palaticanis</i>	<i>Helicobacter_muridarum</i>	-0.5158	0.0099
<i>Rodentibacter_ratti</i>	<i>Gemella_palaticanis</i>	0.8373	0.0099
<i>Rodentibacter_ratti</i>	<i>Bacteroides_uniformis</i>	0.5348	0.0198
<i>Rodentibacter_ratti</i>	<i>Fusobacterium_gastrosuis</i>	0.412	0.0396
<i>Rodentibacter_ratti</i>	<i>Rodentibacter_4</i>	0.4013	0.0198
<i>Rodentibacter_ratti</i>	<i>Helicobacter_muridarum</i>	-0.445	0.0297
<i>Bacteroides_sartorii</i>	<i>Bacteroides_acidifaciens</i>	0.6415	0.0099
<i>Bacteroides_sartorii</i>	<i>Helicobacter_1</i>	-0.3869	0.0495
<i>Fusobacterium_gastrosuis</i>	<i>Rodentibacter_ratti</i>	0.412	0.0396
<i>Fusobacterium_gastrosuis</i>	<i>Helicobacter_1</i>	-0.3983	0.0297
<i>Bacteroides_uniformis</i>	<i>Gemella_palaticanis</i>	0.561	0.0198
<i>Bacteroides_uniformis</i>	<i>Rodentibacter_ratti</i>	0.5348	0.0198
<i>Bacteroides_uniformis</i>	<i>Rodentibacter_4</i>	0.4743	0.0297
<i>Bacteroides_uniformis</i>	<i>RF39_5</i>	-0.412	0.0495
<i>Bacteroides_uniformis</i>	<i>Rodentibacter_1</i>	-0.4128	0.0297
<i>Bacteroides_uniformis</i>	<i>UCG_008_1</i>	-0.4378	0.0297
<i>Bacteroides_uniformis</i>	<i>Helicobacter_muridarum</i>	-0.5107	0.0099

Table S6. Microbial respiration of microbiota. A: anastomosis experimental group, M: control group.

Microbial respiration of microbiota, relative abundances (%)																								
	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	A12	M01	M02	M03	M04	M05	M06	M07	M08	M09	M10	M11	M12
Aerobes	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.2	11.5	0.0	0.0	1.5	0.4	0.0	0.1	0.0	0.0	0.0	0.0
Facultative anaerobes	9.4	58.3	57.6	37.0	82.5	36.8	66.3	47.8	56.3	20.4	47.3	71.4	65.4	22.5	15.1	19.2	19.6	10.7	12.1	0.4	0.0	1.8	1.3	0.0
Obligate anaerobes	90.0	41.7	35.6	56.2	13.4	59.0	32.8	39.6	43.1	78.9	44.5	28.6	0.8	0.5	82.8	80.8	64.6	53.2	54.7	0.3	0.0	4.8	2.7	0.8
Microaerophiles	0.2	0.0	2.5	6.4	3.3	3.4	0.7	11.0	0.1	0.3	7.5	0.0	10.7	65.4	1.7	0.0	13.4	35.5	27.0	99.2	100.0	92.9	95.5	99.2
microaerophile or aerotolerant anaerobes	0.0	0.0	4.0	0.4	0.7	0.6	0.2	0.9	0.4	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.3	4.6	0.0	0.0	0.3	0.5	0.0
Microaerophiles or facultatively anaerobic	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.9	0.0	1.5	0.0	0.0	0.2	0.0	0.0
ND	0.0	0.0	0.3	0.0	0.1	0.2	0.0	0.4	0.1	0.4	0.6	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0

Microbial respiration of microbiota, relative abundances (Log10)																								
	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	A12	M01	M02	M03	M04	M05	M06	M07	M08	M09	M10	M11	M12
Aerobes	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	1.1	0.0	0.0	0.4	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Facultative anaerobes	1.0	1.8	1.8	1.6	1.9	1.6	1.8	1.7	1.8	1.3	1.7	1.9	1.8	1.4	1.2	1.3	1.3	1.1	1.1	0.1	0.0	0.4	0.4	0.0
Obligate anaerobes	2.0	1.6	1.6	1.8	1.2	1.8	1.5	1.6	1.6	1.9	1.7	1.5	0.2	0.2	1.9	1.9	1.8	1.7	1.7	0.1	0.0	0.8	0.6	0.2
Microaerophiles	0.1	0.0	0.5	0.9	0.6	0.6	0.2	1.1	0.0	0.1	0.9	0.0	1.1	1.8	0.4	0.0	1.2	1.6	1.4	2.0	2.0	2.0	2.0	2.0
Microaerophile or aerotolerant anaerobes	0.0	0.0	0.7	0.1	0.2	0.2	0.1	0.3	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.7	0.0	0.0	0.1	0.2	0.0
Microaerophiles or facultatively anaerobic	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.3	0.0	0.4	0.0	0.0	0.1	0.0	0.0
ND	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0

Table S7. Data summary of LEfSe analysis between NLA and AL. Data of taxonomic differences between NLA and AL from Figure 8B. LEfSe/LDA score >2, and a raw P value cutoff of 0.05, Kruskal-Wallis test. NLA: non-leak anastomosis, AL: anastomotic leak.

OPU	Species	P values	FDR	AL	NLA	LDA score
OPU_365	<i>Helicobacter_rodentium</i>	0.037222	0.45694	3170.9	78507	4.58
OPU_114	<i>Lactobacillus_murinus</i>	0.020122	0.45694	882.53	45697	4.35
OPU_116	<i>Ligilactobacillus_1</i>	0.036714	0.45694	0	31283	4.19
OPU_104	<i>Lactobacillus_reuteri</i>	0.036714	0.45694	0	16714	3.92
OPU_355	<i>Rhodospirillales_1</i>	0.036714	0.45694	0	10369	3.71
OPU_31	<i>UCG_005_6</i>	0.036714	0.45694	0	9376.8	3.67
OPU_145	<i>Clostridium_sensu_stricto_1_2</i>	0.036714	0.45694	0	7009.5	3.54
OPU_199	<i>Muribaculaceae_20</i>	0.036714	0.45694	0	1826.1	2.96
OPU_209	<i>Muribaculaceae_30</i>	0.036714	0.45694	0	1159.4	2.76
OPU_113	<i>Lactobacillus_2</i>	0.038015	0.45694	51288	45881	-3.43
OPU_138	<i>Gemella_palaticanis</i>	0.04154	0.45694	3568600	893270	-6.13

Table S8. Correlation coefficient results between NLA and AL. Correlation values in Figure 8C are shown. LEfSe-LDA score >2 and a raw P value < 0.05, Kruskal-Wallis test.

Taxon 1	Taxon 2	Correlation	P Value
<i>Gemella_palaticanis</i>	<i>Helicobacter_rodentium</i>	-0.6012	0.0099
<i>Clostridium_sensu_stricto_1_2</i>	<i>Muribaculaceae_30</i>	0.9367	0.0099
<i>Ligilactobacillus_1</i>	<i>Lactobacillus_marinus</i>	0.6419	0.0396
<i>Lactobacillus_marinus</i>	<i>Rhodospirillales_1</i>	0.5738	0.0396
<i>Rhodospirillales_1</i>	<i>Muribaculaceae_20</i>	0.9122	0.0099
<i>Rhodospirillales_1</i>	UCG_005_6	0.926	0.0099
<i>Muribaculaceae_20</i>	UCG_005_6	0.9034	0.0099