OTUs	Total	pos75	pos50	neg50	neg75	Phylum	Species	Similarity (%)
0	1	1	0	0	0	Firmicutes	*Ruminococcus gnavus*	100
101	2	2	0	0	0	Bacteroidetes	*Bacteroides dorei*	99
130	1	1	0	0	0	Proteobacteria	*Brevundimonas vesicularis*	100
177	2	1	1	0	0	Bacteroidetes	*Bacteroides dorei*	98.6
180	1	0	1	0	0	Firmicutes	*Clostridium spiroforme*	92.7
204	2	2	0	0	0	Bacteroidetes	*Bacteroides dorei*	98.4
226	2	1	0	1	0	Bacteroidetes	*Sediminibacterium salmoneum*	98.1
24	1	1	0	0	0	Firmicutes	*Dorea formicigenerans*	100
270	3	3	0	0	0	Bacteroidetes	*Bacteroides dorei*	98.8
28	1	0	0	1	0	Firmicutes	*Streptococcus mitis*	100
289	4	0	2	2	0	Firmicutes	*Clostridium saccharolyticum*	96.4
310	2	2	0	0	0	NA	*Escherichia/Shigella flexneri*	92.6
49	3	0	3	0	0	Firmicutes	*Roseburia inulinivorans*	99.6
53	1	0	1	0	0	Proteobacteria	*Sutterella wadsworthensis*	100
84	1	0	1	0	0	Bacteroidetes	*Odoribacter splanchnicus*	99.3

Supp. Table 6: OTU correlation network composition deduced from patients at time of surgery

Cluster: Identity of the cluster; OTUs: identity of the Operational Taxonomic Unit specific of each cluster; Total: total number of significant correlations between the identified OTU and other OTUs from the cluster; pos75: number of significant positive correlations (R≥0.75) between the identified OTU and other OTUs from the cluster; pos50: number of significant positive correlations (R≥0.50) between the identified OTU and other OTUs from the cluster; neg50: number of significant negative correlations (R≤-0.5) between the identified OTU and other OTUs from the cluster; Similarity: similarity percentage between the OTU and the first relative species. No significant negative correlation with R≤-0.75 was observed.