

Cluster	Cluster p-value	OTUs	Total	pos75	pos50	neg50	neg75	Phylum	Species	Similarity (%)
1	0.0107	28	5	2	3	0	0	Firmicutes	<i>Streptococcus mitis</i>	100
		163	4	0	3	1	0	Firmicutes	<i>Streptococcus sinensis</i>	98.8
		64	4	1	3	0	0	Firmicutes	<i>Gemella haemolysans</i>	99.8
		124	2	1	1	0	0	Firmicutes	<i>Granulicatella adiacens</i>	100
		176	2	0	2	0	0	Proteobacteria	<i>Acinetobacter johnsonii</i>	99
		227	1	0	1	0	0	Bacteroidetes	<i>Sediminibacterium salmoneum</i>	96
		264	1	0	1	0	0	Actinobacteria	<i>Actinomyces odontolyticus</i>	100
2	5.27e⁻⁰⁴	205	6	2	4	0	0	Proteobacteria	<i>Comamonas aquatica</i>	98.7
		5	6	0	5	1	0	Firmicutes	<i>Ruminococcus bromii</i>	99.8
		108	5	3	2	0	0	Proteobacteria	<i>Pelomonas saccharophila</i>	99
		11	5	2	2	0	1	Firmicutes	<i>Thermanaeromonas toyohensis</i>	85.9
		159	5	0	5	0	0	Firmicutes	<i>Alicyclobacillus pohliae</i>	99
		154	4	2	2	0	0	Proteobacteria	<i>Ralstonia insidiosa</i>	99.7
		76	4	0	4	0	0	Proteobacteria	<i>Mesorhizobium australicum</i>	98.8
		102	3	0	3	0	0	Firmicutes	<i>Oscillibacter valericigenes</i>	91.9
		55	3	0	3	0	0	Proteobacteria	<i>Methylobacterium adhaesivum</i>	98.9
		256	2	0	2	0	0	Proteobacteria	<i>Rhodospirillum rubrum</i>	85.8
		91	2	1	1	0	0	Deinococcus-Thermus	<i>Thermus scotoductus</i>	99.5
		150	1	0	1	0	0	Proteobacteria	<i>Methylobacterium adhaesivum</i>	98.8
		287	1	0	1	0	0	Firmicutes	<i>Dendrosporobacter quercicolus</i>	81.2
		307	1	0	1	0	0	Firmicutes	<i>Veillonella parvula</i>	99.8
3	1.25e⁻⁰⁶	8	13	7	6	0	0	Firmicutes	<i>Blautia glucerasea</i>	98.8
		18	12	4	7	0	1	Firmicutes	<i>Clostridium hylemonae</i>	98.5
		38	12	1	10	1	0	Firmicutes	<i>Clostridium bolteae</i>	99.5
		103	10	1	9	0	0	Proteobacteria	<i>Aeromonas ichthiosmia</i>	100
		193	10	4	6	0	0	Firmicutes	<i>Clostridium bartlettii</i>	99.5
		222	9	0	8	1	0	Firmicutes	<i>Enterococcus faecalis</i>	100
		281	9	3	6	0	0	Firmicutes	<i>Clostridium hylemonae</i>	99.2
		325	9	2	7	0	0	Firmicutes	<i>Ruminococcus gnavus</i>	100
		82	9	2	7	0	0	Firmicutes	<i>Blautia hansenii</i>	100
		191	8	0	7	1	0	Firmicutes	<i>Butyricicoccus pullicaecorum</i>	99.6
		145	7	1	6	0	0	Firmicutes	<i>Clostridium aldenense</i>	98

		188	6	0	6	0	0	Firmicutes	<i>Anaerostipes caccae</i>	99.8
		202	6	0	6	0	0	Bacteroidetes	<i>Parabacteroides distasonis</i>	98.6
		301	6	3	3	0	0	Firmicutes	<i>Ruminococcus schinkii</i>	96.8
		13	5	0	5	0	0	Firmicutes	<i>Clostridium bolteae</i>	100
		23	5	0	4	1	0	Firmicutes	<i>Streptococcus salivarius</i>	100
		6	5	1	0	3	1	Firmicutes	<i>Faecalibacterium prausnitzii</i>	98.8
		85	5	2	3	0	0	Firmicutes	<i>Clostridium bartlettii</i>	99.5
		184	4	0	3	1	0	Proteobacteria	<i>Proteus vulgaris</i>	99.8
		317	4	2	2	0	0	Firmicutes	<i>Ruminococcus gnavus</i>	99.8
		75	4	0	4	0	0	Firmicutes	<i>Clostridium hylemonae</i>	99.2
		0	3	1	2	0	0	Firmicutes	<i>Ruminococcus gnavus</i>	100
		220	3	0	1	2	0	Proteobacteria	<i>Klebsiella pneumoniae</i>	100
		29	3	2	1	0	0	Bacteroidetes	<i>Parabacteroides distasonis</i>	98.3
		316	3	0	3	0	0	Firmicutes	<i>Clostridium bartlettii</i>	99.7
		40	3	0	3	0	0	Firmicutes	<i>Enterococcus durans</i>	100
		2	1	1	0	0	0	Firmicutes	<i>Eubacterium rectale</i>	99.7
		232	1	0	1	0	0	Firmicutes	<i>Phascolarctobacterium faecium</i>	100
		335	1	0	1	0	0	Firmicutes	<i>Enterococcus durans</i>	100
		60	1	0	1	0	0	Firmicutes	<i>Clostridium ramosum</i>	99.8
4	7.54e⁻³	58	7	1	4	2	0	Proteobacteria	<i>Undibacterium oligocarboniphilum</i>	100
		139	4	0	3	0	0	Bacteroidetes	<i>Prevotella enoeca</i>	83.3
		258	4	0	2	2	0	Firmicutes	<i>Desulfotomaculum guttoideum</i>	96.9
		68	4	1	3	0	0	Proteobacteria	<i>Sphingomonas melonis</i>	99.8
		250	2	0	2	0	0	Firmicutes	<i>Staphylococcus warneri</i>	100
		257	2	0	2	0	0	Firmicutes	<i>Faecalibacterium prausnitzii</i>	95
		143	1	0	1	0	0	Bacteroidetes	<i>Lishizhenia tianjinensis</i>	86.9
		170	1	0	1	0	0	Firmicutes	<i>Clostridium hathewayi</i>	99.5
		224	1	0	1	0	0	Proteobacteria	<i>Bradyrhizobium yuanmingense</i>	99.5
		4	1	0	1	0	0	Bacteroidetes	<i>Bacteroides fragilis</i>	98.6
		41	1	0	0	1	0	Firmicutes	<i>Desulfotomaculum guttoideum</i>	95.9
		62	1	0	0	0	0	Firmicutes	<i>Clostridium thermocellum</i>	87.9
5	3.91e⁻⁰⁷	21	12	2	9	0	1	Bacteroidetes	<i>Bacteroides caccae</i>	100
		37	10	2	7	1	0	Firmicutes	<i>Eubacterium hallii</i>	99.7

			117	8	0	8	0	0	Bacteroidetes	<i>Parabacteroides merdae</i>	100
			52	8	0	8	0	0	Bacteroidetes	<i>Prevotella oralis</i>	91.1
			22	7	0	7	0	0	Firmicutes	<i>Clostridium aldenense</i>	96.4
			3	7	0	7	0	0	Bacteroidetes	<i>Bacteroides stercoris</i>	99
			84	7	1	6	0	0	Bacteroidetes	<i>Odoribacter splanchnicus</i>	99.3
			14	6	1	4	0	1	Bacteroidetes	<i>Bacteroides dorei</i>	98.6
			33	6	0	6	0	0	Bacteroidetes	<i>Alistipes onderdonkii</i>	97.1
			7	6	3	3	0	0	Bacteroidetes	<i>Bacteroides uniformis</i>	100
			155	5	0	5	0	0	Firmicutes	<i>Desulfotomaculum guttoideum</i>	96.8
			24	5	0	4	0	0	Firmicutes	<i>Dorea formicigenerans</i>	100
			47	5	0	5	0	0	Firmicutes	<i>Clostridium lactatifermentans</i>	95.2
			20	4	2	2	0	0	Firmicutes	<i>Gemmiger formicilis</i>	99.8
			63	4	0	4	0	0	Actinobacteria	<i>Collinsella aerofaciens</i>	99
			9	4	2	0	2	0	Firmicutes	<i>Blautia wexlerae</i>	99.8
			98	4	0	3	1	0	Firmicutes	<i>Anaerostipes butyraticus</i>	97.6
			166	3	0	3	0	0	Firmicutes	<i>Blautia luti</i>	98.6
			204	3	1	2	0	0	Bacteroidetes	<i>Bacteroides dorei</i>	98.4
			53	3	0	2	1	0	Proteobacteria	<i>Sutterella wadsworthensis</i>	100
			74	3	0	3	0	0	Firmicutes	<i>Clostridium leptum</i>	95.2
			129	2	0	2	0	0	Firmicutes	<i>Ruminococcus schinkii</i>	96.7
			177	2	0	2	0	0	Bacteroidetes	<i>Bacteroides dorei</i>	98.6
			31	2	0	0	1	1	Proteobacteria	<i>Escherichia/Shigella flexneri</i>	99.8
			49	2	0	2	0	0	Firmicutes	<i>Roseburia inulinivorans</i>	99.6
			54	2	0	2	0	0	Firmicutes	<i>Clostridium orbiscindens</i>	95.9
			78	2	0	2	0	0	Firmicutes	<i>Ruminococcus lactaris</i>	96.1
			138	1	0	1	0	0	Bacteroidetes	<i>Alistipes shahii</i>	99.8
			19	1	0	0	1	0	Firmicutes	<i>Ruminococcus albus</i>	95.7
			229	1	0	0	0	0	Firmicutes	<i>Ruminococcus torques</i>	97.6
			327	1	0	1	0	0	Bacteroidetes	<i>Bacteroides nordii</i>	99.5
			80	1	0	1	0	0	Firmicutes	<i>Eubacterium ramulus</i>	99.8
			99	1	0	1	0	0	Firmicutes	<i>Clostridium asparagiforme</i>	95.6
ND	ND		169	8	0	7	1	0	Firmicutes	<i>Ruminococcus obeum</i>	99.8
ND	ND		10	6	1	5	0	0	Firmicutes	<i>Clostridium nexile</i>	99.8

ND	ND	151	4	0	3	1	0	Firmicutes	<i>Ruminococcus obeum</i>	100
ND	ND	123	3	0	3	0	0	Firmicutes	<i>Clostridium hylemonae</i>	97.5
ND	ND	46	2	0	2	0	0	Firmicutes	<i>Blautia hansenii</i>	99.8
ND	ND	59	2	0	0	2	0	Firmicutes	<i>Faecalibacterium prausnitzii</i>	98.8

Supp. Table 5: OTU correlation network composition deduced from patients with endoscopic recurrence 6 months after ICR

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 ($R \geq 0.75$) between the identified OTU and other OTUs from the cluster; pos50: number of significant positive correlations ($R \geq 0.50$) between the identified OTU and other OTUs from the cluster; neg50: number of significant negative correlations ($R \leq -0.5$) 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 $R \leq -0.75$ was observed.