

**Table S4 Taxonomic annotations of identified fifty-two significant and important OTUs**

Name	Top-hit taxon	Similarity (%)	Top-hit taxonomy	Strain and sequence
OTU_4	AB606363_s	98.84	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	Uncultured bacterium; partial sequence
OTU_2430	AB606363_s	96.53	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	Uncultured bacterium; partial sequence
OTU_2488	AB606363_s	96.99	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	Uncultured bacterium; partial sequence
OTU_53	JQ084467_s	99.77	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	Uncultured bacterium; partial sequence
OTU_15	FJ881211_s	98.15	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	Uncultured bacterium; partial sequence
OTU_356	EU506196_s	99.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;AB606282_g	Uncultured bacterium; partial sequence
OTU_25	DQ815300_s	98.6	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;AB606282_g	Uncultured bacterium; partial sequence
OTU_564	EF603862_s	97	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Pseudoflavonifractor	Uncultured bacterium; partial sequence
OTU_152	EU509811_s	99.54	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Pseudoflavonifractor	Uncultured bacterium; partial sequence
OTU_24	JQ083832_s	99.08	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Pseudoflavonifractor	Uncultured bacterium; partial sequence
OTU_1212	KI535319_s	97	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Pseudoflavonifractor	Uncultured bacterium; partial sequence
OTU_33	KE159677_s	99.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	Uncultured bacterium; partial sequence
OTU_30	AB606395_s	98.84	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;EU006213_g	Uncultured bacterium; partial sequence
OTU_58	EU507468_s	99.53	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Acetatifactor	Uncultured bacterium; partial sequence
OTU_40	EU006478_s	98.61	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Acetatifactor	Uncultured bacterium; partial sequence
OTU_77	EF098689_s	98.84	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;JQ084490_g	Uncultured bacterium; partial sequence
OTU_1	KE159600_s	99.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;KE159600_g	Uncultured bacterium; partial sequence
OTU_6	EU506257_s	99.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;KE159600_g	Uncultured bacterium; partial sequence
OTU_27	EF603866_s	98.85	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Clostridium_g7	Uncultured bacterium; partial sequence
OTU_26	Alistipes timonensis	97.56	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Alistipes timonensis JC136; whole genome sequence
OTU_2850	Alistipes timonensis	95.11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Alistipes timonensis JC136; whole genome sequence
OTU_1682	Alistipes timonensis	95.11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Alistipes timonensis JC136; whole genome sequence
OTU_20	Alistipes inops	98.89	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Alistipes inops strain 627; whole genome sequence
OTU_3	EF603419_s	99.11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Uncultured bacterium; partial sequence
OTU_2812	EF603419_s	96.89	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Uncultured bacterium; partial sequence
OTU_12	PAC000670_s	99.11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella	Uncultured bacterium; partial sequence
OTU_23	EU791148_s	98.89	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;HM630235_g	Uncultured bacterium; partial sequence
OTU_18	JQ085186_s	98.9	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Bilophila	Uncultured bacterium; partial sequence
OTU_29	EF406368_s	99.11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;S24-7_f;HM124247_g	Uncultured bacterium; partial sequence
OTU_44	GQ157662_s	99.33	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;S24-7_f;Muribaculum	Uncultured bacterium; partial sequence
OTU_2	AB626927_s	98	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;S24-7_f;AB626927_g	Uncultured bacterium; partial sequence
OTU_3035	AB626927_s	95.78	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;S24-7_f;AB626927_g	Uncultured bacterium; partial sequence
OTU_32	Bacteroides vulgatus	98.67	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	Bacteroides vulgatus ATCC 8482; whole genome sequence
OTU_2325	Bacteroides vulgatus	97.33	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	Bacteroides vulgatus ATCC 8483; whole genome sequence
OTU_875	Bacteroides vulgatus	97.33	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	Bacteroides vulgatus ATCC 8484; whole genome sequence
OTU_2583	Bacteroides dorei	96.89	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	Bacteroides dorei DSM 17855; whole genome sequence
OTU_922	Bacteroides oleiciplenus	97.56	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	Bacteroides oleiciplenus YIT 12058; whole genome sequence
OTU_96	GQ867375_s	92.48	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Alloprevotella	Uncultured bacterium; partial sequence
OTU_48	Alistipes putredinis	96	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Alistipes putredinis DSM 17216; whole genome sequence
OTU_61	DQ815748_s	97.56	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	Uncultured bacterium; partial sequence
OTU_5	HM124297_s	97.67	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Acetatifactor	Uncultured bacterium; partial sequence
OTU_45	AB606330_s	99.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;KE159538_g	Uncultured bacterium; partial sequence
OTU_98	EU511963_s	99.11	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;AY994025_g	Uncultured bacterium; partial sequence
OTU_84	EU457259_s	99.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	Uncultured bacterium; partial sequence
OTU_41	KE159810_s	99.53	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;KE159810_g	Uncultured bacterium; partial sequence
OTU_67	Faecalibaculum rodentium	99.56	Bacteria;Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Faecalibaculum	Faecalibaculum rodentium strain A1017; whole genome sequence
OTU_110	EF603857_s	99.56	Bacteria;Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;ASTB_g	Uncultured bacterium; partial sequence
OTU_125	FJ676605_s	94.95	Bacteria;Tenericutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_g2	Uncultured bacterium; partial sequence
OTU_7	PAC000701_s	99.11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Odoribacteraceae;Odoribacter	Uncultured bacterium; partial sequence
OTU_38	FJ879254_s	98.67	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Parabacteroides	Uncultured bacterium; partial sequence
OTU_42	DQ905725_s	98.6	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eubacterium_g4	Uncultured bacterium; partial sequence
OTU_43	AB606259_s	97.93	Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;GQ422712_g	Uncultured bacterium; partial sequence