

Supplementary Table 8 Spearman's correlations between targeted urinary urolithins and microbiota.

	Urolithin-A-glucuronide	Urolithin-B-glucuronide	Urolithin-C-glucuronide	Total Urolithins (A+B+C)	Family level	Taxonomy
Bifidobacterium adolescentis_msp_0263	-0.18	-0.09	-0.16	-0.18	<i>Bifidobacteriaceae</i>	Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium adolescentis
Bifidobacterium bifidum_msp_0419	-0.12	-0.2	-0.08	-0.13	<i>Bifidobacteriaceae</i>	Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium bifidum
Collinsella aerofaciens_msp_1244	-0.15	-0.06	-0.04	-0.18	<i>Coriobacteriaceae</i>	Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella; Collinsella aerofaciens
unclassified Adlercreutzia_msp_0396	0.09	0.01	0.16	0.12	<i>Eggerthellaceae</i>	Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; Adlercreutzia; unclassified Adlercreutzia
Eggerthella lenta_msp_0573	0.03	-0.15	0.08	0.03	<i>Eggerthellaceae</i>	Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; Eggerthella; Eggerthella lenta
Gordonibacter urolithinifaciens_msp_1339	0.19	-0.05	0.18	0.19	<i>Eggerthellaceae</i>	Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; Gordonibacter; Gordonibacter urolithinifaciens
Bacteroides cellulosilyticus_msp_0003	0.12	0.11	0.15	0.15	<i>Bacteroidaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; Bacteroides cellulosilyticus
Bacteroides dorei_msp_0035	0.12	0.23	0.14	0.19	<i>Bacteroidaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; Bacteroides dorei
Bacteroides faecis_msp_0019	0.09	-0.11	0.15	0.07	<i>Bacteroidaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; Bacteroides faecis
Bacteroides salyersiae_msp_0037	0.17	0.11	0.05	0.17	<i>Bacteroidaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; Bacteroides salyersiae
Bacteroides sp. CAG:144_msp_0412	0.2	0.26	0.15	0.24	<i>Bacteroidaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; Bacteroides sp. CAG:144
Coprobacter secundus == Gabonia massiliensis_msp_0198	0.2	0.13	0.14	0.2	<i>Barnesiellaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Barnesiellaceae; Coprobacter; Coprobacter secundus == Gabonia massiliensis
Alistipes inops == Tidjanibacter massiliensis_msp_0230	0.05	-0.17	0	-0.02	<i>Rikenellaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae; Alistipes; Alistipes inops == Tidjanibacter massiliensis
Alistipes obesi_msp_0225	0.1	0.23	0.08	0.16	<i>Rikenellaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae; Alistipes; Alistipes obesi
Alistipes senegalensis_msp_0381	0.11	0.16	0.02	0.11	<i>Rikenellaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae; Alistipes; Alistipes senegalensis
Parabacteroides goldsteinii_msp_0028	0.2	0.06	0.14	0.17	<i>Tannerellaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Tannerellaceae; Parabacteroides; Parabacteroides goldsteinii
Parabacteroides merdae_msp_0027	-0.02	-0.15	-0.05	-0.09	<i>Tannerellaceae</i>	Bacteroidetes; Bacteroidia; Bacteroidales; Tannerellaceae; Parabacteroides; Parabacteroides merdae
Streptococcus thermophilus_msp_0833	-0.16	-0.06	-0.23	-0.16	<i>Streptococcaceae</i>	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus thermophilus
Butyricoccus sp. 2789STDY5834927 / Clostridia bacterium UC5.1-1D1_msp_1381	-0.06	-0.17	-0.03	-0.05	<i>Clostridiaceae</i>	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Butyricoccus; Butyricoccus sp. 2789STDY5834927 / Clostridia bacterium UC5.1-1D1
Clostridium saudense_msp_0362	-0.15	-0.17	-0.07	-0.17	<i>Clostridiaceae</i>	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; Clostridium saudense
Clostridium sp. 2789STDY5608831_msp_1608c	-0.11	0.16	-0.03	-0.02	<i>Clostridiaceae</i>	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; Clostridium sp. 2789STDY5608831
Clostridium sp. AT4_msp_0066	-0.14	-0.14	-0.14	-0.17	<i>Clostridiaceae</i>	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; Clostridium sp. AT4
unclassified Clostridium_msp_0563	0.19	-0.02	0.12	0.13	<i>Clostridiaceae</i>	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; unclassified Clostridium
Eubacterium eligens_msp_0029	0.18	0.2	0.25	0.26	<i>Eubacteriaceae</i>	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium; Eubacterium eligens

Eubacterium sp. 36_13 & CAG:86_msp_0227	0.19	0.14	0.24	0.24	<i>Eubacteriaceae</i>	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium; Eubacterium sp. 36_13 & CAG:86
Eubacterium sp. CAG:115_msp_0047	0.21	0.06	0.16	0.22	<i>Eubacteriaceae</i>	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium; Eubacterium sp. CAG:115
Eubacterium sp. CAG:180_msp_0271	-0.19	-0.05	-0.13	-0.18	<i>Eubacteriaceae</i>	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium; Eubacterium sp. CAG:180
Eubacterium sp. CAG:248_msp_0161	-0.02	-0.01	-0.15	-0.05	<i>Eubacteriaceae</i>	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium; Eubacterium sp. CAG:248
Blautia massiliensis_msp_0141	-0.18	-0.2	-0.13	-0.21	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Blautia massiliensis
Blautia obeum_msp_0436	0.02	0.15	0.04	0.06	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Blautia obeum
Blautia sp. CAG:237_msp_0189	0.21	-0.03	0.19	0.19	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Blautia sp. CAG:237
Blautia sp. CAG:257_msp_0052	-0.19	-0.15	-0.15	-0.24	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Blautia sp. CAG:257
Blautia sp. Marseille-P3087 / Ruminococcus sp. 2789STDY5608882_msp_0722	-0.16	-0.08	-0.01	-0.14	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Blautia sp. Marseille-P3087 / Ruminococcus sp. 2789STDY5608882
Blautia wexlerae_msp_0076	-0.17	-0.25	-0.1	-0.21	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Blautia wexlerae
Ruminococcus gnavus_msp_0058	-0.2	-0.21	-0.24	-0.26	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Ruminococcus gnavus
Ruminococcus sp. CAG:60 / Blautia sp. 2789STDY5608836_msp_0244	0.23	0.09	0.15	0.19	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Ruminococcus sp. CAG:60 / Blautia sp. 2789STDY5608836
Ruminococcus torques_msp_0126	-0.13	-0.17	-0.15	-0.15	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; Ruminococcus torques
unclassified Blautia_msp_0756	0.14	0.23	0.15	0.16	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; unclassified Blautia
unclassified Blautia_msp_1385	0	0.15	-0.04	0.04	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; unclassified Blautia
Coprococcus catus_msp_0986	-0.01	0.01	0.19	0	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus; Coprococcus catus
Coprococcus comes_msp_0259	-0.2	-0.03	-0.12	-0.15	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus; Coprococcus comes
Coprococcus eutactus 2_msp_0042	0.13	0.16	0.03	0.14	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus; Coprococcus eutactus 2
Dorea formicigenerans_msp_0506	-0.22	-0.15	-0.04	-0.22	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea; Dorea formicigenerans
Dorea longicatena 1_msp_0307	-0.24	-0.03	-0.06	-0.19	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea; Dorea longicatena 1
Eisenbergiella tayi_msp_0014	-0.2	-0.09	0	-0.16	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Eisenbergiella; Eisenbergiella tayi
Clostridium asparagiforme == lavalense_msp_0360	0.09	-0.24	0.04	0.04	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; Clostridium asparagiforme == lavalense
Clostridium bolteae_msp_0009	-0.04	-0.26	-0.02	-0.07	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; Clostridium bolteae
Clostridium clostridioforme 1_msp_0020	-0.09	-0.09	-0.15	-0.08	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; Clostridium clostridioforme 1
Clostridium glycyrrhizinilyticum_msp_0510	-0.16	-0.14	-0.12	-0.2	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; Clostridium glycyrrhizinilyticum
Clostridium symbiosum_msp_0086	-0.01	-0.17	-0.08	-0.05	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; Clostridium symbiosum
unclassified Lachnoclostridium_msp_0049	0.22	-0.06	0.03	0.18	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; unclassified Lachnoclostridium

Lachnospira sp. 2789STDY5834967 / Clostridiales bacterium KLE1615 & 41_12_two_minus_msp_0572	0.15	0.09	0.23	0.19	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira; Lachnospira sp. 2789STDY5834967 / Clostridiales bacterium KLE1615 & 41_12_two_minus
Roseburia faecis_msp_0015	0.15	-0.03	0.11	0.17	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; Roseburia faecis
Roseburia hominis_msp_0071	0.19	0.12	0.27	0.21	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; Roseburia hominis
Roseburia intestinalis_msp_0017	0.19	-0.06	0.13	0.19	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; Roseburia intestinalis
Roseburia sp. CAG:45 & sp. 2789STDY5608886_msp_0057	0.24	-0.02	0.16	0.23	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; Roseburia sp. CAG:45 & sp. 2789STDY5608886
Coprococcus sp. 2789STDY5608819 / Clostridium sp. CAG:264_msp_0133	0.11	0.16	0.05	0.14	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; Coprococcus sp. 2789STDY5608819 / Clostridium sp. CAG:264
Lachnospiraceae bacterium TF01-11 / Clostridium sp. CAG:122_msp_0175	0.14	0.16	0.14	0.17	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; Lachnospiraceae bacterium TF01-11 / Clostridium sp. CAG:122
unclassified Lachnospiraceae_msp_0254	-0.17	-0.14	-0.14	-0.21	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; unclassified Lachnospiraceae
unclassified Lachnospiraceae_msp_0296	0.32	0.2	0.26	0.35	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; unclassified Lachnospiraceae
unclassified Lachnospiraceae_msp_0780	0.1	0.14	0.16	0.12	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; unclassified Lachnospiraceae
unclassified Lachnospiraceae_msp_0930	0.13	0.02	0.2	0.11	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; unclassified Lachnospiraceae
unclassified Lachnospiraceae_msp_1641	0.18	0.03	0.12	0.15	<i>Lachnospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae; unclassified Lachnospiraceae
Oscillibacter sp. 57_20_msp_0903	0.07	0.19	0.21	0.12	<i>Oscillospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; Oscillibacter; Oscillibacter sp. 57_20
Oscillibacter sp. ER4 / Firmicutes bacterium CAG:129_59_24_msp_0763	0.07	0.17	0.16	0.08	<i>Oscillospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; Oscillibacter; Oscillibacter sp. ER4 / Firmicutes bacterium CAG:129_59_24
unclassified Oscillibacter_msp_1062	-0.02	0.31	-0.02	0.02	<i>Oscillospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; Oscillibacter; unclassified Oscillibacter
unclassified Oscillibacter_msp_1143	0.05	0.18	0.05	0.11	<i>Oscillospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; Oscillibacter; unclassified Oscillibacter
Firmicutes bacterium CAG:129_msp_0777	0.18	0.09	0.14	0.18	<i>Oscillospiraceae</i>	Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; unclassified Oscillospiraceae; Firmicutes bacterium CAG:129
Intestinibacter bartlettii_msp_0621	-0.24	-0.04	-0.1	-0.23	<i>Peptostreptococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae; Intestinibacter; Intestinibacter bartlettii
Faecalibacterium prausnitzii 3 (L2-6)_msp_0388	0.1	0.08	0.21	0.15	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium prausnitzii 3 (L2-6)
Faecalibacterium prausnitzii 4 (cf. KLE1255)_msp_0389	0.02	-0.16	-0.05	-0.01	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium prausnitzii 4 (cf. KLE1255)
Faecalibacterium prausnitzii 5_msp_0399	0.09	0.34	-0.06	0.11	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium prausnitzii 5
Faecalibacterium prausnitzii 6_msp_0639	0.18	0.1	0.09	0.15	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium prausnitzii 6
Faecalibacterium prausnitzii 7_msp_0324	-0.14	-0.1	0	-0.15	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium prausnitzii 7
Faecalibacterium sp. CAG:74_msp_0034	0.28	0.21	0.18	0.29	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium sp. CAG:74
Faecalibacterium sp. CAG:82_msp_0457	0.09	0.08	0.2	0.09	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; Faecalibacterium sp. CAG:82
unclassified Faecalibacterium_msp_0265	0.13	0.18	-0.03	0.14	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; unclassified Faecalibacterium

Gemmiger formicilis_msp_0374	-0.07	-0.19	-0.09	-0.12	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Gemmiger; Gemmiger formicilis
unclassified Gemmiger_msp_0456	0.16	0.01	0.1	0.15	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Gemmiger; unclassified Gemmiger
Phocea massiliensis_msp_1724	-0.16	-0.13	-0.12	-0.19	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Phocea; Phocea massiliensis
Eubacterium siraeum_msp_0053	0.06	0.07	0.14	0.15	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminiclostridium; Eubacterium siraeum
Ruminococcus bicirculans_msp_0013	0.2	0.1	0.12	0.2	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; Ruminococcus bicirculans
Ruminococcus bromii_2_msp_0045	0.09	-0.19	0.04	0.03	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; Ruminococcus bromii 2
Ruminococcus faecis_msp_0152	-0.15	-0.02	-0.06	-0.13	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; Ruminococcus faecis
Ruminococcus lactaris_msp_0250	0.06	0.25	0.03	0.1	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; Ruminococcus lactaris
Ruminococcus sp. 2789STDY5608794 & sp. 2789STDY5834890 / Firmicutes bacterium CAG:56_msp_0164	0.1	0.2	0.17	0.16	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; Ruminococcus sp. 2789STDY5608794 & sp. 2789STDY5834890 / Firmicutes bacterium CAG:56
Ruminococcus sp. JC304_msp_1643c	0.15	0.15	0.19	0.16	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; Ruminococcus sp. JC304
unclassified Ruminococcaceae_msp_0124	0.09	-0.04	0.19	0.08	<i>Ruminococcaceae</i>	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; unclassified Ruminococcaceae; unclassified Ruminococcaceae
Flavonifractor plautii_msp_0213	-0.2	-0.15	-0.18	-0.22	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Flavonifractor; Flavonifractor plautii
unclassified Flavonifractor_msp_1323	0	0.15	0.01	0.05	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Flavonifractor; unclassified Flavonifractor
Clostridium sp. 2789STDY5608793_msp_1622	0.09	0.3	-0.02	0.09	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. 2789STDY5608793
Clostridium sp. 2789STDY5608884_msp_0373	0.11	0.22	0.03	0.12	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. 2789STDY5608884
Clostridium sp. 2789STDY5834874 & sp. 2789STDY5608885_msp_0473c	0.09	0.06	0.14	0.12	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. 2789STDY5834874 & sp. 2789STDY5608885
Clostridium sp. 2789STDY5834924_msp_0906	0.23	0.18	0.33	0.27	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. 2789STDY5834924
Clostridium sp. 42_12 & CAG:75_msp_0194	0.14	0.01	0.18	0.14	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. 42_12 & CAG:75
Clostridium sp. CAG:138_msp_0144	0.22	0.01	0.14	0.17	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:138
Clostridium sp. CAG:169_msp_0357	-0.18	-0.17	-0.01	-0.17	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:169
Clostridium sp. CAG:217_msp_0285	0.11	0.02	0.27	0.16	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:217
Clostridium sp. CAG:245_msp_0546	0.05	0.23	0.14	0.18	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:245
Clostridium sp. CAG:343_msp_0586	0.21	0.02	0.17	0.25	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:343
Clostridium sp. CAG:58_msp_0129	-0.15	-0.23	-0.06	-0.18	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:58
Clostridium sp. CAG:62_msp_0093	0.28	0.22	0.34	0.33	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:62
Clostridium sp. CAG:91 & sp. 2789STDY5834873_msp_0075	0.21	0.06	0.17	0.23	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. CAG:91 & sp. 2789STDY5834873
Clostridium sp. KLE 1755 & Clostridiales bacterium VE202-27_msp_0018	0.12	-0.05	0.18	0.13	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; Clostridium sp. KLE 1755 & Clostridiales bacterium VE202-27

unclassified Clostridiales_msp_0056	-0.13	-0.16	-0.16	-0.15	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0317	-0.15	-0.07	-0.07	-0.13	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0424	0.24	0.14	0.24	0.23	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0480	0.19	0.08	0.16	0.18	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0591	-0.15	-0.13	-0.16	-0.17	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0665	0.11	0.21	0.17	0.18	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0761	0.22	0.18	0.06	0.19	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0820	0.14	0.16	0.22	0.18	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_0931	0.11	0.18	-0.1	0.08	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_1428	0.18	0.17	0.13	0.21	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
unclassified Clostridiales_msp_1533	0.06	0.21	-0.03	0.05	<i>unclassified Clostridiales</i>	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; unclassified Clostridiales; unclassified Clostridiales
Clostridia bacterium UC5.1-2E3_msp_0647	0.15	-0.06	0.2	0.18	<i>unclassified Clostridia</i>	Firmicutes; Clostridia; unclassified Clostridia; unclassified Clostridia; unclassified Clostridia; Clostridia bacterium UC5.1-2E3
Clostridium innocuum_msp_0103	-0.06	-0.16	-0.21	-0.11	<i>Erysipelotrichaceae</i>	Firmicutes; Erysipelotrichia; Erysipelotrichales; Erysipelotrichaceae; Erysipelotrichaceae; Erysipelotrichaceae
Erysipelatoclostridium ramosum_msp_0153	0.02	-0.17	-0.06	-0.05	<i>Erysipelotrichaceae</i>	Firmicutes; Erysipelotrichia; Erysipelotrichales; Erysipelotrichaceae; Erysipelotrichaceae; Erysipelotrichaceae
Turicibacter sanguinis 2_msp_1308	-0.13	-0.04	-0.12	-0.18	<i>Erysipelotrichaceae</i>	Firmicutes; Erysipelotrichia; Erysipelotrichales; Erysipelotrichaceae; Turicibacter; Turicibacter sanguinis 2
Phascolarctobacterium sp. CAG:207_msp_0131	0.12	-0.16	0.02	0.04	<i>Acidaminococcaceae</i>	Firmicutes; Negativicutes; Acidaminococcales; Acidaminococcaceae; Phascolarctobacterium; Phascolarctobacterium sp. CAG:207
Dialister invisus_msp_0212	-0.06	-0.15	-0.03	-0.08	<i>Veillonellaceae</i>	Firmicutes; Negativicutes; Veillonellales; Veillonellaceae; Dialister; Dialister invisus
Dialister succinatiphilus_msp_0383	0.07	0.18	-0.09	0.05	<i>Veillonellaceae</i>	Firmicutes; Negativicutes; Veillonellales; Veillonellaceae; Dialister; Dialister succinatiphilus
Veillonella atypica_msp_0884	0.15	-0.06	0.06	0.13	<i>Veillonellaceae</i>	Firmicutes; Negativicutes; Veillonellales; Veillonellaceae; Veillonella; Veillonella atypica
Veillonella rogosae_msp_1219	0.18	0.01	0.17	0.13	<i>Veillonellaceae</i>	Firmicutes; Negativicutes; Veillonellales; Veillonellaceae; Veillonella; Veillonella rogosae
Firmicutes bacterium CAG:103_msp_0654	-0.02	0.03	0.15	-0.02	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; Firmicutes bacterium CAG:103
Firmicutes bacterium CAG:124_msp_0205	0.12	0.1	0.22	0.13	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; Firmicutes bacterium CAG:124
Firmicutes bacterium CAG:212 / Clostridium sp. 2789STDY5834871_msp_0581	-0.16	0.01	0.02	-0.09	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; Firmicutes bacterium CAG:212 / Clostridium sp. 2789STDY5834871
Firmicutes bacterium CAG:41 / Clostridium sp. 2789STDY5834935 & sp. 2789STDY5608853_msp_0468	0.17	0.04	0.23	0.2	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; Firmicutes bacterium CAG:41 / Clostridium sp. 2789STDY5834935 & sp. 2789STDY5608853
Firmicutes bacterium CAG:95_msp_0060	0.23	0.19	0.05	0.21	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; Firmicutes bacterium CAG:95
unclassified Firmicutes_msp_0404	0.16	0.16	0.05	0.16	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes

unclassified Firmicutes_msp_0425	0.09	-0.16	0.07	0.04	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_0596	0.16	0.13	0.12	0.16	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_0622	0.13	0.09	0.25	0.17	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_0679	0.21	0.15	0.1	0.21	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_0723	0.07	0.16	-0.02	0.05	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_0874	0.17	0.18	0.05	0.2	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_1302	0.17	0.22	0.19	0.21	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
unclassified Firmicutes_msp_1342	0.09	0.23	-0.03	0.12	<i>unclassified Firmicutes</i>	Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes; unclassified Firmicutes
Parasutterella excrementihominis_msp_0145	0.23	0.11	0.17	0.24	<i>Sutterellaceae</i>	Proteobacteria; Betaproteobacteria; Burkholderiales; Sutterellaceae; Parasutterella; Parasutterella excrementihominis
Bilophila wadsworthia_msp_0110	-0.16	-0.02	-0.1	-0.13	<i>Desulfovibrionaceae</i>	Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Bilophila; Bilophila wadsworthia
Acinetobacter sp. N54.MGS-139 / Proteobacteria bacterium CAG:139_msp_0202	0.15	0.03	-0.04	0.13	<i>Moraxellaceae</i>	Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter; Acinetobacter sp. N54.MGS-139 / Proteobacteria bacterium CAG:139
Akkermansia muciniphila_msp_0025	0.19	0.05	0.22	0.18	<i>Akkermansiaceae</i>	Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Akkermansiaceae; Akkermansia; Akkermansia muciniphila

Numbers in bold indicate significance at the FDR<0.05 level.