

Lowest Assigned Taxonomy	Taxonomic Level	No. of OTUs	<i>r</i>	FDR
<i>Ralstonia</i>	genus	1	0.91	<0.001
<i>Burkholderiales</i>	order	2	0.61 +/- 0.184	<0.001
<i>Oxalobacter formigenes</i>	species	6	0.61 +/- 0.051	<0.001
<i>Oxalobacteraceae</i>	family	25	0.58 +/- 0.069	<0.001-0.006
<i>Blautia producta</i>	species	1	0.49	<0.001
<i>Allobaculum</i>	genus	4	0.48 +/- 0.015	<0.001
<i>Sutterella</i>	genus	2	0.45 +/- 0.016	<0.001-0.019
<i>ML615J-28</i>	order	17	0.43 +/- 0.016	<0.001-0.009
<i>Roseburia</i>	genus	2	0.42 +/- 0.19	<0.001-0.013
<i>Odoribacter</i>	genus	11	0.42 +/- 0.019	<0.001-0.01
<i>RF39</i>	order	6	0.42 +/- 0.019	0.006-0.043
<i>Rikenellaceae</i>	family	25	0.42 +/- 0.008	<0.001-0.045
<i>Lachnospira</i>	genus	2	0.41 +/- 0.08	<0.001-0.005
<i>Elusimicrobiaceae</i>	family	6	0.41 +/- 0.046	<0.001-0.048
<i>S24-7</i>	family	940	0.39 +/- 0.003	<0.001-0.049
<i>Clostridium</i>	genus	5	0.38 +/- 0.042	<0.001-0.032
<i>Turicibacter</i>	genus	19	0.38 +/- 0.015	<0.001-0.02
<i>Unassigned</i>	NA	236	0.38 +/- 0.005	<0.001-0.049
<i>Clostridiales</i>	order	356	0.38 +/- 0.004	<0.001-0.05
<i>Ruminococcaceae</i>	family	128	0.38 +/- 0.007	<0.001-0.05
<i>Blautia</i>	genus	1	0.38	<0.001
<i>Butyrivibrio</i>	genus	1	0.38	<0.001
<i>Magibacteriaceae</i>	family	1	0.38	<0.001
<i>Bacilli</i>	class	5	0.37 +/- 0.046	<0.001-0.04
<i>Ruminococcus gnavus</i>	species	7	0.37 +/- 0.014	<0.001-0.003
<i>Clostridiaceae</i>	family	2	0.37 +/- 0.009	<0.001-0.001
<i>YS2</i>	order	62	0.37 +/- 0.009	<0.001-0.049
<i>Lachnospiraceae</i>	family	96	0.37 +/- 0.007	<0.001-0.049
<i>Acidobacteriaceae</i>	family	1	0.36	0.001
<i>Adlercreutzia</i>	genus	1	0.36	0.001
<i>Desulfotomaculum</i>	genus	1	0.36	0.001
<i>Streptococcaceae</i>	family	1	0.36	0.001
<i>Veillonella dispar</i>	species	1	0.36	0.001
<i>Erysipelatrichaceae</i>	family	2	0.35 +/- 0.037	<0.001-0.01
<i>Enterococcus</i>	genus	3	0.35 +/- 0.026	<0.001-0.006
<i>Bacteroidales</i>	order	4	0.35 +/- 0.019	<0.001-0.007
<i>Bacteroides caccae</i>	species	7	0.35 +/- 0.019	<0.001-0.016
<i>Oscillospira</i>	genus	42	0.35 +/- 0.017	<0.001-0.047
<i>Desulfovibrio</i>	genus	21	0.35 +/- 0.016	<0.001-0.042
<i>Ruminococcus</i>	genus	30	0.35 +/- 0.014	<0.001-0.045
<i>Lactobacillus reuteri</i>	species	3	0.35 +/- 0.012	<0.001-0.005
<i>Bacteroides</i>	genus	23	0.35 +/- 0.01	<0.001-0.027
<i>Ruminococcus flavefaciens</i>	species	33	0.35 +/- 0.01	<0.001-0.049
<i>Lactobacillus</i>	genus	52	0.35 +/- 0.007	<0.001-0.038
<i>Granulicatella</i>	genus	1	0.35	0.002
<i>Bacillales</i>	order	3	0.34 +/- 0.054	<0.001-0.03
<i>Bifidobacterium</i>	genus	8	0.34 +/- 0.024	<0.001-0.034
<i>Faecalibacterium prausnitzii</i>	species	2	0.34 +/- 0.017	0.001-0.005
<i>Coprococcus</i>	genus	13	0.34 +/- 0.012	<0.001-0.026
<i>Parabacteroides</i>	genus	4	0.33 +/- 0.036	<0.001-0.045
<i>Coriobacteriaceae</i>	family	4	0.33 +/- 0.02	0.001-0.034
<i>RF32</i>	order	3	0.33 +/- 0.001	0.005
<i>Anaerostipes</i>	genus	1	0.33	0.004
<i>Oxalobacter</i>	genus	1	0.33	0.005
<i>Lactobacillaceae</i>	family	3	0.32 +/- 0.022	0.001-0.019
<i>Streptococcus</i>	genus	15	0.32 +/- 0.006	0.001-0.034
<i>Barnesiellaceae</i>	family	1	0.32	0.008
<i>Collinsella aerofaciens</i>	species	4	0.31 +/- 0.075	0.006-0.019
<i>Bilophila</i>	genus	6	0.31 +/- 0.02	<0.001-0.05
<i>Lactobacillales</i>	order	2	0.31 +/- 0.016	0.006-0.02
<i>Actinomyces</i>	genus	2	0.30 +/- 0.03	0.003-0.039
<i>Bifidobacteriaceae</i>	family	1	0.30 +/- 0.03	0.014
<i>Parabacteroides distasonis</i>	species	1	0.30	0.013
<i>Akkermansia</i>	genus	2	0.29 +/- 0.03	0.006-0.05
<i>Coprobacillus</i>	genus	1	0.29 +/- 0.03	0.02
<i>Desulfovibrionaceae</i>	family	5	0.29 +/- 0.014	0.002-0.042
<i>Enterococcaceae</i>	family	1	0.29	0.014
<i>Acinetobacter</i>	genus	1	0.28	0.034
<i>Bifidobacterium pseudolongum</i>	species	1	0.28	0.034
<i>Enterobacteriaceae</i>	family	1	0.28	0.029
<i>Pediococcus</i>	genus	1	0.28	0.034
<i>S24-7</i>	family	4	-0.28 +/- 0.008	0.01-0.042

Table S1. Microbial OTUs (out of 32,927) exhibiting a positive significant Pearson's correlation with the relative abundance of *Oxalobacteraceae*.