

Appendix 1. Members of gut microbiome significantly correlated to fecal levels of indole-3-lactate (significance level = 3,  $p \leq 0.001$ ) in healthy individuals

№	Members of the gut microbial population	Spearman's rank correlation coefficient
1	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_1</i>	0.372
2	<i>f__Lachnospiraceae; g__Blautia; s__OTU_1</i>	0.369
3	<i>f__Lachnospiraceae; g__Lachnospiraceae_ND3007_group; s__OTU_2</i>	0.366
4	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_2</i>	0.362
5	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_3</i>	0.328
6	<i>f__Lachnospiraceae; g__Lachnospiraceae; s__OTU_1</i>	0.321
7	<i>f__Lachnospiraceae; g__OTU_1; s__OTU_1</i>	0.318
8	<i>f__Akkermansiaceae; g__Akkermansia; s__OTU_1</i>	0.315
9	<i>f__Lachnospiraceae; g__Lachnospiraceae_ND3007_group; s__OTU_1</i>	0.315
10	<i>f__Barnesiellaceae; g__Barnesiella; s__OTU_1</i>	0.312
11	<i>f__Lachnospiraceae; g__Lachnospiraceae_UCG-001; s__OTU_1</i>	0.306
12	<i>f__Lachnospiraceae; g__[Eubacterium]_hallii_group; s__OTU_1</i>	0.302
13	<i>f__Lachnospiraceae; g__Lachnospiraceae_UCG-010; s__OTU_5</i>	0.302
14	<i>f__Lachnospiraceae; g__Blautia; s__OTU_2</i>	0.302
15	<i>f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group; s__OTU_6</i>	0.297
16	<i>f__Lachnospiraceae; g__Fusicatenibacter; s__OTU_1</i>	0.296
17	<i>f__Monoglobaceae; g__Monoglobus; s__OTU_1</i>	0.295
18	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_4</i>	0.295
19	<i>f__Lachnospiraceae; g__Roseburia; s__OTU_1</i>	0.295
20	<i>f__Lachnospiraceae; g__Lachnospiraceae_ND3007_group; s__OTU_2</i>	0.293
21	<i>f__Tannerellaceae; g__Parabacteroides; s__OTU_1</i>	0.289
22	<i>f__Lachnospiraceae; g__Blautia; s__OTU_3</i>	0.289
23	<i>f__Bacteroidaceae; g__Bacteroides; s__OTU_1</i>	0.289
24	<i>f__Monoglobaceae; g__Monoglobus; s__OTU_2</i>	0.286
25	<i>f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group; s__OTU_7</i>	0.285
26	<i>f__Ruminococcaceae; g__Subdoligranulum; s__OTU_1</i>	0.285
27	<i>f__Pasteurellaceae; g__Haemophilus; s__OTU_1</i>	0.284
28	<i>f__Bacteroidaceae; g__Bacteroides; s__OTU_2</i>	0.283
29	<i>f__Monoglobaceae; g__Monoglobus; s__OTU_3</i>	0.282
30	<i>f__Lachnospiraceae; g__Blautia; s__OTU_4</i>	0.282
31	<i>f__Christensenellaceae; g__Christensenellaceae_R-7_group; s__OTU_1</i>	0.280
32	<i>f__Lachnospiraceae; g__Blautia; s__OTU_5</i>	0.280
33	<i>f__Bacteroidaceae; g__Bacteroides; s__OTU_2</i>	0.279
34	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_5</i>	0.278
35	<i>f__Lachnospiraceae; g__[Eubacterium]_eligens_group; s__OTU_1</i>	0.278
36	<i>f__Lachnospiraceae; g__Blautia; s__OTU_6</i>	0.276
37	<i>f__Lachnospiraceae; g__[Eubacterium]_hallii_group; s__OTU_2</i>	0.276
38	<i>f__Bacteroidaceae; g__Bacteroides; s__OTU_3</i>	0.276
39	<i>f__Lachnospiraceae; g__Anaerostipes; s__OTU_1</i>	0.275
40	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_6</i>	0.275
41	<i>f__Lachnospiraceae; g__Blautia; s__OTU_7</i>	0.275
42	<i>f__Ruminococcaceae; g__Faecalibacterium; s__OTU_7</i>	0.274
43	<i>f__Lachnospiraceae; g__Fusicatenibacter; s__OTU_2</i>	0.273
44	<i>f__Rikenellaceae; g__Alistipes; s__OTU_1</i>	0.273
45	<i>f__Lachnospiraceae; g__Lachnospiraceae_ND3007_group; s__OTU_3</i>	0.273
46	<i>f__Lachnospiraceae; g__OTU_1; s__OTU_1</i>	0.273
47	<i>f__Lachnospiraceae; g__[Ruminococcus]_torques_group; s__OTU_1</i>	0.272
48	<i>f__Lachnospiraceae; g__Fusicatenibacter; s__OTU_3</i>	0.270
49	<i>f__Bacteroidaceae; g__Bacteroides; s__OTU_4</i>	0.270
50	<i>f__Lachnospiraceae; g__Fusicatenibacter; s__OTU_4</i>	0.269
51	<i>f__Lachnospiraceae; g__Fusicatenibacter; s__OTU_5</i>	0.268
52	<i>f__Monoglobaceae; g__Monoglobus; s__OTU_4</i>	0.268
53	<i>f__Lachnospiraceae; g__Lachnospira; s__OTU_1</i>	0.268
54	<i>f__Lachnospiraceae; g__Lachnospiraceae_ND3007_group; s__OTU_4</i>	0.267