

## SUPPLEMENTAL MATERIALS

**Supplemental Table 1.** Abundances of mucosa-associated *Faecalibacterium prausnitzii* and its phylogroups, and the indices including *Escherichia coli* load in control subjects (H) and patients with irritable bowel syndrome (IBS), colorectal cancer (CRC), Ulcerative colitis (UC) and Crohn's disease (CD).

	n patients (samples)	FP <sup>1</sup>	PHGI <sup>1</sup>	PHGII <sup>1</sup>	FP-E <sup>2</sup>	PHGI-E <sup>2</sup>	PHGII-E <sup>2</sup>
<b>H</b>	<b>31(48)</b>	<b>5.28±0.58</b>	<b>3.36±0.87</b>	<b>2.98±1.51</b>	<b>0.19±0.19</b>	<b>-0.12±0.23</b>	<b>-0.18±0.31</b>
<b>IBS</b>	<b>10(19)</b>	<b>5.10±0.54</b>	<b>2.33±1.22</b>	<b>2.47±1.06</b>	<b>0.25±0.18</b>	<b>-0.21±0.22</b>	<b>-0.19±0.26</b>
<b>CRC</b>	<b>20(20)</b>	<b>4.39±0.58</b>	<b>2.42±0.91</b>	<b>2.39±1.14</b>	<b>-0.09±0.21</b>	<b>-0.42±0.38</b>	<b>-0.41±0.32</b>
<b>UC</b>	<b>25(50)</b>	<b>4.88±0.62</b>	<b>2.28±1.24</b>	<b>2.71±0.99</b>	<b>0.26±0.19</b>	<b>-0.16±0.29</b>	<b>-0.09±0.27</b>
<i>Location</i>							
Ulcerative proctitis (E1)	6(14)	5.11±0.29	2.81±0.38	3.19±0.43	0.33±0.08	-0.06±0.11	0.01±0.13
Distal UC (E2)	11(22)	4.75±0.59	2.41±1.15	2.58±0.93	0.28±0.24	-0.09±0.36	-0.06±0.33
Extensive UC or ulcerative pancolitis (E3)	6(10)	5.14±0.69	1.79±1.6	2.90±1.02	0.16±0.12	-0.37±0.19	-0.2±0.26
<b>CD</b>	<b>45(63)</b>	<b>4.18±1.34</b>	<b>1.21±1.65</b>	<b>1.75±1.47</b>	<b>0.004±0.29</b>	<b>-0.46±0.32</b>	<b>-0.39±0.32</b>
<i>Location</i>							
Ileal-CD (L1)	19(25)	3.55±1.42	0.59±1.33	1.49±1.54	-0.08±0.30	-0.51±0.29	-0.38±0.33
Colonic-CD (L2)	11(17)	4.79±1.07	1.50±1.71	2.00±1.51	0.06±0.23	-0.50±0.31	-0.42±0.32
Ileocolonic-CD (L3)	14(18)	4.23±1.12	1.44±1.72	1.53±1.12	0.01±0.32	-0.42±0.35	-0.42±0.32

<sup>1</sup> Mean log<sub>10</sub> 16S rRNA gene copies/million bacterial 16S rRNA gene copies±standard deviations

<sup>2</sup> Mean indices±standard deviations. Indices have been calculated following formulas depicted in methods section.

**Supplemental Table 2.** Abundances of faecal *Faecalibacterium prausnitzii* and its phylogroups, and the indices including *Escherichia coli* load in patients with Ulcerative colitis (UC) and Crohn’s disease (CD).

	n samples	FP <sup>1</sup>	PHGI <sup>1</sup>	PHGII <sup>1</sup>	FP-E <sup>2</sup>	PHGI-E <sup>2</sup>	PHGII-E <sup>2</sup>
<b>UC</b>	<b>10</b>	<b>4.83±1.97</b>	<b>3.81±2.71</b>	<b>3.17±2.71</b>	<b>1.23±0.58</b>	<b>0.98±0.64</b>	<b>0.80±0.50</b>
<i>Location</i>							
Distal UC (E2)	3	4.88±2.64	3.94±2.93	2.39±2.84	1.49±0.89	1.24±0.85	0.77±0.51
Extensive UC or ulcerative pancolitis (E3)	7	4.81±1.87	3.76±2.86	3.5±2.81	1.12±0.43	0.87±0.58	0.82±0.53
<b>CD</b>	<b>19</b>	<b>4.74±1.65</b>	<b>2.57±2.73</b>	<b>2.05±2.31</b>	<b>1.33±0.54</b>	<b>0.82±0.72</b>	<b>0.71±0.54</b>
<i>Location</i>							
Ileal-CD (L1)	10	4.03±1.60	2.82±2.41	2.02±1.18	0.56±0.90	0.65±0.69	0.69±0.47
Colonic-CD (L2)	3	4.87±0.85	-0.05±1.51	1.68±2.44	0.32±0.19	0.32±0.75	0.75±0.61
Ileocolonic-CD (L3)	6	5.85±1.55	3.48±3.22	3.05±1.47	0.58±1.02	0.86±0.72	0.72±0.70

<sup>1</sup> Mean log<sub>10</sub> 16S rRNA gene copies/million bacterial 16S rRNA gene copies±standard deviations

<sup>2</sup> Mean indices±standard deviations. Indices have been calculated following formulas depicted in methods section.