



**Supplementary Figure 1.** PCA model based on the results of gut microbiota profiling. Green dots represent data from UC patients, red dots from CD patients and blue dots from the control group

**Supplementary Table SI.** Statistically significant differences between study and control groups at species level

Group	Significantly increased species of bacteria
IBD	<i>Actinobacillus porcinus</i> , <i>Actinobacillus rossii</i> , <i>Bacteroides dorei</i> , <i>Bifidobacterium catenulatum</i> , <i>Escherichia coli</i> , <i>Fusobacterium nucleatum</i> , <i>Helicobacter suncus</i> , <i>Peptostreptococcus stomatis</i> , <i>Sutterella sanguinus</i> , <i>Sutterella wadsworthensis</i> , <i>Veillonella denticariosi</i> , <i>Veillonella parvula</i>
Control	<i>Actinomyces cardiffensis</i> , <i>Actinomyces naturae</i> , <i>Agromyces salentinus</i> , <i>Anaerobranca zavarzinii</i> , <i>Anaerofilum agile</i> , <i>Anaerofustis stercorihominis</i> , <i>Anoxybacillus ayderensis</i> , <i>Bifidobacterium angulatum</i> , <i>Bifidobacterium gallicum</i> , <i>Brevibacterium album</i> , <i>Caloramator mitchellensis</i> , <i>Candidatus Liberibacter africanus</i> , <i>Catonella morbi</i> , <i>Clostridium cadaveris</i> , <i>Clostridium cellulolyticum</i> , <i>Clostridium chartatabidum</i> , <i>Clostridium saccharoperbutylaceticum</i> , <i>Clostridium thermoalcaliphilum</i> , <i>Coprococcus catus</i> , <i>Cyanobacterium aponinum</i> , <i>Desulfonatronum thiosulfatophilum</i> , <i>Desulfonauticus autotrophicus</i> , <i>Desulfotomaculum indicum</i> , <i>Dethiobacter alkaliphilus</i> , <i>Eubacterium bifforme</i> , <i>Heliorestis baculata</i> , <i>Herbaspirillum chlorophenolicum</i> , <i>Lachnospira pectinoschiza</i> , <i>Lachnospira pectinoschiza</i> , <i>Lactococcus fujiensis</i> , <i>Leptospira licerasiae</i> , <i>Leuconostoc mesenteroides</i> , <i>Methanobrevibacter acididurans</i> , <i>Methanobrevibacter smithii</i> , <i>Mogibacterium neglectum</i> , <i>Muricauda lutimaris</i> , <i>Mycoplasma edwardii</i> , <i>Natronincola peptidivorans</i> , <i>Oxalobacter formigenes</i> , <i>Paenibacillus filicis</i> , <i>Peptoniphilus coxii</i> , <i>Peptoniphilus olsenii</i> , <i>Rikenella microfusus</i> , <i>Ruminococcus albus</i> , <i>Sarcina maxima</i> , <i>Sharpea azabuensis</i> , <i>Slackia faecicanis</i> , <i>Streptococcus gallinaceus</i> , <i>Tindallia magadiensis</i>

IBD – inflammatory bowel disease.

**Supplementary Table SII.** Demographic and clinical characteristic of IBD patients divided according to PCA analysis of gut microbiome

Characteristics	Group A (n = 11)	Group B (n = 7)	P-value
CD	6	3	NA
UC	5	4	NA
Age [years]	11 (8–16)	11 (12–16)	NS
ESR, median (range) [mm/h]	20 (6–63)	14 (5–68)	NS
CRP, median (range) [mg/l]	8.09 (0.51–156)	11.9 (0.45–150)	NS
WBC, median (range) [10 <sup>3</sup> /μl]	6.64 (5.66–11.6)	8.33 (6.08–18.93)	NS
PLT, median (range) [10 <sup>3</sup> /μl]	293 (200–554)	341 (245–494)	NS
Ferritin, median (range) [ng/ml]	35.2 (5.27–113.8)	50.8 (5.7–170.6)	NS
Albumin, median (range) [g/dl]	4.47 (3.52–4.91)	4.41 (2.78–4.74)	NS
fCal, median (range) [μg/g]	1552.6 (415–2551.6)	1997.4 (522–2497.5)	NS
PCDAI/PUCAI	30 (10–55)	30 (15–70)	NS
Mild*	6	1	NS
Moderate*	5	5	NS
Severe*	0	1	NA

CD – Crohn's disease, UC – ulcerative colitis, ESR – erythrocyte sedimentation rate, CRP – C-reactive protein, WBC – white blood count, PLT – platelet count, fCal – fecal calprotectin, PCDAI – Pediatric Crohn's Disease Activity Index, PUCAI – Pediatric Ulcerative Colitis Activity Index, NA – not applicable, \*according to PCDAI/PUCAI.