

Supplementary Table S1. Statistically significant differences in the gut microbiota of CD patients with different community types.

	mean±SD		P value (Kruskal-Wallis test)
	Community type I	Community type II	
Diversity			
N OTUs	1576.34±577.62	679.83±319.72	<0.001
Shannon's index	7.09±0.76	5.33±0.99	<0.001
Phylum (%)			
<i>Bacteroidetes</i>	22.60±15.96	14.86±19.21	0.002
<i>Fusobacteria</i>	0.03±0.15	1.42±3.13	0.016
<i>Proteobacteria</i>	3.43±4.13	13.96±15.23	<0.001
<i>Tenericutes</i>	0.22±0.66	0.01±0.06	<0.001
<i>Verrucomicrobia</i>	0.99±2.63	2.29±9.04	0.004
Family (%)			
<i>Corynebacteriaceae</i>	0.002±0.005	0.02±0.05	0.010
<i>Micrococcaceae</i>	0.01±0.02	0.08±0.14	<0.001
<i>Nocardiaceae</i>	0.00±0.00	0.002±0.01	0.021
<i>Coriobacteriaceae</i>	2.12±1.87	1.68±3.00	<0.001
<i>o__Bacteroidales;f__</i>	0.34±1.67	0.14±0.79	<0.001
<i>Bacteroidaceae</i>	13.86±12.46	10.42±15.41	0.002
<i>Porphyromonadaceae</i>	1.34±1.63	1.46±3.05	<0.001
<i>Prevotellaceae</i>	3.80±7.64	1.05±2.37	0.001
<i>Rikenellaceae</i>	1.49±1.82	0.54±1.05	<0.001
<i>[Barnesiellaceae]</i>	0.61±1.44	0.26±0.88	<0.001
<i>[Odoribacteraceae]</i>	0.33±0.46	0.26±0.53	0.001
<i>[Paraprevotellaceae]</i>	0.45±0.68	0.58±2.10	<0.001
<i>Bacillaceae</i>	0.01±0.01	0.04±0.10	0.001
<i>Staphylococcaceae</i>	0.01±0.03	0.01±0.03	0.006
<i>Gemellaceae</i>	0.01±0.03	0.06±0.16	0.016
<i>Aerococcaceae</i>	0.0002±0.001	0.003±0.01	0.017

<i>Carnobacteriaceae</i>	0.01±0.02	0.11±0.32	<0.001
<i>Enterococcaceae</i>	0.30±0.95	4.89±8.80	0.012
<i>Streptococcaceae</i>	2.86±4.15	8.10±13.92	0.024
<i>o__Clostridiales;Other</i>	1.06±1.16	0.30±0.46	<0.001
<i>o__Clostridiales;f__</i>	3.36±2.61	0.80±1.20	<0.001
<i>Christensenellaceae</i>	0.47±1.18	0.06±0.33	<0.001
<i>Dehalobacteriaceae</i>	0.01±0.01	0.002±0.01	<0.001
<i>Lachnospiraceae</i>	24.33±10.84	20.82±21.49	0.015
<i>Peptococcaceae</i>	0.05±0.14	0.001±0.002	<0.001
<i>Ruminococcaceae</i>	23.58±9.56	6.46±8.27	<0.001
<i>[Mogibacteriaceae]</i>	0.18±0.23	0.05±0.09	<0.001
<i>Erysipelotrichaceae</i>	2.85±2.82	1.90±3.08	0.001
<i>Leptotrichiaceae</i>	0.0001±0.001	0.07±0.41	0.013
<i>Victivallaceae</i>	0.01±0.03	0.002±0.01	0.021
<i>c__Alphaproteobacteria;o__RF32;f__</i>	0.12±0.34	0.03±0.11	<0.001
<i>Alcaligenaceae</i>	0.49±0.68	1.10±2.14	0.034
<i>Desulfovibrionaceae</i>	0.18±0.22	0.26±0.78	<0.001
<i>Enterobacteriaceae</i>	2.23±4.00	10.29±14.62	<0.001
<i>Legionellaceae</i>	0.00±0.00	0.002±0.01	0.021
<i>Halomonadaceae</i>	0.0002±0.001	0.001±0.004	0.049
<i>Pseudomonadaceae</i>	0.001±0.002	0.003±0.01	0.047
<i>Anaeroplasmataceae</i>	0.14±0.64	0.01±0.06	0.001
<i>[Cerasiococcaceae]</i>	0.02±0.09	0.0001±0.001	0.027
<i>Verrucomicrobiaceae</i>	0.97±2.63	2.29±9.04	0.010

Supplementary Table S2. Inclusion/exclusion criteria for CD patients and healthy subjects.

<p>Inclusion criteria for CD patients:</p> <ul style="list-style-type: none"> • m/f, 18-60 years old • CD diagnosis established by clinical and endoscopic evidence, corroborated by histopathological findings
<p>Exclusion criteria for CD patients:</p> <ul style="list-style-type: none"> • Presence of concomitant diseases/conditions which can lead to sufficient changes of the gut microbiota (e.g., oncological pathology, and prior GI surgery) • The subject has identified congenital or acquired immunodeficiency • Extensive colonic resection, or ≥ 3 small bowel resections, or short bowel syndrome. Ileostomy or colostomy • The subject has a history or evidence of colonic mucosal dysplasia • <i>C. difficile</i> infection or clinically significant infections, including viral hepatitis, tuberculosis, pneumonia • Intake of prebiotics or/and probiotics within 3 months prior to the visit for biosample collection; antibiotics within 6 months prior to the visit for biosample collection • Pregnancy or breastfeeding
<p>Inclusion criteria for healthy volunteers:</p> <ul style="list-style-type: none"> • m/f, 18-60 years old
<p>Exclusion criteria for healthy volunteers:</p> <ul style="list-style-type: none"> • Presence of concomitant diseases/conditions which can lead to sufficient changes of the gut microbiota (e.g., oncological pathology, and prior GI surgery) • Presence of chronic decompensated cardiovascular, respiratory, liver, kidney, or endocrine diseases • The subject has identified congenital or acquired immunodeficiency • <i>C. difficile</i> infection or clinically significant infections, including viral hepatitis, tuberculosis, pneumonia • Presence of diarrhea (stool frequency more than 3 times a day) within at least 3 consecutive days during the last month • Intake of prebiotics or/and probiotics within 3 months prior to the visit for biosample collection; antibiotics within 6 months prior to the visit for biosample collection • Pregnancy or breastfeeding

Supplementary Table S3. Studied SNPs

#	SNP	Gene	PCR primers
1	rs2241880 [110–112]	<i>ATG16L1</i>	5'-AGGAGACGCTCTGTCTCTTCC-3'
			5'-CACTTCTTTACCAGAACCAGGATG-3'
2	Rs9858542 [27–29]	<i>BSN</i>	5'-GGAGAGCGTGTTCTCCAAGAT-3'
			5'-CCAGTTGCAGGCAGTGCATA-3'
3	rs6908425 [113,114]	<i>CDKAL1</i>	5'-GGTGACACCCACAAAAGAAAAAGA-3'
			5'-TGCCCTAAGCTAGGGGTAC-3'
4	rs6596075 [115,116]	<i>IBD5</i>	5'-GACCTGAAGAGCTCTGCCTTCAAA-3'
			5'-TCACTGAGGTTCAAGTCACCAGC-3'
5	rs11805303 [117,118]	<i>IL23R</i>	5'-TGTATGCTTGCAAACAGAGAACT-3'
			5'-AGATTCCTCTTAGTCGGAGCTTTG-3'
6	rs1004819 [119–121]	<i>IL23R</i>	5'-CTGGATTGCACTGACCTGCT-3'
			5'-GCACAAGCATTCTAGGACCC-3'
7	rs10489629 [122,123]	<i>IL23R</i>	5'-AAGCTTGTTTGATTATGATGTCAGC-3'
			5'-GTCATGCCCAGTTTCCGCTT-3'
8	rs11209026 [111,124]	<i>IL23R</i>	5'-TGTCAATTCTTTCTTTGATTGGGAT-3'
			5'-AGAAATTCTGCAAAAACCTACCC-3'
9	rs2522057 [125]	<i>IRF1-AS1</i>	5'-TTCATTCATGTCCCTGACACA-3'
			5'-TGCTCACATCTGCCATCTCA-3'
10	rs13361189 [126,127]	<i>IRGM</i>	5'-TCTCTCCTCCAAGGCTCCTC-3'
			5'-CCCTTTCTAAACTGTACCCGC-3'
11	rs4958847 [128,129]	<i>IRGM</i>	5'-CCTCTCACTGGGAGAAGCTTTA-3'
			5'-TGCATCACAAATTTCTCCTGTTAGT-3'
12	rs2274910 [130]	<i>ITLN1</i>	5'-GGAGCCTTTAGGCCATGTCTC-3'
			5'-CAGTGCGGAGAAAATACAGGC-3'
13	Rs1793004 [33,97]	<i>NELL1</i>	5'-TGGATCAGGGCCACAATCTT-3'
			5'-TTATGAAGAACTGGGTTTCCAAGC-3'
14	rs2836878 [131–134]	<i>PSMG1</i>	5'-CCAGGCACAAGGACTCTTGA-3'
			5'-AGGCTGGGAGAGGAGATGAG-3'
15	rs1992662 [97]	<i>PTGER4</i>	5'-TGCACATTGTGAGCACACATAAA-3'

			5'-TGGTTTCCTTCTATACATATCCGT-3'
16	rs8111071 [135]	<i>RSPH6A</i>	5'-CACGCATGACCCTGCAATAC-3'
			5'-TCTGTTGAACCAATGAATGGATGG-3'
17	Rs2631367 [136–138]	<i>SLC22A5</i>	5'-CGCTCTGCCTGCCAGC-3'
			5'-GCGGCTGGCCTTACATAGG-3'
18	Rs3816769 [30,31]	<i>STAT3</i>	5'-GTCCACTGATAGGAAGATGACTCT-3'
			5'-CTGGTCTTGCAGGGAAGCTA-3'
19	rs7753394 [139,140]	<i>TNFAIP3</i>	5'-ATCTCTCACCCCTTCTCCTGAAAGA-3'
			5'-GCCCCACATGGTGTAATTTATGC-3'
20	rs1456893 [141]	intergen	5'-ATGTGCCTCTGACCATGACA-3'
			5'-TGCCATGACTAGCTTCTAGGT-3'
21	rs224136 [142,143]	intergen	5'-TAATAGGGCTGTTCACTGGA-3'
			5'-ATTCATCCAAGTGCCCAAGTGA-3'
22	rs6601764 [144]	intergen	5'-GGGGGAAGTAGAGAGTTGGAC-3'
			5'-GGAGCATTCAAGTGTGCTTACA-3'
23	rs7807268 [145,146]	intergen	5'-GGAAGGGTGATTTCTCCTGTT-3'
			5'-CCCTTCGCTACAGACATTGG-3'
24	rs12037606 [147,148]	intergen	5'-TGACAAGCTTTATCACAGCTGATT-3'
			5'-TGCCCTAAGCTAGGGGTTAC-3'