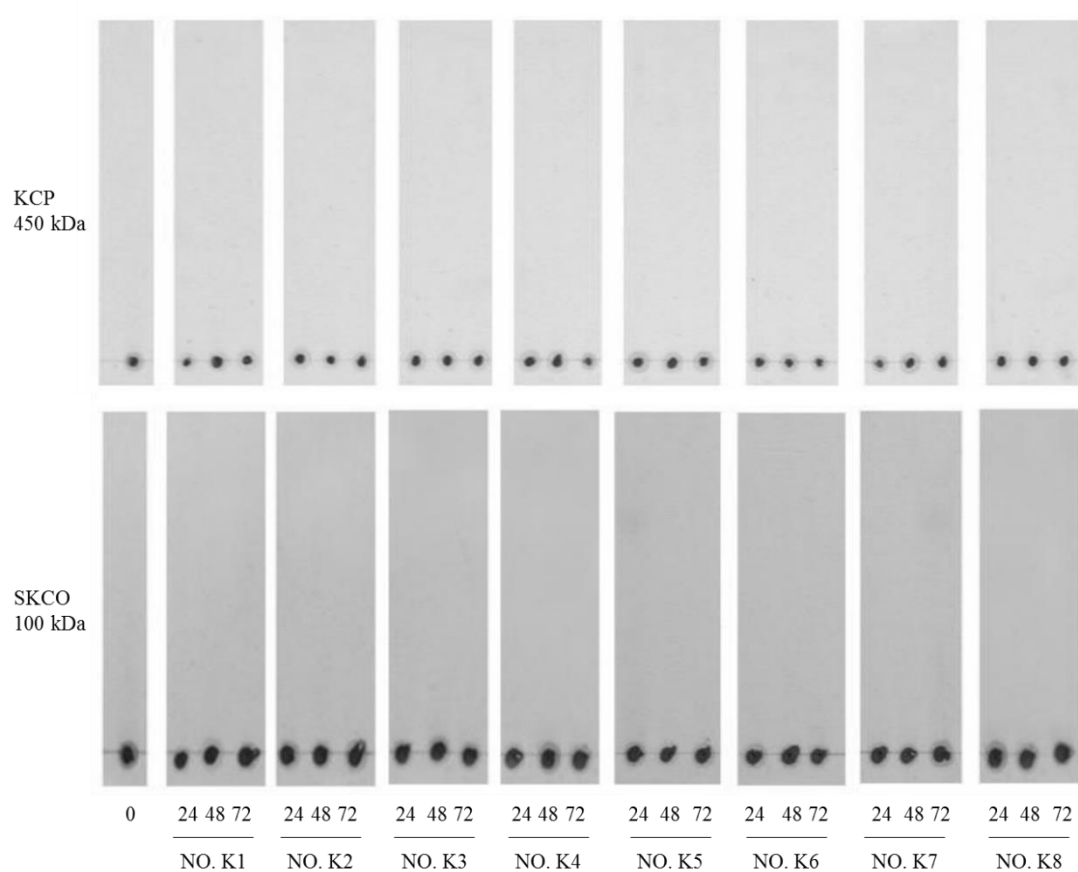


Supplementary Figure S1. The degradation of KCP and SKCO by different volunteers' fecal microbiota.

The degradation of KCP and SKCO by human gut microbiota was evaluated after fermenting 24, 48 and 72 hours in the batch chemostat system using TLC. NO. K1-NO. K8 represent fecal microbiota collected from these volunteers that were inoculated in the batch chemostat.



Supplementary Figure S2. BLAST analysis of two predicted CGN-degrading genes.

Two potential CGN-degrading genes were identified in *B.xylanisolvens* genome sequence, and were named as C0 and C1. A, BLAST results of C0. B, BLAST results of C1.

A

kappa-carrageenase precursor [Bacteroides ovatus]
Sequence ID: [KWR60852.1](#) Length: 346 Number of Matches: 1

Range 1: 45 to 341 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
236 bits(602)	4e-72	Compositional matrix adjust.	143/310(46%)	184/310(59%)	28/310(9%)	+1
Query 133	VVTPHTDPQLFEVVEQYTDFFNGTEIDKSKWNTPCR-PFATVSPSPDNVKQEDGMLNITI			309		
Sbjct 45	MCTPYNSDK-FEKQILYSCEFDGRG-FDTEYWENPKDDKFATWTFPPENVETRDGKLELKI			102		
Query 310	KGHEHDFSKAPPHYFQSGMLNSKGVITYGYFEARIKGAHVFRGTCFAFWLYSLFGDGKK			489		
Sbjct 103	K+++H + YF SGML SK KV YGI+EARIKGA V+ GTC AFWLY+ P + KYYKH--KRGTKDLYFTSGMLRSKSKVGYGYEARIKGADVWFGTCSAFWLYTFPSEIDN			160		
Query 490	IKPQKENTVVYNEIDIIELQQVFKDFHIMSCNHYHIMVLKFDGTFDGEKFTNKFHPQS			669		
Sbjct 161	+K N VVYNEID+IELQQVFK I+S N HI +L D N +P+ SWGKK-NDVVYNEIDVIELQQVFKSFKILSQNMHIWILDEDLKNQ-----IKAGQYFK-			213		
Query 670	MWGHNETVVDWDSRDDYHLYACENRFDSDIWIYIDNKRVASVPNYWHLGMYITLSMEPRT			849		
Sbjct 214	G NET V W+ DDYH+YA ENRPDS+++Y+DN EVAS PNY+WH+ MY+TIS+ RT -LGKNETTVSWNPEDDYHVYAVENRPDSVVVYVDNVRVASKPNYFHWMDMYLTLISLGLRT			272		
Query 850	PFEKWN-NGKRYPV---PTTKEQADAAG-----PFSTMKVDYIRTRRRKDYSPFK			987		
Sbjct 273	PFEK+ +G+R V K D G F S M VDYIR++R DY F+ PFEKYEADGQRLAVNPDGLDKSVLDNEGEFINPESPQRFTSVMYVDYIRSWKR-DYENFE			331		
Query 988	SSKREYNPD 1017					
Sbjct 332	SSKR + D SSKRAFTDED 341					

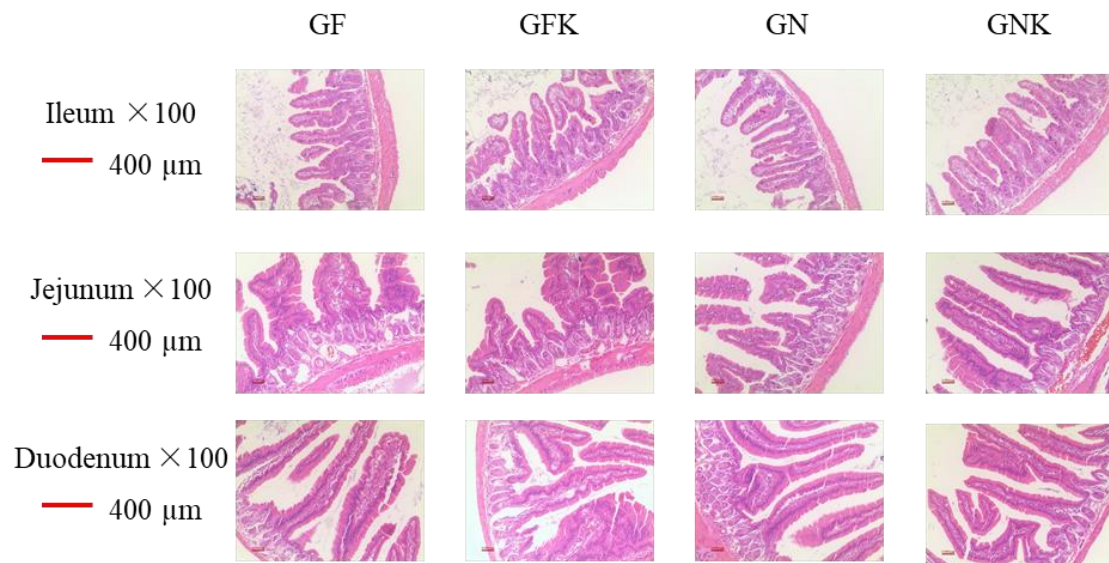
B

kappa-carrageenase precursor [Bacteroides ovatus]
Sequence ID: [KWR60852.1](#) Length: 346 Number of Matches: 1

Range 1: 38 to 346 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
642 bits(1655)	0.0	Compositional matrix adjust.	309/309(100%)	309/309(100%)	0/309(0%)	+1
Query 181	TDRVSPFMCTPYNSDKFEKQILYSCEFDGRGFDTEYWENPKDDKFATWTFPPENVETRDGK			360		
Sbjct 38	TDRVSPFMCTPYNSDKFEKQILYSCEFDGRGFDTEYWENPKDDKFATWTFPPENVETRDGK			97		
Query 361	LELKIKYKHKRGTCDLYFTSGMLRSKSKVGYGYEARIKGADVWFGTCSAFWLYTFPSE			540		
Sbjct 98	LELKIKYKHKRGTCDLYFTSGMLRSKSKVGYGYEARIKGADVWFGTCSAFWLYTFPSE			157		
Query 541	IDNSNGKENDVYNEIDVIELQQVFKSFKILSQNMHIWILDEDLKNQIKAGQYPKLGKN			720		
Sbjct 158	IDNSNGKENDVYNEIDVIELQQVFKSFKILSQNMHIWILDEDLKNQIKAGQYPKLGKN			217		
Query 721	ETTWSWNPEDDYHVYAVENRPDSVVVYVDNVRVASKPNYFHWMDMYLTLISLGLRTPFEKY			900		
Sbjct 218	ETTWSWNPEDDYHVYAVENRPDSVVVYVDNVRVASKPNYFHWMDMYLTLISLGLRTPFEKY			277		
Query 901	EADGQRLAVNPDGLDKSVLDNEGEFINPESPQRFTSVMYVDYIRSWKRDIENFESSKRAF			1080		
Sbjct 278	EADGQRLAVNPDGLDKSVLDNEGEFINPESPQRFTSVMYVDYIRSWKRDIENFESSKRAF			337		
Query 1081	TDEDKQRFK 1107					
Sbjct 338	TDEDKQRFK 346					

Figure S3. Pathological changes in the sections of duodenum, jejunum and ileum evaluated by H&E staining.



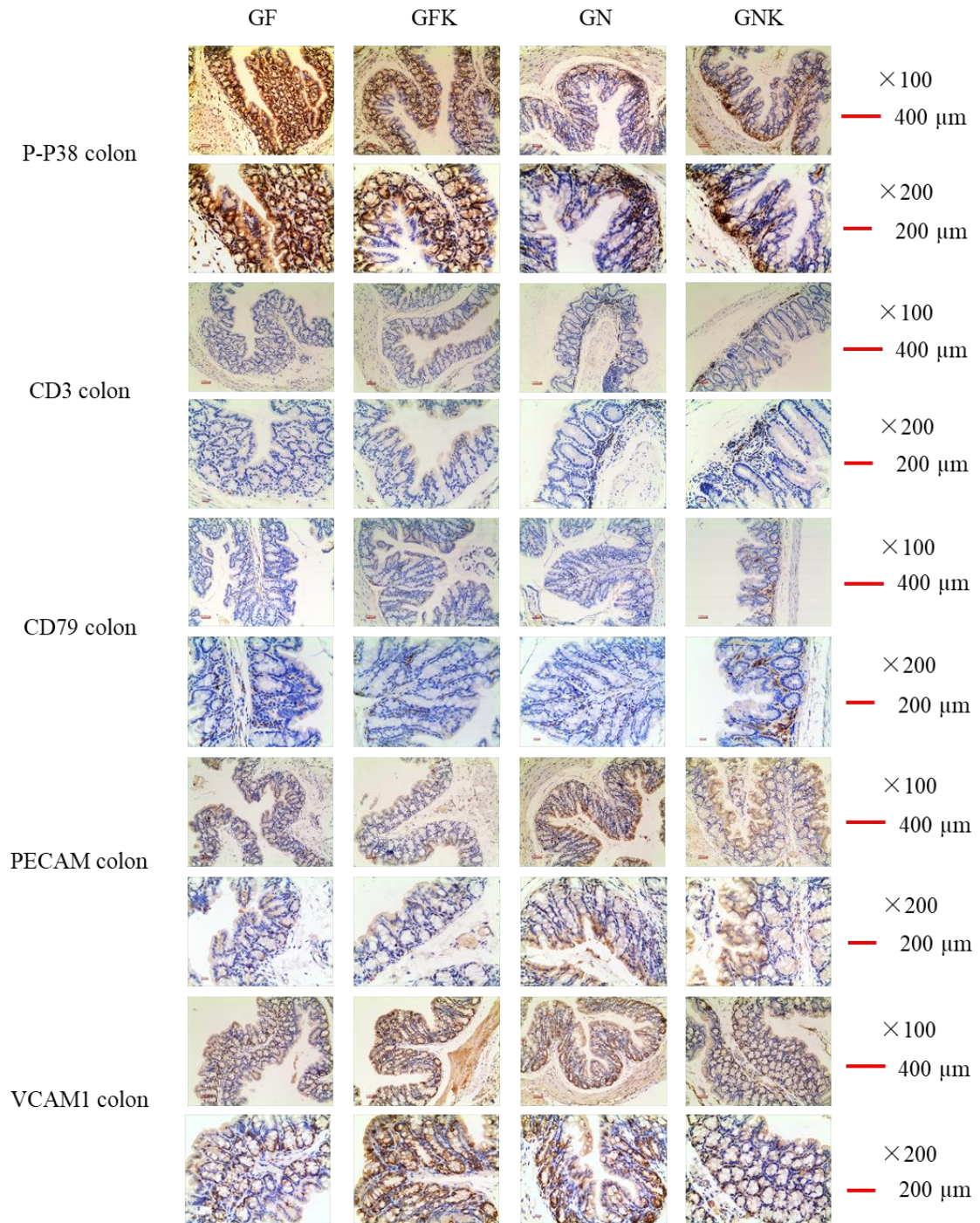
Supplementary Figure S4. Distribution and map of the RNA-seq reads on the chromosomes of mouse genome.

chromosome	Reads Mapped Counts												Gene of Home Mouse
	GF2	GF3	GF4	GFR2	GFK3	GFK4	GN2	GN3	GN4	Chk2	Chk3	Chk4	
1	1534812	1445706	1082239	1071164	1043643	1119719	1611087	1482916	1621832	1289414	1122711	1863482	1242
2	1730737	1621785	1230446	1224561	1277883	1321347	1922378	1606408	1737536	1449019	1368098	2074282	1842
3	1199923	1164587	836453	926390	1086528	994679	1259749	1212480	1199022	980470	905420	1321909	1051
4	1833423	1245900	941702	984667	1053495	1053618	1502904	1272076	1368448	1170263	1130286	1699906	1350
5	1403715	1289748	975312	984099	1106185	1076576	1571321	1323803	1389416	1268275	1180414	1817077	1303
6	1204286	1073195	790968	795840	837287	871470	1272363	1141236	100462	914722	826211	1285948	1162
7	1947828	1903928	1442496	1440776	1619914	1550174	2355616	1894939	1923110	1922771	1881106	2629198	2044
8	1040474	984167	750167	739990	841409	784393	1203852	984218	1032100	923525	881406	1450503	1072
9	1502721	1375244	1030674	1030829	1158079	1089862	1698610	1400917	1585992	1144057	1046934	1772716	1264
10	1206141	1167425	884975	884016	963654	938059	1432328	1167362	1132712	1066257	998045	1460893	1040
11	2209843	2008497	1517444	1538933	1611102	1714243	2451888	2090587	2181547	2019192	1969177	2757110	1633
12	802340	733821	523286	541322	549128	595359	933614	804600	755810	696233	577493	907852	694
13	698726	662712	481732	501451	558511	542764	741283	682350	723481	581738	538586	817353	863
14	732930	676620	513267	535493	566872	577539	828837	698375	745537	633973	590868	898505	924
15	999676	949053	714768	716750	766646	777131	166766	968898	1046670	935608	886080	1311947	797
16	767827	662674	502852	492515	562402	532781	797140	703411	847163	598772	566062	977123	665
17	1192191	1071650	80249	810808	1098966	883118	1418081	1087557	1086017	1158317	1070972	1833560	1091
18	531657	520442	384077	408773	405789	419879	629378	516343	533919	490779	442715	680842	492
19	911155	783092	602838	587258	661711	654339	963092	797591	912273	799318	770321	220428	719
X	680464	616222	456379	466852	476935	502258	709397	608101	713702	483471	440496	777926	947
Y	1601	722	773	687	792	1197	1798	4222	5474	6356	7424	5900	377
MT	741758	768835	520559	553827	782798	561024	727487	565446	678709	664033	673563	933283	13
SUM	24374228	22726020	16985852	17217001	19032729	18561529	27193969	23013836	24514532	21146563	19874388	30347743	22585

Supplementary Figure S5. Immunohistochemical staining analysis of colon samples.

Four groups of germ-free mice were included in the experiment, which lasted for 4 months. Mice were treated with KCO (5% in drinking water, GFK group), KCO plus *B. xylanisolvens* and *E. coli* (5×10^8 , GNK group), only *B. xylanisolvens* and *E. coli* (5×10^8 , GN group), or distilled water (GF, control group). A. Photomicrographs of IHC staining against P-P38, CD3a and CD79a, VCAM1 and PECAM1 in colon tissue samples. B. Histopathological scores representing the severity of inflammation in colon, after IHC staining results. Results are expressed as mean \pm SEM ($n = 6$).

A



B

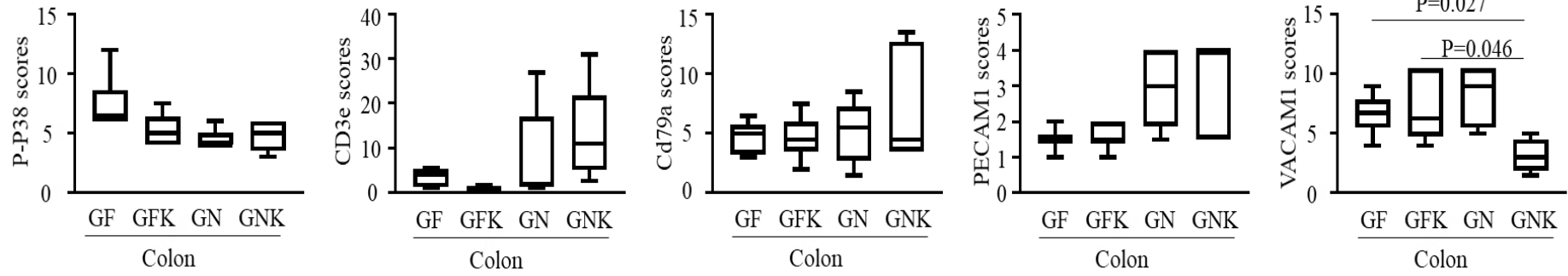
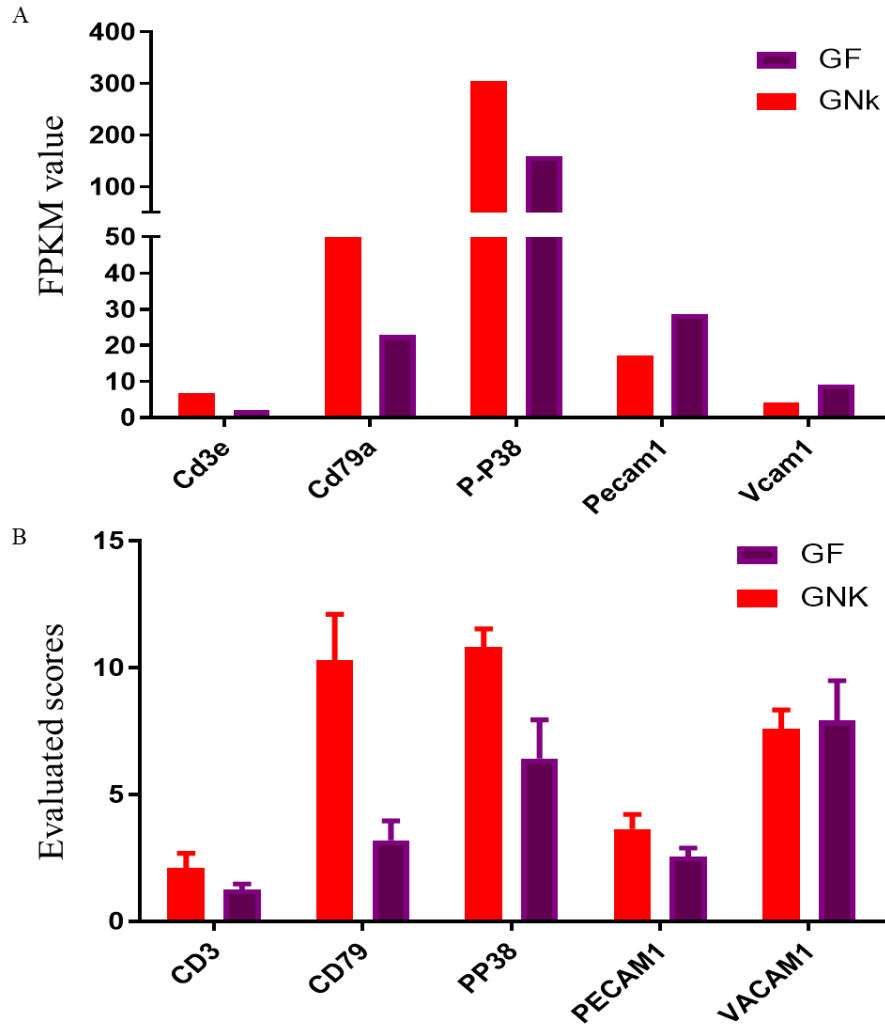


Figure S6. Comparison analysis of RNA-Seq and immunohistochemical results from rectum.



Supplementary Table S1. Analysis of bacterial communities using real time PCR.

No.	Time(h)	Total bacteria	<i>Bacteroides-Prevotella</i> group	<i>Bifidobacterium</i> genus	<i>Clostridium</i> cluster XIVab	<i>Enterobacteriaceae</i>	<i>Lactobacillus</i> group	<i>Desulfovibrio</i>
K1	0	10.86	8.93	8.43	9.13	6.73	5.22	6.92
	48	10.81	8.08	8.25	8.28	8.44	5.41	7.75
K2	0	11.05	9.27	7.71	9.47	7.28	5.05	6.41
	48	11.49	9.66	8.84	9.86	7.97	5.05	7.17
K3	0	10.47	8.14	7.76	8.34	7.24	4.83	5.51
	48	11.16	8.89	8.21	9.09	8.33	5.09	7.57
K4	0	10.88	8.66	7.79	8.86	7.77	5.27	6.96
	48	11.65	8.98	8.39	9.18	9.51	7.42	8.69
K5	0	11.01	8.93	8.49	9.13	6.49	5.46	6.77
	48	11.08	8.94	8.68	9.14	9.26	7.28	8.77
K6	0	11.01	9.08	8.22	9.28	8.80	5.44	6.35
	48	11.07	9.16	8.79	9.36	8.19	5.58	8.91
K7	0	10.75	8.66	7.40	8.86	7.34	6.90	6.63
	48	11.25	9.26	8.37	9.46	8.21	5.45	7.95
K8	0	10.87	8.90	8.51	9.10	7.52	5.02	6.95
	48	11.25	9.38	9.32	9.58	8.90	5.71	8.21
Average	0	10.86 ± 0.07	8.82 ± 0.12	8.04 ± 0.15	9.02 ± 0.12	7.34 ± 0.25	5.39 ± 0.23	6.56 ± 0.17
Average	48	11.22 ± 0.09	9.04 ± 0.16	8.60 ± 0.13	9.24 ± 0.16	8.60 ± 0.20	5.87 ± 0.33	8.13 ± 0.22
P value		0.007	0.2942	0.0135	0.2942	0.0019	0.2574	<0.0001

Supplementary Table S2. Distribution of the sequenced clone numbers*.

No. of mouse	No. of <i>B. xylanisolvans</i> clones	No. of <i>E. coli</i> clones
1	6	4
2	2	7
3	4	6
4	8	2
5	3	6
7	4	6

*Ten clones were picked up randomly from the plates of each mouse. Clones then were sent out for sequencing. The distribution of these sequences were identified according to the BLAST results.

Supplementary Table S3. Primers used in this study.

Target group	Primer sequences (5'-3')	Amplicon size	Annealing temperature	Reference
<i>Bacteroides-Prevotella</i> group	Bac303F: GAAGGTCCCCCACATTG	418 bp	56 °C	[1]
	Bac708R: CAATCGGAGTTCTTCGTG			
<i>Bifidobacterium</i> genus	Bif164F: GGGTGGTAATGCCGGATG	440 bp	59 °C	[1]
	Bif601: TAAGCCATGGACTTTCACACC			
<i>Clostridium</i> cluster X I Vab	CloXIV-F: GAWGAAGTATYTCGGTATGT	150 bp	54 °C	[1]
	CloXIV-R: CTACGCWCCCTTTACAC			
<i>Enterobacteriaceae</i>	Eco-F: CATTGACGTTACCCGCAGAAGAAGC	189 bp	63 °C	[1]
	Eco-R: CTCTACGAGACTCAAGCTTGC			
<i>Lactobacillus</i> group	Lac-F: AGCAGTAGGGAATCTTCCA	344 bp	58 °C	[2]
	Lac-R: ATTYCACCGCTACACATG			
<i>Desulfovibrio</i>	DSV691-F: CCGTAGATATCTGGAGGAACATCAG	135 bp	62 °C	[3]
	DSV826-R: ACATCTAGCATCCATCGTTTACAGC			

Supplementary Table S4. Statistic differentially expressed genes in the pathway of leukocyte transendothelial migration between GNK and GF groups.

	Gene description	Gene Symbol	Fold Change	Pval
GNK Down regulation	Claudin-1	Cldn1 (CAMs)	0.164	0.000
	Integrin, Alpha M	Itgam	0.235	0.000
	Matrix metalloprotein 9	Mmp9	0.243	0.000
	Matrix metalloprotein 2	Mmp2	0.251	0.000
	Junction adhesion molecule 2	Jam2	0.302	0.000
	Chemokine ligand 12	Cxcl12 (CXCR)	0.419	0.001
	Cadherin 5	Cdh5	0.421	0.004
	Vascular cell adhesion molecule 1	Vcam1	0.459	0.002
	Guanine nucleotide binding protein (G protein), alpha inhibiting 1	Gnai1 (Gi)	0.475	0.019
	Junction adhesion molecule 3	Jam3	0.520	0.041
	Integrin beta 1	Itgb1	0.520	0.014
	RAS related protein 1b	Rap1b	0.586	0.023
	Platelet/endothelial cell adhesion molecule 1	Pecam1	0.590	0.076
	RAS-related protein 1a	Rap1a	0.606	0.038
GNK Up regulation	Breast cancer anti-estrogen resistance 1	Bcar1 (PI30cas)	1.593	0.064
	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	Pik3cd (PI3K)	1.810	0.049
	Claudin 3	Cldn3	1.832	0.019
	Ezrin	Ezr (ERM)	1.845	0.019
	Mitogen-activated protein kinase 13	Mapk13	1.934	0.014
	Actin, beta	Actb	2.140	0.003
	Claudin 23	Cldn23	2.316	0.004

References

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2. Walter J, Hertel C, Tannock GW, Lis CM, Munro K, Hammes WP: Detection of *Lactobacillus*, *Pediococcus*, *Leuconostoc*, and *Weissella* species in human feces by using group-specific PCR primers and denaturing gradient gel electrophoresis. *Appl Environ Microbiol.* 2001; 67(6):2578-2585.
3. Fite A, Macfarlane GT, Cummings JH, Hopkins MJ, Kong SC, Furrie E, Macfarlane S: Identification and quantitation of mucosal and faecal desulfovibrios using real time polymerase chain reaction. *Gut.* 2004; 53(4):523-529.