Supplementary Materials

Fig. S1 In-house program used for processing of raw pyrosequencing data and analysis of the pyrosequencing data at species level.

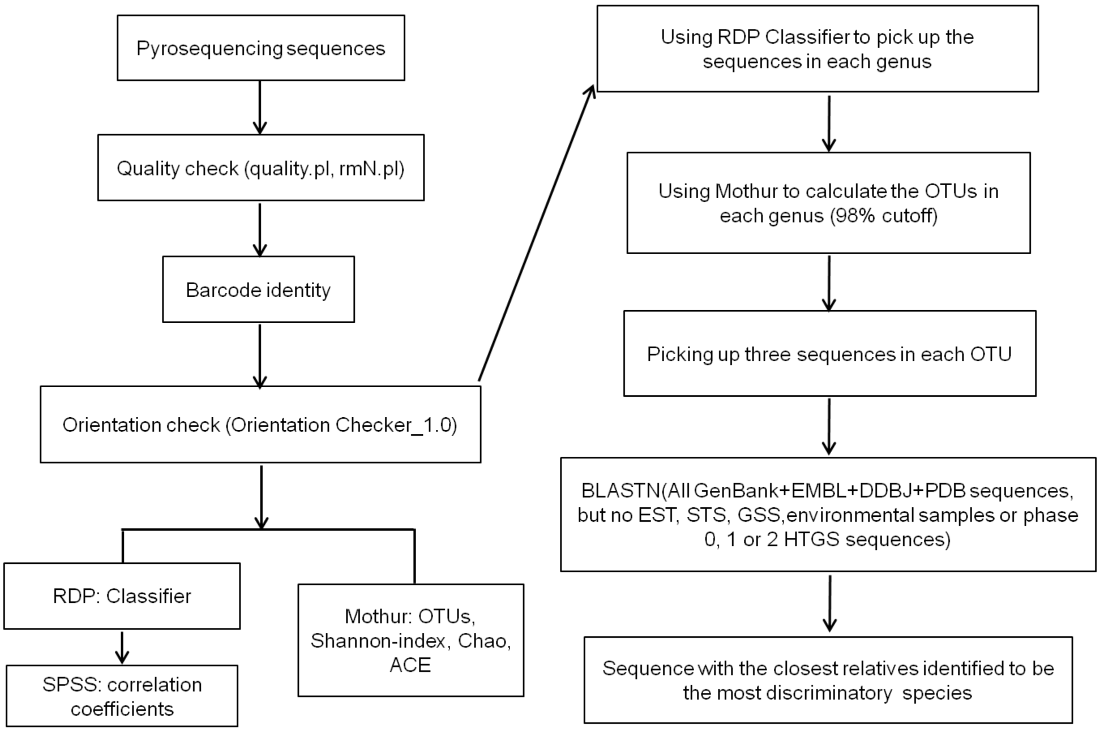

Fig. S2 PCR-DGGE profiles of duplicated chemostat experiments conducted under the same operation conditions with two inocula collected from the same donor at ten months intermittence. A. DGGE profile of V3 region of 16S rRNA gene[a]; B. Phylogenetic tree based on UPGMA method analyzed by Quantity One.

[a] HU08 and HU09 represent the different fecal inocula of the same donor collected in 2008 and 2009. HF represents the chemostat samples inoculated with human feces. 08VI, 09VI, 08VL and 09VL represent the chemostat samples cultured with VI and VL media in 2008 and 2009. M represents markers used for DGGE profiles.

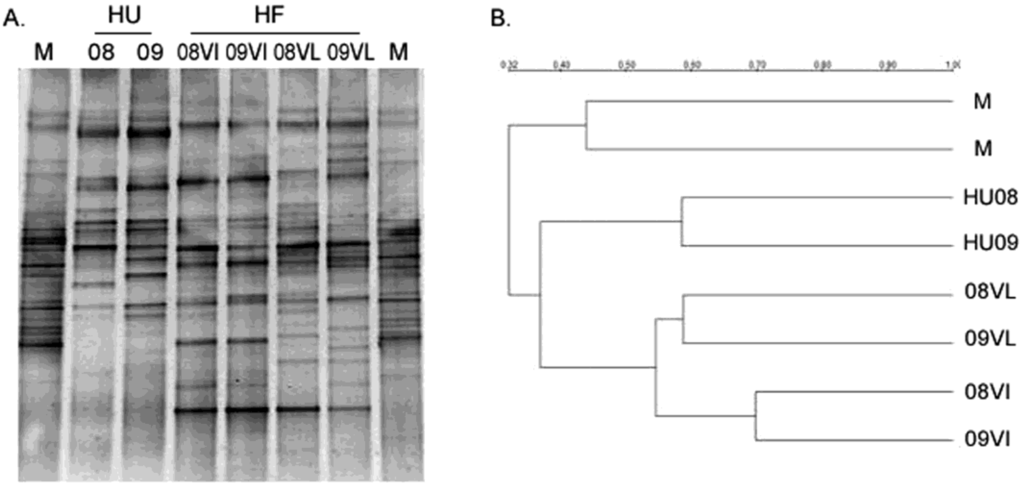

Fig. S3 The microbiota compositions analyzed by 454 pyrosequencing[a].

[a] Samples were collected from duplicated chemostat experiments conducted under the same operation conditions with two human fecal inocula taken from the same donor at ten months intermittence. HU08 and HU09 represent the different fecal inocula of the same donor collected in 2008 and 2009. HF08VI, HF09VI, HF08VL and HF09VL represent the chemostats samples with VI and VL media conducted in 2008 and 2009. Un represents unclassified.

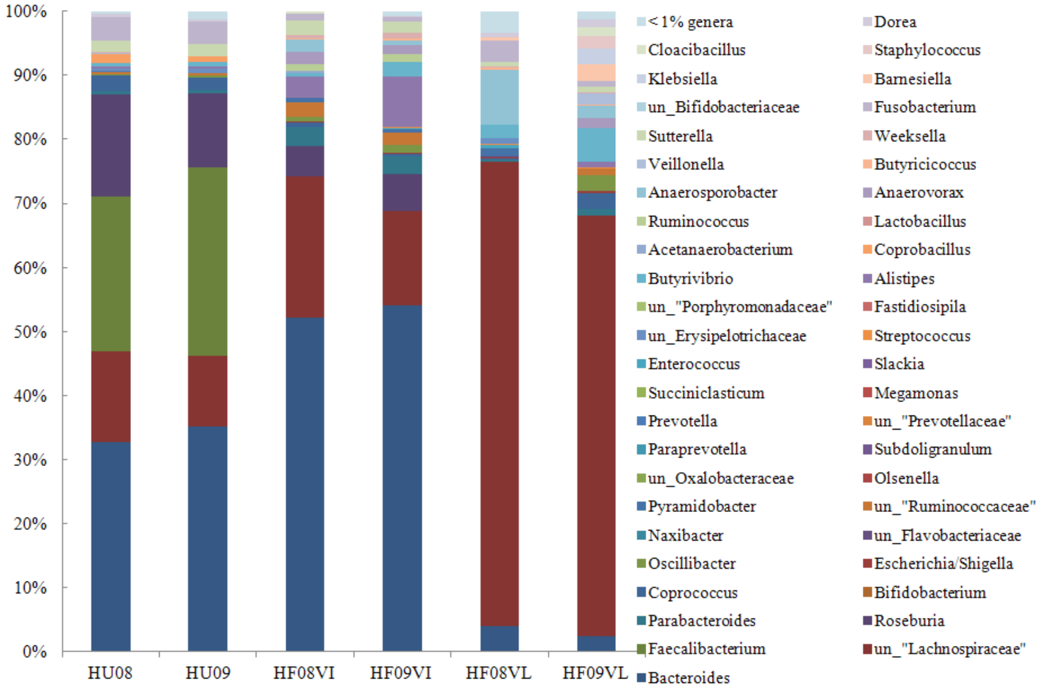

Fig. S4 The effect of sequencing reads on the patterns of human fecal microbiota compositions[a].

[a] Pearson correlation between samples was analyzed by SPSS software based on the percentage of each bacterial classification unit at genus levels. Un represents unclassified.

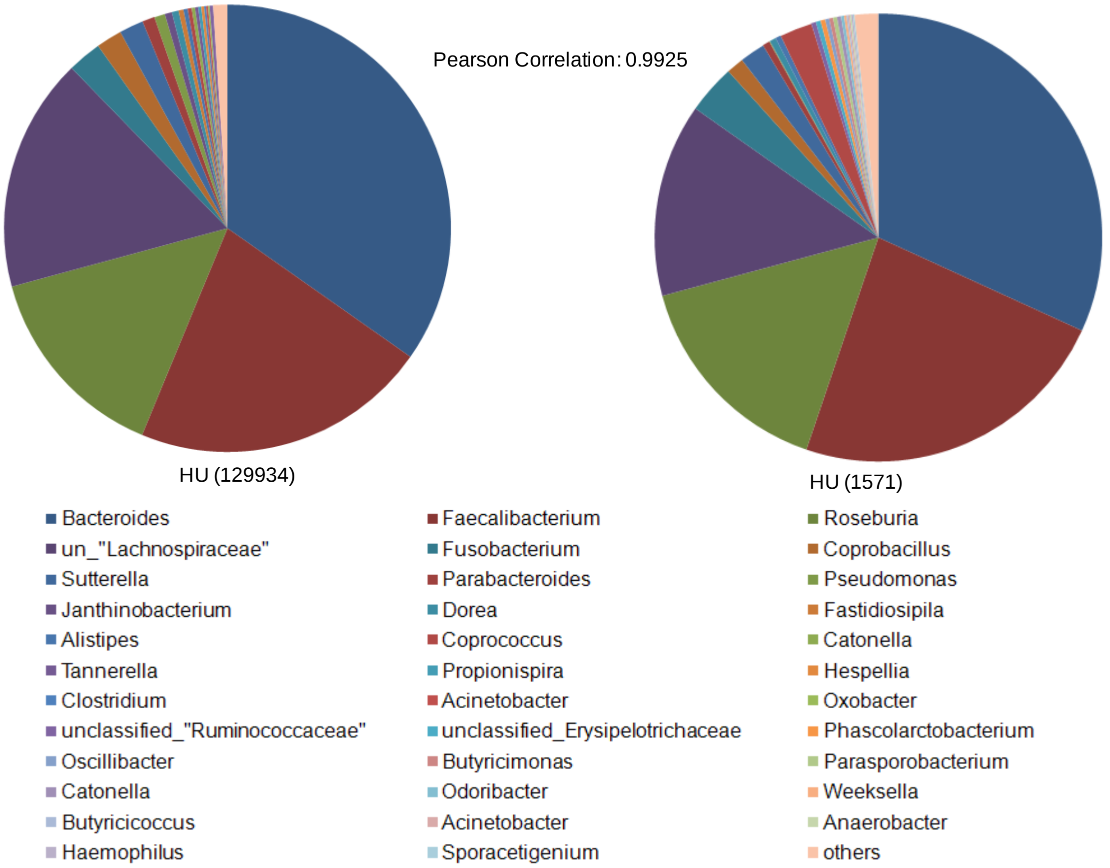

Table S1 PCR primers used for qPCR assay.

Target bacterial group	Primer name	Primer sequence (5′-3′)	Amplicon size (bp)	Annealing temp (℃)	Reference
Total bacteria	Bac1114F	CGGCAACGAGCGCAACCC	161	66	(5)
	Bac1275R	CCATTGTAGCACGTGTGTAGCC			
Bacteroides group	Bfra-F	ATAGCCTTTCGAAAGRAAGAT	495	50	(8)
	Bfra-R	CCAGTATCAACTGCAATTTTA			
Clostridium coccoides–Eubacterium group	CcocF	CGGTACCTGACTAAGAAGC	429	55	(11)
	CcocR	AGTTTYATTCTTGCGAACG			
Enterobacteriaceae	Eco1457F	CATTGACGTTACCCGCAGAAGAAGC	195	63	(1)
	Eco1652R	CTCTACGAGACTCAAGCTTGC			
Bifidobacterium genus	Bif164F	GGGTGGTAATGCCGGATG	437	59	(1)
	Bif601R	TAAGCCATGGACTTTCACACC			
Lactobacillus group	LactoF	TGGAAACAGRTGCTAATACCG	233	62	(6)
	LactoR	GTCCATTGTGGAAGATTCCC			

Table S2 Basic information for biodiversity analysis of pyrosequencing[a].

Subjects[b]	HU	HFVI	HFVL	CH	CFVI	CFVL
No of sequences	1751	1456	1043	1684	1643	1082
No of OTUs (98% cutoff)	141	143	96	308	69	91
ACE	280.58	221.04	247.65	864.66	173.71	218.92
Shannon	3.38	3.38	2.35	4.75	1.46	2.7
Chao	200.04	204.11	172.56	568.55	128.5	164.93
Evenness[c]	0.45	0.46	0.34	0.64	0.20	0.39
Good's coverage (%)	96.69	95.95	95.21	90.68	97.87	95.75

[a] Basic information calculated using Mothur (version 1.11.0).

[b] HU and CH represent inocula of human feces and chicken cecal contents. HFVI, HFVL, CFVI and CFVL represent chemostat products of human fecal and chicken cecal microbiota grown in VI and VL media.

[c] The Shannon index of evenness was calculated with the formula E = H/ln(S), where H is the Shannon diversity index and S is the total number of sequences in that group.

Table S3 Comparative composition of major genera at species level between human fecal and chicken cecal microbiota[a]

Genus	**HU**[b]		**CH**[b]	
Faecalibacterium	*Faecalibacterium prausnitzii*	23.47%	*Faecalibacterium prausnitzii*	7.66%
Bacteroides	*Bacteroides vulgatus*	31.88%	*Bacteroides plebeius*	6.77%
			Bacteroides uniformis	1.43%
			Bacteroides clarus	1.71%
			Bacteroides faecis	0.95%
			Bacteroides barnesiae	0.51%
		31.88%		11.37%
Unclassified Lachnospiraceae	*Eubacterium eligens*	1.00%	*Eubacterium xylanophilum*	3.38%
	Eubacterium fissicatena	0.86%	*Eubacterium fissicatena*	0.83%
	Eubacteriaceae bacterium	1.14%	*Ruminococcus gnavus*	0.48%
	Butyrate-producing bacterium	0.69%	*Coprococcus comes*	0.48%
	Eggerthella lenta	1.88%		
	Lachnospira pectinoschiza	5.54%		
	Lachnospiraceae bacterium	1.58%	*Clostridium methylpentosum*	0.47%
	Clostridium saccharolyticum	0.99%	*Clostridium hathewayi*	0.36%
	Clostridium populeti	0.29%	*Clostridium populeti*	1.66%
		13.97%		7.66%
Parabacteroides	*Parabacteroides merdae*	0.34%	*Parabacteroides merdae*	11.46%
	Parabacteroides distasonis	0.18%	*Parabacteroides johnsonii*	2.08%
		0.52%		13.54%
Roseburia	*Roseburia intestinalis*	15.63%	*Roseburia faecis*	3.21%

[a] Sequences with 98% similarity are regarded as the same OTU.

[b] HU, human fecal microbiota; CH, chicken cecal microbiota.

Table S4 Comparative microbiota compositions of human fecal and chicken cecal inocula and their corresponded chemostat products grown in VI and VL media at genus level[a]

Genus	% in total sequences					
	HU[b]	HFVI	HFVL	CH	CFVI	CFVL
Parabacteroides	0.51	2.95	0.38	11.76	0	0.46
Bacteroides	31.81	50.62	3.84	9.98	0.12	12.85
unclassified Lachnospiraceae	13.94	21.43	70.76	6.83	0	4.07
Faecalibacterium	23.42	0	0	6.65	0	0.19
Naxibacter	0	0	0	5.17	0	0
unclassified Ruminococcaceae	0.34	2.20	0	3.27	0	8.97
Olsenella	0	0	0	3.09	0	0
unclassified Oxalobacteraceae	0	0	0	3.09	0	0
Roseburia	15.59	4.46	0	2.79	0	0.09
Subdoligranulum	0	0	0	2.32	0	3.51
Paraprevotella	0	0	0	2.26	0	0.000
Escherichia/Shigella	0	0.07	0.10	2.14	0.06	0.09
Oscillibacter	0.29	0.76	0	2.08	0.06	9.98
unclassified Flavobacteriaceae	0	0.07	0.10	2.02	0	0
unclassified Prevotellaceae	0	0	0	1.96	0	0.19
Prevotella	0.06	0	0	1.84	0	4.71
Megamonas	0	0	0	1.54	0	0
Succiniclasticum	0	0	0	1.49	0	0
unclassified Erysipelotrichaceae	0.34	0.07	0.86	1.37	0	0.09
Enterococcus	0	0	0.48	1.37	0	0
Streptococcus	0	0	0.10	1.37	0	0
Slackia	0	0	0	1.37	0	0
Fastidiosipila	0	0	0	1.31	0	15.62
unclassified Porphyromonadaceae	0	0	0	0.95	0	4.62
Cloacibacillus	0	0.28	0	0.71	0	0
Janthinobacterium	0	0	0.19	0.65	0	0.19
Alistipes	0.40	3.30	0.	0.59	0	0
Bifidobacterium	0	0	0	0.53	79.37	0
unclassified Comamonadaceae	0	0	0	0.53	0	0
unclassified Coriobacteriaceae	0	0	0	0.48	0.06	0
Massilia	0	0	0	0.48	0	0
Coprococcus	2.34	0.69	0.19	0.36	0	2.96
Eubacterium	0	0	0	0.36	0	0
Pseudomonas	0.06	0	0.10	0.30	0.24	0
Hespellia	0.06	0	0	0.30	0	0
Collinsella	0	0	0	0.30	0	0

Butyricicoccus	0.11	0.14	0.29	0.24	0	0.92
Blautia	0.57	0	0.38	0.24	0	0
Methylobacterium	0.06	0	0	0.24	0	0
Peptococcus	0	0	0	0.24	0	0
Marvinbryantia	0	0	0	0.24	0	0
Pseudoramibacter	0	0	0	0.24	0	0
Butyrivibrio	0.57	0.41	2.01	0.18	0	0.28
Desulfonatronum	0	0	0	0.18	0	0.19
Coprobacillus	1.26	0	0	0.18	0	0
Catenibacterium	0	0	0.10	0.18	0	0
Hallella	0	0	0	0.18	0	0
unclassified Veillonellaceae	0	0	0	0.18	0	0
Acetanaerobacterium	0	0.34	0	0.12	0	2.31
Moryella	0	0	0	0.12	0	0
Lactococcus	0	0	0.77	0.06	0	0.09
Dorea	0.46	0	0.77	0.06	0	0
Butyricimonas	0.29	0	0	0.06	0	0
Barnesiella	0	0	0.38	0.06	0	0
Anaerofilum	0	0	0	0.06	0	0
TM7	0	0	0	0.06	0	0
Megasphaera	0	0	0	0.06	0	0
unclassified Actinosynnemataceae	0	0	0	0.06	0	0
unclassified Alcaligenaceae	0	0	0	0.06	0	0
Weeksella	0.17	0.55	0.10	0	0	9.34
Desulfovibrio	0	0	0	0	0	0.65
Hydrogenoanaerobacterium	0	0	0	0	0	0.37
Ethanoligenens	0	0.07	0	0	0	0.19
Clostridium	0	0	0.67	0	0.18	0.09
unclassified Clostridiaceae 1	0	0	0	0	0	0.09
Veillonella	0.06	0	0.10	0	8.34	0
Lactobacillus	0	0	0	0	7.30	0
unclassified Bifidobacteriaceae	0	0	0	0	3.53	0
Alloscardovia	0	0	0	0	0.43	0
Eggerthella	0	0	0	0	0.24	0
Fusobacterium	3.54	1.10	3.26	0	0	0
Sutterella	1.83	2.20	0.77	0	0	0
Phascolarctobacterium	0.34	0.07	0.19	0	0	0
Parasporobacterium	0.29	0	0	0	0	0
Catonella	0.29	0	0	0	0	0
Odoribacter	0.23	0	0	0	0	0
Acinetobacter	0.11	0	0	0	0	0
Anaerobacter	0.11	0	0	0	0	0
Haemophilus	0.11	0	0	0	0	0
Sporacetigenium	0.11	0	0	0	0	0

Sporobacterium	0.06	0.34	0	0	0	0
Turicibacter	0.06	0	0	0	0	0
Anaerosporobacter	0	1.79	8.44	0	0	0
Pyramidobacter	0	0.55	1.34	0	0	0
Pantoea	0	0	0.96	0	0	0
Anaerostipes	0	0	0.67	0	0	0
Dialister	0	0	0.58	0	0	0
unclassified Enterobacteriaceae	0	0	0.29	0	0	0
Enterobacter	0	0	0.29	0	0	0
Solobacterium	0	0	0.19	0	0	0
Providencia	0	0.28	0.10	0	0	0
Cronobacter	0	0	0.10	0	0	0
Anaerovorax	0	1.92	0	0	0	0
Ruminococcus	0	1.03	0	0	0	0
Lawsonia	0	0.14	0	0	0	0
Erysipelothrix	0	0.14	0	0	0	0
Holdemania	0	0.14	0	0	0	0
Akkermansia	0	0.07	0	0	0	0
Anaerotruncus	0	0.07	0	0	0	0
Pseudobutyrivibrio	0	0.07	0	0	0	0

[a] Results are expressed as the percentage of specified sequence in total bacterial sequences. The phylogenetic assignment was based on RDP Classifier.

[b] HU and CH represent inocula of human feces and chicken cecal contents. HFVI, HFVL, CFVI and CFVL represent chemostat products of human fecal and chicken cecal microbiota grown in VI and VL media.

Table S5 Comparison of post-ileal digestibility of major nutrients from chicken and human samples[&].

Samples	Dry matter		Crude protein		Starch		NSP[×]		Sugars	
	Chicken	Human	Chicken	Human	Chicken	Human	Chicken	Human	Chicken	Human
Terminal ileal (g d^{-1})	20.3±0.13[§]	101.30	2.51±0.05	17.20	1.37±0.06	1.30	0.17±0.01	23.30	4.02±0.04	20.8
Feces (g d^{-1})	17.8±0.15	34.10	0.30±0.04 (1.92±0.09)[¥]	9.80	0.88±0.08	0.30	0.09±0.01	8.30	0.48±0.05	0.4
Post-ileal digestibility (%)	12.32	66.34	88.05 (23.51)[¥]	43.02	35.77	76.92	47.06	64.38	88.06	98.08

[&] All data for chicken are shown as mean and SD, n=18. The post-ileal digestibility was calculated as the difference between the terminal ileal output (g d^{-1}) and feces (g d^{-1}) relative to the terminal ileal output (g d^{-1}). All data for humans were cited by Coles *et al*. (3).

[§] The daily ileal output in dry matter for adult chickens is predicted with the daily total dry matter in excreta plus 2.5 gram based on a previous study on intact and cecectomized adult chickens (10).

[¥] The data outside of the brackets represent true protein, excluding non-protein nitrogen (uric acid). The data inside the brackets represent the crude protein, including both protein and non-protein nitrogen.

[×] Non-starch polysaccharides.

Table S6 Molar ratios of VFA in chemostats, SHIME[§] or batch fermentation inoculated with human fecal microbiota studied by different countries.

Carbohydrates (%)	Techniques	Inocula source	Acetate	Propionate	Butyrate	Reference
starch 0.2; pectin 0.05; inulin 0.05; xylan 0.05; arabinogalactan 0.05; guar gum 0.05	chemostats	British	70	17	13	(7)
			83	9	8	
starch 0.3, arabinogalactan 0.1, pectin 0.2, xylan 0.1, glucose 0.04	SHIME[§]	American	51	15	22	(4)
starch 0.2; pectin 0.05; Raftiline LS 0.05; xylan 0.05; arabinogalactan 0.05; guar gum 0.05	chemostats	British	61	24	15	(2)
Konjac glucomannan (KGM) 0.2%	Batch fermentation	Japanese	50	30	13	(9)
carrageenan oligosaccharides (KCO) 0.8%	chemostats	Chinese	44	40	16	Unpublished data in our lab
carrageenan oligosaccharides (KCO) 0.8%	Batch fermentation	Chinese	53	29	18	Unpublished data in our lab

[§] SHIME was represent for Simulator of the Human Intestinal Microbial Ecosystem.

Appendix

The sequence of the phylotype of unclassified *Lachnospiraceae* coming from human microbiota which was enriched in the VL medium *in vitro* chemostat system.

```
>the phylotype
CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGAT
CCAGCGACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCA
GCAGGGAAGAAAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGT
GCCAGCAGCCGCGGTAAT
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