The method of FBP preparation

In brief, the blueberry pomace (Jilin province Pulan High Tech Co., Ltd., Changchun, China) was mixed with distilled water at $g_{pomace}:V_{distilled\ water}$ = 1:1.25. Subsequently, the mixture was pasteurized (80℃, 15 min) to eliminate the indigenous microbiota. After being reactivated at MRS broth for two times (180 rpm for 12 h per time at 37℃), *Lactobacillus casei* (7.00 Log CFU/mL, CICC 20280) was inoculated into sterile blueberry pomace mixture at 5% inoculation volume. The fermentation of *Lactobacillus casei* on blueberry pomace mixture was carried out at 37°C for 42 h without agitation. After the freeze drying, the FBP was collected and stored at -20℃.

The expression of functional proteins related to sIgA-producing in PPs

Homogenates of PPs were prepared in lysis buffer (Dingguo Changsheng Biological Technology Co., Ltd., Beijing, China), containing 5× amount of phosphorylation protease inhibitors (Servicebio Biotechnology Co., Ltd., Wuhan, China) to extract protein. The BCA method (Dingguo Changsheng Biological Technology Co., Ltd., Beijing, China) was applied to determine the protein concentration. The protein solutions were diluted to 4.5 μg/μL in lysis buffer with adding 5× SDS loading buffer (EpiZyme Biotechnology Co., Ltd., Shanghai, China). Subsequently, the mixture was denatured at 100°C for 10 min. Aliquots of the mixture (40 μg protein in total) were separated on the 12.5% SDS-polyacrylamide gel (80V, 2h) and then electroblotted onto PVDF membranes (0.2 μm, Merck Millipore Ltd., USA). Membranes were blocked for 1.5 h in 5% (w/v) skimmed milk powder (Servicebio Biotechnology Co., Ltd., Wuhan, China). Then, the blocked PVDF membranes were

washed three times by using TBST (20 min) to remove the skimmed milk powder solution and subsequently incubated in the primary antibodies overnight at 4°C. After finishing the PVDF membranes washing steps, the PVDF membranes were incubated with anti-rabbit secondary antibody (HRP conjugated) for 2 h at room temperature. Again, PVDF membranes were washed three times by using TBST (10 min). The conjugates were visualized by the ECL system (LI-COR, USA) and analyzed by Image Studio Ver 5.2 (LI-COR, USA).

The antibodies used in this studies were as follows: β-actin (YM3607, 1:2000, ImmunoWay Biotechnology, UAS); TGF-β (21898-1-AP, 1:3000, Proteintech, Wuhan, China); CD 40 (YT0763, 1:2000, ImmunoWay Biotechnology, USA); Integrin-α4β7 (LM10435, 2:1000, Annoron, Beijing, China); MAdCAM-1 (YN0883, 1:2000, ImmunoWay Biotechnology, USA); CCL25 (YN1321, 1:2000, ImmunoWay Biotechnology, USA); CCR9 (YN2513, 1:2000, ImmunoWay Biotechnology, USA); IgA (60099-1-Ig, 1:5000, Proteintech, Wuhan, China); J chain (LM12334, 1:2000, Annoron, Beijing, China); SC (15288-1-AP, 1:2000, Proteintech, Wuhan, China); pIgR (YN2028, 1:2000, ImmunoWay Biotechnology, USA); HRP*Goat anti-rabbit IgG (wjRS0002, 1:5000, Ruiying Biological, Suzhou, China).

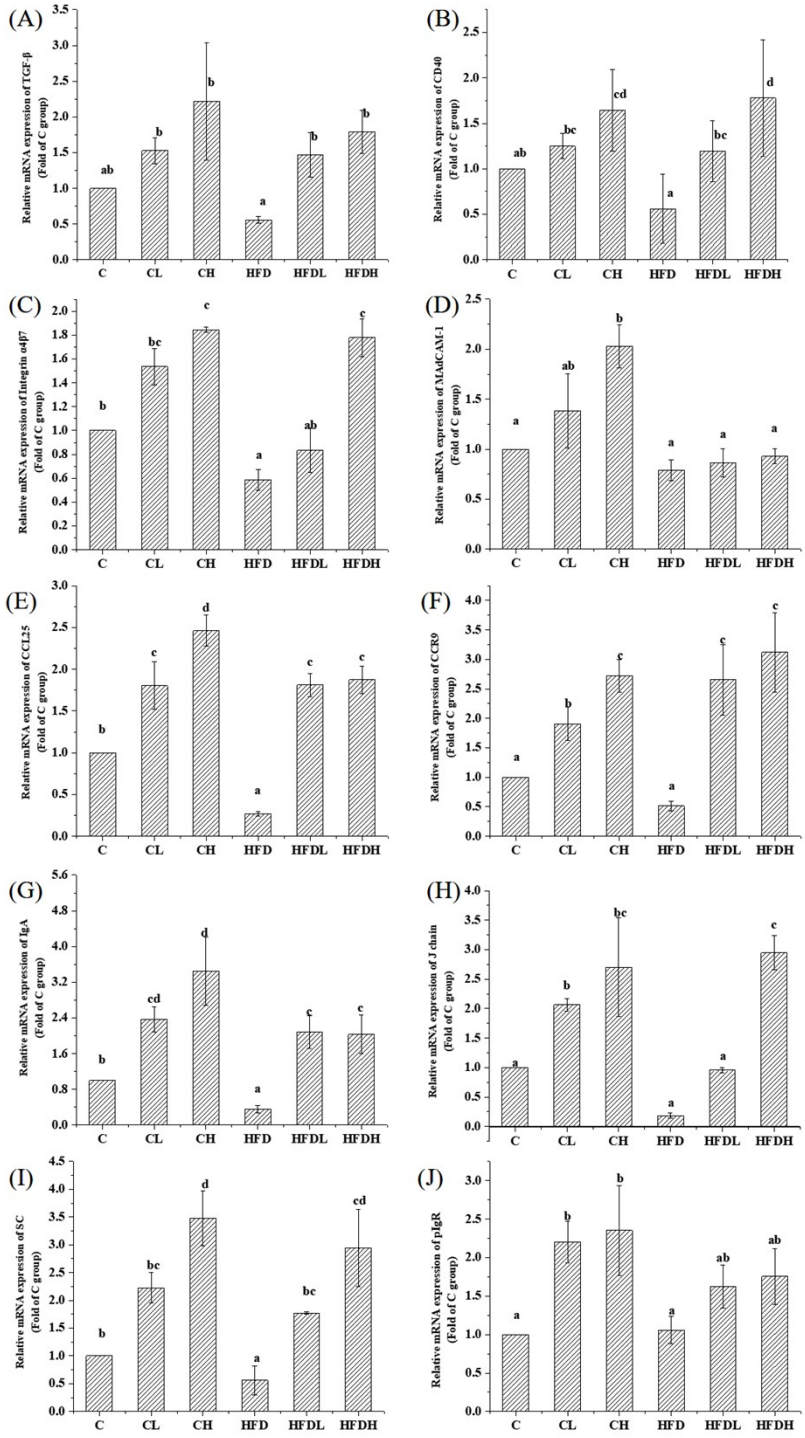
Analysis of indigenous microbiota in the interior of PPs by 16S rRNA Illumina sequencing data

Total DNA of indigenous microbiota in the interior of PPs were extracted using MN NucleoSpin Kit (Biomarker Technologies Co, Ltd., Beijing, China) according to the manufacturer's instructions. The V3 - V4 regions of the 16S rDNA were amplified

by using universal primers (Forward primer: 5'-ACTCCTACGGGAGGCAGCAG-3'; Reverse primer: 5'-GGACTACHVGGGTWTCTAAT-3'). Dual-index barcodes were used to tag each sample. The quality and concentration of PCR products were measured by using QuantiFluor-ST Fluorometer (Promega, USA). PCR products with bright main bands between 400 and 450 bp were selected for further experiments. The Illumina HiSeq platforms according to the manufacturer's manual at Biomarker Technologies Co, Ltd, Beijing, China.

Determination of acetic, propionic and butyric acids in the caecal contents by gas chromatography

Caecal contents (100 mg) were suspended in 2 mL water and homogenized for 5 min. After centrifugation (13, 000 g, 20 min, 4°C), the supernatant (0.4 mL) was mixed with 80 μL H_2SO_4 (50%) for 10 min and the mixture was fully acidified for 1 h at 4℃. Then 0.4 mL ethyl acetate was added and vortexed for 5 min. The mixture was incubated at 4℃ for 10 min and centrifuged at 13, 000 g for 5 min. Samples (1 μL) were analyzed at 1:10 spilt ratio by gas chromatography (Agilent 6890N, USA) on a DB-FFAP chromatographic capillary column (30 m × 0.25 mm × 0.50 μm; Agilent, USA) under the following conditions: initial temperature of 105°C for 3 min, heating to 170°C at 10°C/min, and heating to 240°C at 70°C/min maintained for 2 min. The signal was detected at 250°C with an FID detector.



Supplementary Figure S1. Effects of FBP on sIgA production at mRNA level in small intestine via class-switch recombination (A-B), the homing of IgA^+ plasma cells (C-F) as well as IgA production and sIgA secretion (G-J). Means with different letters in each figure were significantly different at $p < 0.05$ ($n = 7$).

Supplementary Table S1. Ingredients of maintenance purified diet.

	Feed ratio (g/kg)	
Ingredient	TP23522	TP23520
Casein	190	258
Corn Starch	480	0
Maltodextrin	118	162
Sucrose	65	89
Soybean Oil	24	32
Lard	19	317
Cellulose	47	65
Mineral Mix, M1022	43	58
Vitamin Mix, V1000	9	13
L-Cystine	3	4
Choline Bitartrate	2	3
TBHQ	0.01	0.07
	Total: 1000	Total: 1000
	Feed heat ratio (%)	
	TP23522	TP23520
Protein	20	20
Carbohydrate	70	20
fat	10	60
	Total: 100	Total: 100
	Feed heat (Kcal/g)	
	TP23522	TP23520
	3.9	5.3

Supplementary Table S2. Primers used in this research.

Gene	Primers	Melting Temperature	Length	Gene Bank ID/ References
Firmicutes	F: GGAGYATGTGGTTTAATTCGAAGCA R: AGCTGACGACAACCATGCAC	55℃	126 bp	[1]
Bacteroides	F:ATAGCCTTTCGAAAGRAAGAT R:CCAGTATCAACTGCAATTTTA	55℃	238 bp	[2]
Bifidobacterium	F: GGGTGGTAATGCCGGATG R: TAAGCGATGGACTTTCACACC	55℃	224 bp	[3]
Lactobacillus	F: AGCAGTAGGGAATCTTCCA R: CACCGCTACACATGGAG	55℃	341 bp	[1]
Butyric acid bacteria	F:GCIGAICATTTCACITGGAAYWSITGGCAYATG R:CCTGCCTTTGCAATRTCIACRAANGC	55℃	530 bp	[4]
Escherichia coli	F:GTTAATACCTTTGCTCATTA R:ACCAGGGTATCTTAATCCTGTT	55℃	340 bp	[5]
Akkermansia	F:CAGCACGTGAAGGTGGGGAC R:CCTTGCGGTTGGCTTCAGAT	55℃	327 bp	[6]
Internal reference gene	F:ACTCCTACGGGAGGCAGCAG R:GGACTACHVGGGTWTCTAAT	55℃	400-440 bp	[7]
TGF-β	F: GCTAATGGTGGACCGCAACAAC R: GGCACTGCTTCCCGAATGTCT	57℃	102 bp	NM-011577.2
CD40	F: GGTCATAACACCGCTGCTCCAG R: GCTATGCTGTCTGTCACCTGCC	57℃	119 bp	NM-011611.2
Integrin-α4β7	F: TCCTCCAGCACAGCCTACAT R: TAGCATAGTCCCATCCGTCGTA	57℃	100 bp	HW-3644659.1
MAdCAM-1	F: GACACAACGCTGGCGGTTAC R: AGGTGAGGTCTGGCTCTGTAGT	57℃	136 bp	NM-013591.2
CCL25	F: AGCTGGAGGATGGGAGGAGTCT R: ACGTTGGTGGGTCTGGTCTTGT	57℃	107 bp	NM-009138.3
CCR9	F: TGCTCCCAATCCACTTCTGTGT R: AAAGGCTAGGTTCCCACCATCC	57℃	150 bp	NM-001166625.1
IgA	F:ACAAGCGTGTTGCGTGTATCAG R:GGTCGATGGTCTTCTGGGTGAA	57℃	100 bp	NG-005838.1
SC	F:GTGCCCGCCAATCTTCTGTGAG R:CCCACACCAGTACCAGCCTTCA	57℃	101 bp	DL-232588.1
J chain	F: GGTGTTCCTGAGACCTGCTACA R: GTCAAGGCTGCTTGCACCATT	57℃	104 bp	NM-152839.3
pIgR	F: CACATCCTGCCAAGCCATGAC R: CCACACCAGTACCAGCCTTCA	57℃	125 bp	NM-011082.3
CCL28	F: TCATCCTGTGGTGCTCCTGGGA R: GCTGCTTGCTTCTTGGTGGTGT	57℃	102 bp	NM-020279.3

CCR10	F: CAGTCTTCGTGTGGCTGTTGTC R: TGCGTGAGGCTTTCGGGAAA	57℃	118 bp	NM-007721.4
β-actin	F: GGCTGTATTCCCTCCATCG R: CCAGTTGGTAACAATGCCATG	57℃	240 bp	[8]

Supplementary Table S3. Organ indexes of mice.

	C	CL	CH	HFD	HFDL	HFDH
Heart index (%)	0.53 ± 0.05 ^{abc}	0.60 ± 0.05 ^{bc}	0.61 ± 0.07 ^{c}	0.48 ± 0.04 ^{a}	0.52 ± 0.06 ^{ab}	0.50 ± 0.06 ^{a}
Liver index (%)	3.24 ± 0.14 ^{a}	3.38 ± 0.19 ^{a}	3.53 ± 0.19 ^{a}	3.48 ± 0.30 ^{a}	3.38 ± 0.44 ^{a}	3.56 ± 0.26 ^{a}
Kidney index (%)	0.94 ± 0.06 ^{a}	0.99 ± 0.06 ^{a}	1.03 ± 0.11 ^{a}	0.92 ± 0.07 ^{a}	0.95 ± 0.11 ^{a}	1.00 ± 0.09 ^{a}
Spleen index (%)	0.21 ± 0.02 ^{a}	0.19 ± 0.01 ^{a}	0.23 ± 0.04 ^{a}	0.21 ± 0.03 ^{a}	0.22 ± 0.04 ^{a}	0.23 ± 0.04 ^{a}
Empty cecum weight (%)	0.33 ± 0.04 ^{a}	0.40 ± 0.06 ^{ab}	0.45 ± 0.09 ^{b}	0.47 ± 0.06 ^{b}	0.45 ± 0.06 ^{b}	0.50 ± 0.07 ^{b}
Cecal contents (%)	0.30 ± 0.05 ^{a}	0.49 ± 0.10 ^{b}	0.44 ± 0.08 ^{ab}	0.45 ± 0.10 ^{b}	0.49 ± 0.12 ^{b}	0.46 ± 0.09 ^{b}

Data were expressed as mean ± standard deviation (n = 7). Means with different letters were significantly different at $p < 0.05$.

Supplementary Table S4. The α diversity of internal microbiota in Peyer's Patches.

Group	Shannon	Simposon	Ace	Chao 1
C	1.69 ± 0.04 ^{ab}	0.41 ± 0.03 ^{bc}	263.62 ± 10.10 ^{ab}	282.29 ± 16.95 ^{ab}
CL	2.16 ± 0.10 ^{b}	0.29 ± 0.03 ^{b}	286.54 ± 23.89 ^{ab}	284.00 ± 26.61 ^{ab}
CH	3.58 ± 0.18 ^{c}	0.08 ± 0.02 ^{a}	310.26 ± 13.74 ^{b}	322.84 ± 17.61 ^{b}
HFD	1.37 ± 0.09 ^{a}	0.53 ± 0.05 ^{c}	227.52 ± 10.70 ^{a}	232.07 ± 13.01 ^{a}
HFDL	1.98 ± 0.13 ^{b}	0.28 ± 0.04 ^{b}	261.84 ± 8.14 ^{ab}	263.68 ± 17.77 ^{ab}
HFDH	3.25 ± 0.09 ^{c}	0.11 ± 0.01 ^{a}	273.24 ± 12.96 ^{ab}	278.50 ± 13.69 ^{ab}

Data were expressed as mean ± standard deviation (n = 5). Means with different letters were significantly different at $p < 0.05$.

Supplementary Table S5. Effects of different diets on diversity of internal microbiota

Microbiota	C	CL	CH	HFD	HFDL	HFDH
Phylum						
Firmicutes	86.48% ± 3.54% ^{bc}	65.83% ± 16.03% ^{abc}	75.85% ± 10.55% ^{abc}	88.20% ± 8.32% ^{d}	57.55% ± 8.79% ^{a}	59.99% ± 9.03% ^{ab}
Actinobacteria	6.38% ± 1.00% ^{a}	14.21% ± 7.65% ^{ab}	10.11% ± 4.78% ^{ab}	7.74% ± 5 .09% ^{ab}	26.57% ± 7 .74% ^{b}	17.90% ± 11.98% ^{ab}
Proteobacteria	1.70% ± 0.47% ^{a}	1.88% ± 1.40% ^{a}	5.31% ± 2.98% ^{a}	1.01% ± 0.35% ^{a}	2.38% ± 0.55% ^{a}	7.95% ± 2.67% ^{a}
Bacteroidetes	3.55% ± 3.15% ^{a}	3.34% ± 2.47% ^{a}	3.39% ± 0.86% ^{a}	0.58% ± 0.12% ^{a}	3.18% ± 2.06% ^{a}	6.33% ± 3.51% ^{a}
Cyanobacteria	1.44% ± 0.65% ^{a}	2.02% ± 1.55% ^{a}	3.14% ± 1.55% ^{a}	0.32% ± 0.29% ^{a}	6.17% ± 4.29% ^{a}	3.29% ± 2.86% ^{a}
Verrucomicrobia	0.16% ± 0.1% ^{a}	2.26% ± 1.16% ^{b}	0.26% ± 0.06% ^{a}	1.70% ± 0.65% ^{ab}	3.50% ± 1.14% ^{b}	0.14% ± 0.08% ^{a}
Patescibacteria	0.15% ± 0.04% ^{a}	0.98% ± 0.46% ^{ab}	0.18% ± 0.08% ^{a}	0.24% ± 0.09% ^{a}	0.25% ± 0.13% ^{a}	2.14% ± 1.50% ^{b}
Tenericutes	0.02% ± 0.00% ^{a}	0.88% ± 0.43% ^{c}	0.12% ± 0.07% ^{a}	0.18% ± 0.10% ^{ab}	0.14% ± 0.09% ^{a}	0.67% ± 0.07% ^{bc}
Firmicutes/ Bacteroidetes	19.38 ± 5.52 ^{a}	31.35 ± 23.46 ^{a}	22.841 ± 2.76 ^{a}	154.54 ± 18.012 ^{b}	24.76 ± 16.48 ^{a}	11.52 ± 5.80 ^{a}
Genus						
Faecalibaculum	53.93% ± 22.76% ^{ab}	37.43% ± 27.47% ^{ab}	63.07% ± 12.98% ^{b}	60.05% ± 20.81% ^{ab}	22.96% ± 8.80% ^{ab}	10.10% ± 9.33% ^{a}
Dubosiella	11.66% ± 3.00% ^{a}	11.80% ± 7.45% ^{a}	7.07% ± 3.73% ^{a}	21.09% ± 13.12% ^{a}	17.02% ± 3.66% ^{a}	6.03% ± 2.73% ^{a}
Lactobacillus	1.52% ± 0.20% ^{a}	8.37% ± 3.32% ^{ab}	2.52% ± 0.96% ^{a}	2.94% ± 0.63% ^{a}	6.46% ± 3.35% ^{ab}	13.02% ± 5.55% ^{b}
Coriobacteriaceae_ UCG-002	3.47% ± 2.10% ^{a}	8.02% ± 5.53% ^{a}	2.89% ± 1.27% ^{a}	2.80% ± 1.77% ^{a}	7.91% ± 4.18% ^{a}	1.48% ± 0.85% ^{a}
uncultured_bacterium _f_Muribaculaceae	5.23% ± 2.51% ^{ab}	12.84% ± 7.10% ^{b}	2.81% ± 1.820% ^{a}	0.53% ± 0.147% ^{a}	5.86% ± 2.74% ^{ab}	3.48% ± 1.77% ^{ab}
Bifidobacterium	1.38% ± 0.59% ^{ab}	2.04% ± 0.93% ^{ab}	2.40% ± 0.36% ^{b}	0.56% ± 0.04% ^{a}	1.28% ± 0.96% ^{ab}	0.54% ± 0.18% ^{a}
Nicotiana_otophora	1.55% ± 0.77% ^{a}	1.46% ± 0.51% ^{a}	1.81% ± 0.70% ^{a}	1.14% ± 0.08% ^{a}	4.98% ± 1.37% ^{b}	8.52% ± 1.65% ^{c}
Romboutsia	6.30% ± 4.09% ^{a}	2.67% ± 1.87% ^{a}	0.14% ± 0.03% ^{a}	0.87% ± 0.37% ^{a}	6.42% ± 4.60% ^{a}	2.52% ± 1.48% ^{a}
Rhodococcus	2.21% ± 1.17% ^{a}	1.07% ± 0.85% ^{a}	4.25% ± 1.61% ^{ab}	1.01% ± 0.54% ^{a}	2.99% ± 1.19% ^{a}	7.47% ± 1.69% ^{b}
Streptococcus	0.77% ± 0.16% ^{a}	0.85% ± 0.31% ^{ab}	0.72% ± 0.31% ^{a}	2.72% ± 1.31% ^{b}	1.85% ± 0.94% ^{ab}	0.77% ± 0.06% ^{a}
Akkermansia	0.04% ± 0.02% ^{a}	0.53% ± 0.19% ^{a}	0.48% ± 0.22% ^{a}	0.13% ± 0.06% ^{a}	4.91% ± 2.30% ^{b}	0.17% ± 0.07% ^{a}
Ochrobactrum	0.79% ± 0.36% ^{ab}	0.19% ± 0.10% ^{a}	1.65% ± 1.01% ^{ab}	0.47% ± 0.07% ^{a}	1.51% ± 0.64% ^{ab}	3.69% ± 2.38% ^{b}
Candidatus_ Saccharimonas	0.83% ± 0.04% ^{b}	0.00% ± 0.00% ^{a}	0.00% ± 0.00% ^{a}	0.00% ± 0.00% ^{a}	0.04% ± 0.01% ^{a}	0.01% ± 0.01% ^{a}
Desulfovibrio	0.64% ± 0.11% ^{b}	0.00% ± 0.00% ^{a}	0.00% ± 0.00% ^{a}	0.00% ± 0.00% ^{a}	0.04% ± 0.04% ^{a}	0.07% ± 0.03% ^{a}
Enterorhabdus	0.41% ± 0.09% ^{b}	1.40% ± 0.14% ^{d}	0.15% ± 0.03% ^{a}	0.22% ± 0.09% ^{ab}	1.14% ± 0.08% ^{c}	0.28% ± 0.04% ^{ab}
Ruegeria	0.19% ± 0.06% ^{a}	1.10% ± 0.34% ^{c}	0.36% ± 0.26% ^{ab}	0.13% ± 0.03% ^{a}	0.74% ± 0.18% ^{bc}	0.29% ± 0.10% ^{ab}
Methylotenera	0.27% ± 0.06% ^{a}	0.87% ± 0.33% ^{b}	0.33% ± 0.05% ^{a}	0.03% ± 0.01% ^{a}	0.18% ± 0.02% ^{a}	0.13% ± 0.05% ^{a}
Ruminococcaceae_ UCG-014	0.14%±0.08% ^{a}	0.18% ± 0.07% ^{a}	0.56% ± 0.17% ^{b}	0.07% ± 0.03% ^{a}	0.13% ± 0.05% ^{a}	0.18% ± 0.10% ^{a}
Lachnospiraceae_ NK4A136_group	0.82%±0.06% ^{bc}	0.44% ± 0.05% ^{ab}	0.46% ± 0.15% ^{ab}	0.22% ± 0.04% ^{a}	0.45% ± 0.03% ^{ab}	1.06% ± 0.48% ^{c}
Blautia	0.12%±0.03% ^{a}	0.27% ± 0.11% ^{a}	0.62% ± 0.06% ^{bc}	0.95% ± 0.16% ^{d}	0.36% ± 0.03% ^{ab}	0.83% ± 0.19% ^{cd}

in Peyer's Patches (n = 5).

References of supplementary Table S2

1. M. A. Gorzelak, S. K. Gill, T. Nishat, A. V. Zahra, J. Michael and D. L. Gibson, Methods for improving human gut microbiome data by reducing variability through sample processing and storage of stool, *Plos One*, 2015, **10**, e0139529.
2. J. Maukonen, C. Simões and M. Saarela, The currently used commercial DNA-extraction methods give different results of *Clostridial* and *Actinobacterial* populations derived from human fecal samples, *Fems Microbiol. Ecol.*, 2012, **79**, 697-708.
3. A. E. Bernhard and K. G. Field, Identification of nonpoint sources of fecal pollution in coastal waters by using host-specific 16S ribosomal DNA genetic markers from fecal anaerobes, *Appl. Environ. Microbiol.*, 2000, **66**, 1587-1594.
4. P. Louis and H. J. Flint, Development of a semiquantitative degenerate real-time PCR-based assay for estimation of numbers of butyryl-coenzyme A (CoA) CoA transferase genes in complex bacterial samples, *Appl. Environ. Microbiol.*, 2007, **73**, 2009-2012.
5. I. Aloisio, C. Santini, B. Biavati, G. Dinelli, A. Cencič, W. Chingwaru, L. Mogna and D. D. Gioia, Characterization of *Bifidobacterium* spp. strains for the treatment of enteric disorders in newborns, *Appl. Microbiol. Biot.*, 2012, **96**, 1561-1576.
6. X. Jie, A. Irini Lazou, P. Olena, O. Crister, A. Siv and M. Ran, Intake of blueberry fermented by *Lactobacillus plantarum* affects the gut microbiota of

L-NAME treated rats, *Evidence-Based Complementray and Alternative Medicine*, 2013, **2013**, 809128.

7. X. Nan, G. Tan, H. Wang and X. Gai, Effect of biochar additions to soil on nitrogen leaching, microbial biomass and bacterial community structure, *Eur. J. Soil Biol.*, 2016, **74**, 1-8.

8. G. Chang, Y. Shi, G. Le, Z. Xu, J. Sun and J. Li, Effects of *Lactobacillus plantarum* on genes expression pattern in mice jejunal Peyer's patches, *Cell Immunol.*, 2009, **258**, 1-8.