SUPPORTING INFORMATION

Using PacBio long-read high-throughput microbial gene amplicon sequencing to evaluate infant formula safety

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Figure S1. Rarefaction analysis (A) and Shannon diversity (B) estimates of the SMRT sequencing reads of bacteria in infant formula. Red and blue lines represent samples from the domestic and imported groups, respectively.

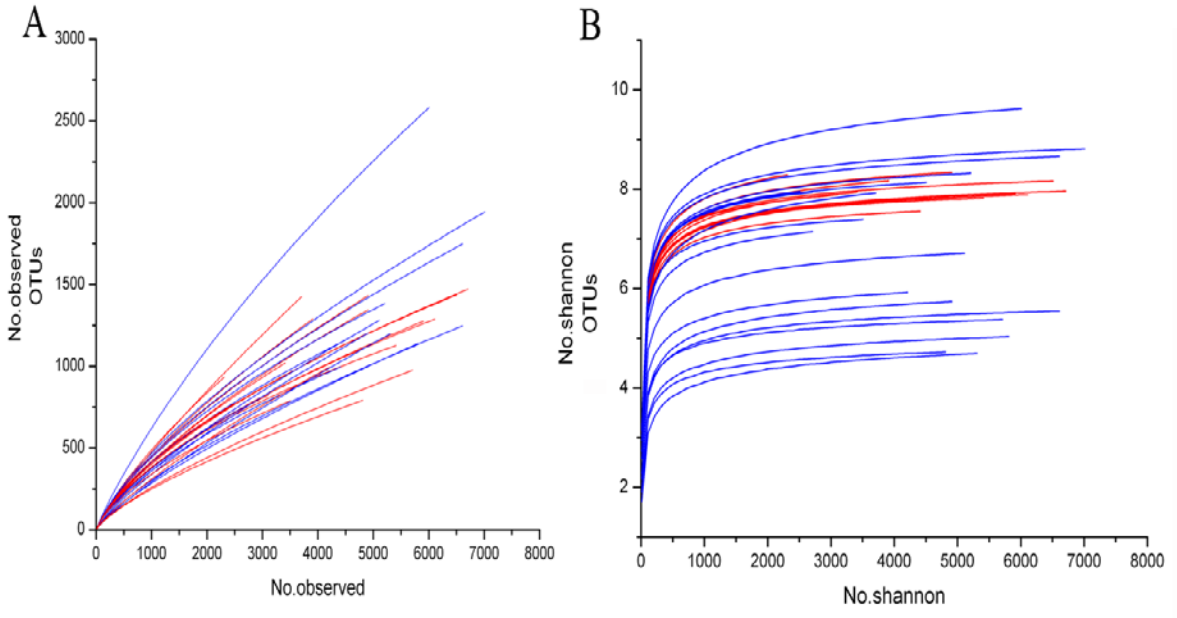

Figure S2. Relative abundances and bacterial diversity at phylum level.

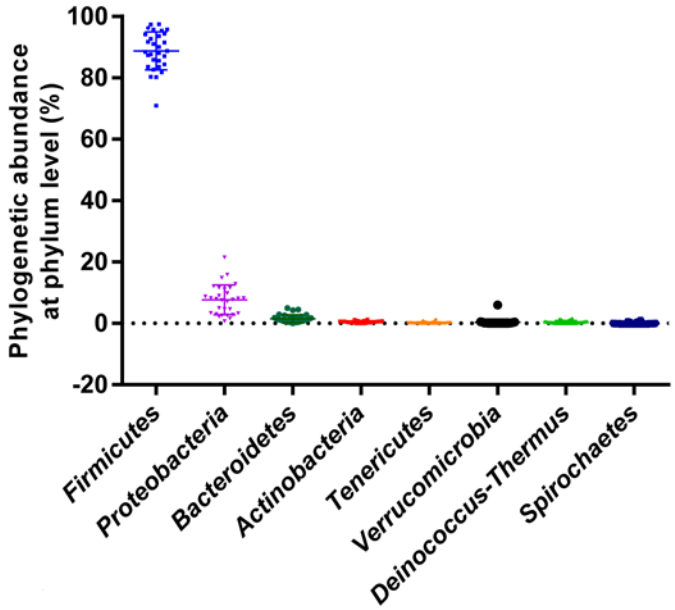

Table S1 Nutrition information of all samples

Sample	Whey Protein Nitrogen Index (WPNI)	Protein	Fat	Linoleic Acid	α-linolenic Acid	Carbohydrate	Vitamin A	Vitamin D	Vitamin E	Vitamin K1	Vitamin B1	Vitamin B2	Vitamin B6	Vitamin B12	Niacin	Folic Acid	Pantothenic Acid	Vitamin C	Biotin	Sodium	Potassium	Copper	Magnesium	Iron	Zinc	Manganese	Calcium	Phosphorus	Iodine	Chlorine	Selenium
		g	g	mg	mg	g	ug Retinol Equivalents	μg	mg a-Tocopherol	μg	μg	μg	μg	μg	μg	μg	μg	mg	μg	mg	mg	μg	mg	mg	mg	μg	mg	mg	μg	mg	μg
D1	5.41	10.50	26.30	3600.00	360.00	54.70	369.00	10.00	5.50	45.00	400.00	1020.00	240.00	1.20	75.00	75.00	2800.00	68.00	11.00	125.00	350.00	300.00	32.00	3.00	3.20	32.00	358.00	220.00	85.00	265.00	13.00
D2	6.73	10.50	26.30	3600.00	360.00	54.70	369.00	10.00	5.50	45.00	400.00	1020.00	240.00	1.20	75.00	75.00	2800.00	68.00	11.00	125.00	350.00	300.00	32.00	3.00	3.20	32.00	358.00	220.00	85.00	265.00	13.00
D3	7.39	10.50	26.30	3600.00	360.00	54.70	369.00	10.00	5.50	45.00	400.00	1020.00	240.00	1.20	75.00	75.00	2800.00	68.00	11.00	125.00	350.00	300.00	32.00	3.00	3.20	32.00	358.00	220.00	85.00	265.00	13.00
D4	7.55	16.20	22.00	3000.00	270.00	52.80	425.00	8.00	5.50	45.00	700.00	1020.00	400.00	1.20	100.00	100.00	3300.00	68.00	12.60	173.00	550.00	300.00	30.00	6.20	3.30	85.00	546.00	336.00	90.00	410.00	15.00
D5	6.26	16.20	22.00	3000.00	270.00	52.80	425.00	8.00	5.50	45.00	700.00	1020.00	400.00	1.20	100.00	100.00	3300.00	68.00	12.60	173.00	550.00	300.00	30.00	6.20	3.30	85.00	546.00	336.00	90.00	410.00	15.00
D6	6.54	16.20	22.00	3000.00	270.00	52.80	425.00	8.00	5.50	45.00	700.00	1020.00	400.00	1.20	100.00	100.00	3300.00	68.00	12.60	173.00	550.00	300.00	30.00	6.20	3.30	85.00	546.00	336.00	90.00	410.00	15.00
D7	6.05	17.00	20.00	2100.00	210.00	53.50	430.00	10.00	5.50	44.00	700.00	1020.00	400.00	1.00	100.00	100.00	3360.00	71.00	13.50	176.00	550.00	300.00	30.00	6.20	3.40	78.00	545.00	336.00	90.00	410.00	13.00
D8	6.60	17.00	20.00	2100.00	210.00	53.50	430.00	10.00	5.50	44.00	700.00	1020.00	400.00	1.00	100.00	100.00	3360.00	71.00	13.50	176.00	550.00	300.00	30.00	6.20	3.40	78.00	545.00	336.00	90.00	410.00	13.00
D9	6.74	17.00	20.00	2100.00	210.00	53.50	430.00	10.00	5.50	44.00	700.00	1020.00	400.00	1.00	100.00	100.00	3360.00	71.00	13.50	176.00	550.00	300.00	30.00	6.20	3.40	78.00	545.00	336.00	90.00	410.00	13.00
D10	6.41	17.00	20.00	2100.00	210.00	53.50	430.00	10.00	5.50	44.00	700.00	1020.00	400.00	1.00	100.00	100.00	3360.00	71.00	13.50	176.00	550.00	300.00	30.00	6.20	3.40	78.00	545.00	336.00	90.00	410.00	13.00
D11	6.48	17.00	20.00	2100.00	210.00	53.50	430.00	10.00	5.50	44.00	700.00	1020.00	400.00	1.00	100.00	100.00	3360.00	71.00	13.50	176.00	550.00	300.00	30.00	6.20	3.40	78.00	545.00	336.00	90.00	410.00	13.00
D12	6.28	17.00	20.00	2100.00	210.00	53.50	430.00	10.00	5.50	44.00	700.00	1020.00	400.00	1.00	100.00	100.00	3360.00	71.00	13.50	176.00	550.00	300.00	30.00	6.20	3.40	78.00	545.00	336.00	90.00	410.00	13.00
Means±SD	6.54 ±0.57	15.18±2.84	22.08±2.69	2175.53±1424.31	262.5±64.12	53.63±0.71	413.5±26.92	9.5±0.9	5.5±0	44.5±0.52	625±135.68	1020±0	360±72.36	1.1±0.1	93.75±11.31	93.75±11.31	3205±245.56	69.5±1.57	12.65±1.07	162.5±22.65	500±90.45	300±0	30.5±0.9	5.4±1.45	3.33±0.09	68.25±22.06	498.5±84.73	307±52.46	88.75±2.26	373.75±65.58	13.5±0.9
IA1	6.10	11.80	25.00	1900.00	316.00	56.70	379.00	6.50	3.16	27.40	379.00	506.00	223.00	0.65	65.00	65.00	2528.00	65.30	10.50	126.00	379.00	223.00	32.00	2.70	3.16	32.00	316.00	169.00	65.30	316.00	12.60
IA2	7.20	15.00	22.50	1820.00	400.00	53.50	465.00	6.30	3.84	26.30	283.00	283.00	279.00	1.01	26.00	26.00	1780.00	46.50	10.10	≤405	465.00	178.00	36.00	6.30	2.63	6.00	425.00	223.00	36.40	≤1052	12.10
IA3	5.89	15.00	19.00	1750.00	0.00	56.80	448.00	6.00	3.70	25.30	273.00	273.00	269.00	0.97	25.00	25.00	1715.00	44.80	9.70	150.00	448.00	172.00	35.00	6.00	2.53	6.00	409.00	214.00	35.10	380.00	0.00
IA4	5.29	15.00	19.00	1750.00	0.00	56.80	448.00	6.00	3.70	25.30	273.00	273.00	269.00	0.97	25.00	25.00	1715.00	44.80	9.70	150.00	448.00	172.00	35.00	6.00	2.53	6.00	409.00	214.00	35.10	380.00	0.00
IA5	5.58	15.00	19.00	1750.00	0.00	56.80	448.00	6.00	3.70	25.30	273.00	273.00	269.00	0.97	25.00	25.00	1715.00	44.80	9.70	150.00	448.00	172.00	35.00	6.00	2.53	6.00	409.00	214.00	35.10	380.00	0.00
Means±SD	6.01 ±0.73	14.36±1.43	20.9±2.75	1794±66.56	143.2±198.32	56.12±1.47	437.6±33.58	6.16±0.23	3.62±0.26	25.92±0.93	296.2±46.49	321.6±103.17	261.8±22.12	0.91±0.15	33.2±17.78	33.2±17.78	1890.6±357.43	49.24±9.01	9.94±0.36	144±12	437.6±33.58	183.4±22.29	34.6±1.52	5.4±1.51	2.68±0.27	11.2±11.63	393.6±43.93	206.8±21.49	41.4±13.37	364±32	4.94±6.77
IB1	4.41	10.40	28.00	4.03	326.00	54.00	563.00	9.30	5.70	52.00	775.00	853.00	426.00	1.40	83.00	83.00	2713.00	70.00	16.00	124.00	504.00	334.00	35.00	6.20	4.70	39.00	349.00	194.00	78.00	336.00	11.00
IB2	2.83	15.00	22.00	3237.00	266.00	55.00	521.00	8.10	5.00	40.00	367.00	1007.00	288.00	1.30	58.00	58.00	2518.00	65.00	9.40	180.00	647.00	209.00	61.00	8.60	4.30	252.00	647.00	396.00	50.00	504.00	19.00
IB3	3.50	15.00	16.00	3829.00	380.00	59.00	553.00	8.90	3.40	41.00	347.00	568.00	284.00	1.20	57.00	57.00	2290.00	68.00	9.10	241.00	852.00	256.00	45.00	8.00	2.80	227.00	568.00	347.00	85.00	455.00	11.00
Means±SD	3.58 ±0.79	2.04±2.66	4±6	1568.43±2058.84	38.67±57.03	2±2.65	16.44±21.94	0.44±0.61	0.87±1.18	5.11±6.66	185.78±241.54	160.89±222.73	62.22±80.85	0.07±0.1	11.33±14.73	11.33±14.73	144.67±211.71	1.78±2.52	3±3.9	39.56±58.52	122.89±174.92	45.11±63.14	9.33±13.11	0.93±1.25	0.76±1	89.11±116.43	114.89±154.38	78.89±105.37	14±18.52	63.78±86.4	3.56±4.62
IC1	7.60	10.50	26.00	3600.00	280.00	58.00	440.00	7.25	5.40	35.00	350.00	800.00	270.00	1.75	85.00	85.00	2600.00	100.00	14.00	125.00	550.00	330.00	35.00	6.30	4.00	90.00	380.00	230.00	60.00	310.00	12.50
IC2	6.59	10.50	26.00	3600.00	280.00	58.00	440.00	7.25	5.40	35.00	350.00	800.00	270.00	1.75	85.00	85.00	2600.00	100.00	14.00	125.00	550.00	330.00	35.00	6.30	4.00	90.00	380.00	230.00	60.00	310.00	12.50
IC3	8.13	15.20	18.90	1790.00	166.00	59.00	410.00	6.40	5.30	32.00	350.00	920.00	320.00	2.30	74.00	74.00	3000.00	92.00	13.80	200.00	780.00	280.00	46.00	6.40	3.70	82.00	520.00	320.00	74.00	510.00	11.50
IC4	8.40	15.20	18.90	1790.00	166.00	59.00	410.00	6.40	5.30	32.00	350.00	920.00	320.00	2.30	74.00	74.00	3000.00	92.00	13.80	200.00	780.00	280.00	46.00	6.40	3.70	82.00	520.00	320.00	74.00	510.00	11.50
IC5	0.89	17.50	16.50	1760.00	180.00	58.00	440.00	6.80	4.20	26.00	480.00	1270.00	480.00	1.80	80.00	80.00	2500.00	53.00	11.00	220.00	900.00	200.00	63.00	6.80	5.00	41.00	650.00	450.00	34.00	500.00	0.00
IC6	0.78	17.50	16.50	1760.00	180.00	58.00	440.00	6.80	4.20	26.00	480.00	1270.00	480.00	1.80	80.00	80.00	2500.00	53.00	11.00	220.00	900.00	200.00	63.00	6.80	5.00	41.00	650.00	450.00	34.00	500.00	0.00
Means±SD	5.40 ±3.59	14.40±3.19	20.47±4.42	2383.33±942.52	208.67±55.61	58.33±0.52	430±15.49	6.82±0.38	4.97±0.6	31±4.1	393.33±67.13	996.67±218.42	356.67±98.12	1.95±0.27	79.67±4.93	79.67±4.93	2700±236.64	81.67±22.49	12.93±1.5	181.67±44.8	743.33±159.08	270±58.65	48±12.62	6.5±0.24	4.23±0.61	71±23.51	516.67±120.78	333.33±98.93	56±18.15	440±100.8	8±6.21
ID1	5.89	10.60	26.00	4720.00	450.00	55.20	473.00	275.00	14.10	52.00	480.00	1260.00	400.00	1.80	75.00	75.00	2311.00	75.00	22.00	138.00	596.00	360.00	34.00	6.00	3.20	62.50	410.00	230.00	69.00	342.00	13.80
ID2	1.44	17.00	23.80	4140.00	390.00	49.95	519.00	308.00	13.00	48.00	620.00	1200.00	450.00	2.49	85.00	85.00	3100.00	72.00	26.00	239.00	700.00	370.00	45.00	7.00	4.50	60.00	756.00	436.00	50.00	494.00	11.80
ID3	0.41	17.00	23.80	4140.00	390.00	49.95	390.00	236.00	11.00	34.00	620.00	1200.00	450.00	2.49	85.00	85.00	3100.00	72.00	26.00	239.00	783.00	370.00	51.00	7.00	4.50	51.00	756.00	436.00	50.00	518.00	11.80
ID4	0.22	17.00	23.80	4140.00	390.00	49.95	390.00	236.00	11.00	34.00	620.00	1200.00	450.00	2.49	85.00	85.00	3100.00	72.00	26.00	239.00	783.00	370.00	51.00	7.00	4.50	51.00	756.00	436.00	50.00	518.00	11.80
Means±SD	1.99 ±2.66	15.40±3.2	24.35±1.1	4285±290	405±30	51.26±2.63	443±64.02	263.75±34.76	12.28±1.54	42±9.38	585±70	1215±30	437.5±25	2.32±0.35	82.5±5	82.5±5	2902.75±394.5	72.75±1.5	25±2	213.75±50.5	715.5±88.76	367.5±5	45.25±8.02	6.75±0.5	4.18±0.65	56.13±6.01	669.5±173	384.5±103	54.75±9.5	468±84.76	12.3±1

Table S2 Quantitative PCR primer information and culture conditions for standard bacterial strains

Target bacterial group	Primers' DNA sequence (3'-5')	Predicted PCR product size (bp)	Annealing Temperature (^{o}C)	Reference	qPCR efficiency (%)	Coefficient of determination $(R)^2$	Standard bacterial strains	Culture media	Culture conditions
Staphylococcus aureus	GGCCGTGTTGAACGTGGTC AAATCA	279	48	22	99.1	0.99	*Staphylococcus aureus* NBRC 12732	Baird-Parker Agar Plate	37℃,45 h
Escherichia coli	TIACCATTTCAGTACCTTCTG GTAA CATGCCGCGTGTATGAA GAA CGGGTAACGTCAATGA GCAAA	428	60	23	96.8	0.99	*Escherichia coli* ATCC 11775	Nutrient agar	37℃, 20 h
Salmonella sp.	GTGAAATTATCGCCACGTTC GGGCAA TCATCGCACCGTCAAAGGA ACC	285	55	24	98.5	0.99	*Salmonella enterica* ATCC 19585	Xylose Lysine Deoxycholate Salt Agar	37℃, 20 h

Table S3 Culture conditions for bacterial plate count

Target bacterial group	Plate count method	Culture conditions for plate count	Enrichment media	Enrichment conditions	Selective media	Conditions for selective cultivation	Typical morphology of target bacteria	Confirmatory test	Culture conditions for confirmatory tests	Chinese National Standards Used
Total bacteria	Plate Count Agar	37 ℃, 36 h	–	–	–	–	–	–	–	GB 4789.2—2010
Coliforms	–	–	–	–	Violet Red Bile Agar	37℃,20 h	Characteristic colonies are pink to red or purple , with or without precipitation haloes.(0.5 mm to 1mm in diameter after incubation)	Brilliant Green Lactose Bile	37 ℃, 36 h	GB 4789.3—2010
Salmonella	–	–	Tetrathionate Broth Base, Selenite Cystine Broth	42 ℃, 36 h	Bismuth Sulfite Agar, Xylose Lysine Deoxycholate Salt Agar	37 ℃, 46 h /37 ℃, 20 h	Typical colonies are shining black or chocolate-brown,grey with or without black or brown edge.	Salmonella Biochemical Identification Kit	–	GB 4789.4—2010
Staphylococcus aureus	–	–	–	–	Baird-Parker Agar Plate	37 ℃,45h	Typical colonies are black or grey (2 mm to 3 mm in diameter after incubation for 48 h) and surrounded by a clear zone which may be partially opaque.	Coagulase Test	37℃, 20 h	GB 4789.10—2010
Enterobacter sakazakii	–	–	Modified Lauryl Sulfate Tryptose Broth-Vancomycin	44 ℃, 24 h	Chromogenic Enterbacter Sakazakii Agar/Trypticase Soy Agar	37 ℃, 18 h/ 25 ℃, 50 h	Characteristic colonies are yellow	Enterobacter sakazakii Biochemical Identification Kit	–	GB 4789.40—2010

Table S4 The relative abundance (in percentage) of bacteria at phylum, class, order, family, genus and species level

Species	2A	2B	2C	2D	2E	2F	2G	3A	3B	3C	3D	3E	3F	3G	4A	4B	4C	4D	4E	4F	4G	5A	5B	5C	5D	5E	5F	5G	Mean
Acidobacteria	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
*Actin

Pseudomonas_viridiflava	0	0	0.028935	0	0	0.014758	0.032383	0.03996	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.003868
Pseudoxanthomonas_mexicana	0	0	0	0.04008	0	0.029516	0	0	0	0	0	0	0	0	0	0	0.017191	0	0	0	0	0	0.034959	0.058343	0	0.075415	0	0.297788	0.032954	0.022031	0.253807	0.10846	0.032351
Pseudoxanthomonas_taiwanensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.016477	0	0	0	0.000549
Pseudoxanthomonas_yeongjuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.015083	0	0	0	0	0	0	0.000503
Psychrobacillus_psychrodurans	0	0.042355	0	0	0	0	0.016192	0.01998	0.015168	0	0.016661	0	0	0	0	0	0	0	0.027709	0.038161	0	0	0	0	0	0	0.042541	0	0	0.01493	0	0.00779
Psychrobacter_arenosus	0	0	0	0	0	0	0.016192	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.019448	0	0	0	0.01418	0	0.022031	0.01493	0	0.002893
Psychrobacter_cibarius	0.024981	0	0	0	0	0	0.032383	0.01998	0.045503	0.022599	0.033322	0.128617	0	0	0	0	0	0	0.076321	0.036603	0.017479	0	0	0.015083	0	0.028361	0.016477	0.110156	0.119439	0	0.024244
Psychrobacter_cryohalolentis	0	0	0	0	0	0	0.016192	0	0	0	0	0	0	0	0	0	0.017191	0	0	0	0	0	0.019448	0	0.015083	0	0	0	0	0	0	0.002264
Psychrobacter_faecalis	0.024981	0	0	0	0.018372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0	0	0.002179
Psychrobacter_fozii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01418	0.032954	0.044063	0	0	0.00304
Psychrobacter_fulvigenes	0	0	0	0	0	0	0.032383	0	0	0	0	0.032154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.042541	0	0	0.01493	0	0.004067
Psychrobacter_maritimus	0	0	0	0	0.018372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000612
Pusillimonas_ginsengisoli	0	0	0	0	0.018372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000612
Pusillimonas_noertemannii	0	0	0	0	0	0	0	0	0	0	0.016661	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000555
Rahnella_aquatilis	0	0.042355	0.05787	0.06012	0.055117	0.029516	0.048575	0	0	0.022599	0.083306	0	0	0.120482	0.430063	0.017191	0	0	0	0	0	0	0	0	0	0.015083	0.357143	0.042541	0	0	0	0	0.046065
Ralstonia_mannitolilytica	0	0	0	0	0.036744	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.015083	0	0	0	0	0	0	0.001728
Ralstonia_pickettii	0	0	0	0	0	0	0	0	0	0	0.016661	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000555
Raoultella_ornithinolytica	0.024981	0.042355	0.144676	0	0	0.07379	0.064767	0.07992	0.166844	0.045198	0.066644	0.032154	0	0.02008	0.614376	0.085955	0	0.027709	0	0	0	0	0	0	0	0	0	0	0.016477	0	0	0.180766	0.056223
Raoultella_terrigena	0.049963	0	0	0	0	0	0.080959	0	0.015168	0	0	0	0.018755	0	0.020479	0.051573	0	0	0.01908	0	0	0	0	0	0	0	0	0	0	0.032954	0	0	0.072307	0.012041
Rhizobium_radiobacter	0	0	0	0	0	0	0.016192	0.01998	0	0	0	0.032154	0	0	0	0	0	0	0	0	0.036603	0	0	0	0	0	0	0.042541	0.016477	0	0.01493	0.072307	0.008373
Rhizobium_skierniewicense	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01908	0	0	0	0	0	0	0	0.01418	0	0	0.01493	0	0.001606
Rhodobacter_blasticus	0	0	0	0	0.018372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000612
Rhodocytophaga_aerolata	0	0	0.028935	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000965
Rikenella_microfusus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.032954	0	0	0	0.001098
Roseburia_faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01908	0	0	0	0	0	0	0	0	0.016477	0	0.01493	0	0.001683
Roseburia_intestinalis	0	0	0	0.02004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000668
Roseomonas_ludipueritiae	0	0	0	0.02004	0	0.014758	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0.01493	0	0.002392
Roseomonas_vinacea	0	0	0	0	0.018372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000612
Rothia_nasimurium	0	0	0	0	0	0	0	0	0	0.022599	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000753
Ruminobacter_amylophilus	0.024981	0	0.028935	0.06012	0.036744	0	0	0.13986	0.015168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.039683	0	0	0	0	0.072307	0.013927
Ruminococcus_albus	0	0	0	0	0	0	0	0.01998	0	0	0	0	0	0	0	0	0	0	0	0.01908	0.036603	0	0	0	0.015083	0.039683	0	0.065909	0	0	0	0	0.006545
Ruminococcus_bromii	0.099925	0	0	0.02004	0	0	0	0	0.030335	0	0	0	0	0.02008	0	0	0	0	0	0	0	0	0	0	0.023485	0.015083	0	0.028361	0	0	0	0.036153	0.009115
Ruminococcus_callidus	0	0	0	0.02004	0	0	0	0.01998	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001334
Ruminococcus_flavefaciens	0	0.08471	0.028935	0.08016	0	0.014758	0	0	0.015168	0	0	0	0	0	0	0	0	0	0	0.01908	0	0	0.038895	0	0.015083	0.039683	0.042541	0.131817	0	0.044789	0	0.018521
Ruminococcus_gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017479	0	0	0	0.119048	0.01418	0	0	0.02986	0	0.006019
Ruminococcus_lactaris	0	0	0.028935	0.02004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001633
Saccharofermentans_acetigenes	0	0	0	0.02004	0	0.014758	0.016192	0	0	0	0.016661	0	0	0	0	0	0	0	0	0.01908	0.10981	0	0	0	0.015083	0.119048	0.01418	0.411929	0.022031	0.01493	0.072307	0.028868
Salinicoccus_alkaliphilus	0.024981	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000833
Salmonella_enterica	0.049963	0.042355	0	0.04008	0	0.088548	0.016192	0.05994	0.045503	0.045198	0.066644	0.128617	0	0	0	0	0	0	0	0	0.073206	0	0	0	0	0.045249	0	0.099263	0.049432	0	0.134368	0	0.032819
Sarcina_maxima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01418	0.049432	0	0	0	0.00212
Schlegelella_aquatica	0	0.08471	0	0	0	0.029516	0.048575	0	0.030335	0	0	0	0	0.02008	0	0	0	0.083126	0.01908	0.183016	0	0.038895	0	0.060332	0.119048	0.085082	0.032954	0	0.119439	0	0.031806
Selenomonas_ruminantium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.039683	0	0	0	0	0	0.001323
Serratia_fonticola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.020479	0.034382	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001829
Serratia_grimesii	0	0	0	0	0	0	0	0	0	0	0	0	0	0.140562	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004685
Serratia_marcescens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.020479	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000683
Serratia_proteamaculans	0.099925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.003331
Serratia_quinivorans	0.049963	0	0	0	0	0.014758	0.016192	0	0	0	0.066644	0	0	0	0	0.051573	0	0	0.114482	0	0	0	0	0	0	0	0	0	0.016477	0.022031	0	0	0.011737
Shewanella_baltica	0	0	0	0	0.036744	0.014758	0.016192	0	0.015168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002762
Shinella_granuli	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.036153	0.001205
Simplicispira_psychrophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.039683	0	0	0	0	0	0.001323
Solibacillus_silvestris	3.822133	2.498941	3.96412	1.683367	4.317472	3.92562	3.092617	2.077922	2.699833	2.80226	2.799067	3.247588	0.900225	0.301205	1.04444	0.395393	0.375536	2.937102	3.300897	3.879941	0.699178	1.08907	0.681071	1.191554	2.81746	4.424277	1.449992	4.62657	4.762616	4.663774	2.549041
Solirubrobacter_soli	0	0	0	0	0	0	0	0	0.015168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000506
Sphaerochaeta_pleomorpha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.036603	0	0	0	0	0	0	0	0.016477	0	0	0	0.001769
Sphingobacterium_faecium	0	0	0	0.02004	0.036744	0.014758	0.032383	0	0	0	0	0.032154	0	0	0	0.017191	0	0	0.01908	0	0	0	0	0	0.030166	0	0.042541	0	0	0.01493	0.072307	0.011077
Sphingobacterium_kitahiroshimense	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017191	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000573
Sphingomonas_aerolata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.057241	0	0	0	0	0	0	0.039683	0	0	0.044063	0	0.072307	0.00711
Sphingomonas_changbaiensis	0	0	0.05787	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001929
Sphingomonas_panni	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0	0	0.000734
Sphingopyxis_alaskensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01418	0	0	0.01493	0	0.00097
Sphingopyxis_bauzanensis	0	0	0	0	0	0	0	0	0.015168	0	0	0	0	0	0	0	0	0	0	0	0	0	0.019448	0	0	0	0	0.056721	0	0	0.059719	0	0.005035
Sporobacter_termitidis	0	0	0	0	0	0	0	0	0.015168	0.022599	0	0	0	0	0	0	0	0	0	0	0	0	0.019448	0	0	0	0	0	0.082386	0	0.01493	0	0.005151
Sporosarcina_aquimarina	0	0	0	0	0.018372	0	0	0	0	0	0	0	0	0.02008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.036153	0.002487
Sporosarcina_ginsengi	0	0	0	0	0	0	0	0	0.015168	0	0.016661	0	0	0	0	0	0	0.027709	0	0	0	0	0.019448	0	0	0.039683	0	0	0.022031	0	0	0	0.00469
Sporosarcina_koreensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0	0	0.000734
Sporosarcina_luteola	0	0.042355	0.028935	0.02004	0	0	0	0	0	0	0	0	0	0	0	0.017191	0	0.055417	0.01908	0	0.017479	0.038895	0	0	0	0	0.042541	0	0.022031	0	0.036153	0.011337
Sporosarcina_newyorkensis	0.524607	0.508259	0.462963	0.360721	0.698144	0.265643	0.016192	0	0.015168	0	0.033322	0	0.037509	0	0.020479	0	0	0.138543	0.381607	0.10981	0.052438	0	0	0	0.198413	0.042541	0	0.022031	0.02986	0.723066	0.154711
Sporosarcina_soli	0.074944	0.127065	0.289352	0.04008	0.16535	0.22137	0.09715	0	0.015168	0.022599	0.016661	0.032154	0.037509	0.02008	0.040958	0.068764	0.026824	0.083126	0.038161	0.256223	0.017479	0	0.023485	0.030166	0.198413	0.184345	0.065909	0.198282	0.089579	0.253073	0.091142
Staphylococcus_aureus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.039683	0.028361	0	0	0	0	0	0.002268
Staphylococcus_capitis	0	0	0	0	0	0	0	0	0	0.022599	0	0	0.018755	0	0	0	0	0	0	0	0.036603	0	0	0	0.060332	0	0	0	0.022031	0	0	0	0.005344
Staphylococcus_epidermidis	0	0.08471	0.028935	0.06012	0	0.014758	0	0	0.015168	0	0	0.032154	0.018755	0	0	0	0	0	0.209884	0.073206	0	0.038895	0.023485	0	0	0.113443	0.016477	0.022031	0.119439	0	0.029049
Staphylococcus_equorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0	0	0.000734
Staphylococcus_haemolyticus	0	0	0	0.02004	0	0	0	0.01998	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.023485	0	0	0	0.01418	0	0	0	0	0	0.00259
Staphylococcus_hominis	0.024981	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01908	0.036603	0	0	0	0	0	0	0	0	0	0	0	0	0.002689
Staphylococcus_sciuri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0	0	0.000734
Staphylococcus_simulans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022031	0	0	0.000734
Staphylococcus_warneri	0.024981	0.042355	0.028935	0	0	0.014758	0	0	0	0	0	0	0.018755	0	0	0	0	0.027709	0	0	0	0.058343	0	0.015083	0	0.01418	0	0.022031	0	0	0	0	0.008904
Stenotrophomonas_chelatiphaga	0	0.042355	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01418	0	0	0	0	0.001885
Stenotrophomonas_geniculata	0	0	0	0.04008	0	0.014758	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01493	0	0.002326
Stenotrophomonas_maltophilia	0	0	0	0.02004	0	0	0	0.01998	0.075838	0	0.016661	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004417
Stenotrophomonas_rhizophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.016477	0	0	0	0.000549
Streptococcus_agalactiae	0.374719	0.465904	0.752315	0.180361	0.845122	0.590319	0.631477	0.579421	0.515698	0.384181	1.249583	0.610932	0.037509	0	0	0.137528	0.026824	0.55417	0.324366	0.475842	0	0.058343	0.023485	0.135747	0.634921	0.553035	0.214203	1.03547	0.671842	0.650759	0.423803
Streptococcus_australis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.073206	0	0	0	0	0	0	0	0	0	0	0	0	0.00244
Streptococcus_cristatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.019448	0	0	0	0	0	0	0	0	0	0	0.000648
Streptococcus_dysgalactiae	0	0	0	0	0	0	0.016192	0	0	0.022599	0	0.032154	0.018755	0	0	0	0	0	0	0	0	0	0	0.015083	0.15873	0.01418	0	0.044063	0.01493	0.036153	0.012428
Streptococcus_gallolyticus	0	0	0	0	0	0.014758	0	0.01998	0	0	0	0	0	0	0.020479	0	0	0	0	0	0	0	0	0	0	0	0.01418	0	0	0	0	0	0.002313
Streptococcus_gordonii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.023485	0	0	0	0	0	0	0	0	0	0.000783
Streptococcus_infantarius	0	0.127065	0	0	0.036744	0.103306	0	0.01998	0.06067	0.045198	0.066644	0	0.037509	0	0	0	0.026824	0	0	0	0	0.019448	0	0	0.079365	0.226886	0	0	0	0	0	0	0.028321
Streptococcus_mitis	0.049963	0	0.028935	0	0	0.014758	0.016192	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01493	0.036153	0.005364
Streptococcus_parauberis	0.024981	0	0.05787	0.04008	0.036744	0.014758	0.09715	0.03996	0.091006	0.090395	0.016661	0.032154	0	0	0.020479	0	0	0.055417	0.076321	0.146413	0	0	0	0.015083	0	0.028361	0	0.044063	0.089579	0	0.033916
Streptococcus_salivarius	8.743442	7.539178	7.841435	5.971944	10.28844	11.3046	8.306347	8.791209	10.42014	11.23164	8.747084	5.62701	73.06827	68.29317	72.72169	74.05879	39.6191	5.901912	8.872353	23.24305	74.42755	42.06534	12.63504	68.64253	7.34127	2.977879	8.897677	0.572813	0.447895	0.542299	22.97137
Streptococcus_sanguinis	0	0	0	0	0	0.014758	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000492
Streptococcus_sinensis	0	0	0	0	0.018372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000612
Streptococcus_uberis	0	0	0.028935	0	0.018372	0.014758	0.016192	0.01998	0	0	0.016661	0	0	0.060241	0	0	0	0	0.038161	0.036603	0	0	0	0	0.15873	0.028361	0	0.066094	0.01493	0.036153	0.018472
Streptococcus_vestibularis	0.024981	0.042355	0	0	0	0	0	0	0	0	0	0	0.037509	0.02008	0	0	0	0	0	0	0.017479	0	0	0.030166	0	0	0.016477	0	0	0	0	0	0.006302
Subdoligranulum_variabile	0	0	0.05787	0	0	0	0	0	0	0	0	0

Table S5 Simpson and Chao1 indexes in infant formula samples

Sample	Simpson index	Chao1 index
D1	0.98	3117.12
D2	0.99	3811.34
D3	0.98	2415.26
D4	0.98	2548.47
D5	0.98	1581.86
D6	0.98	2017.02
D7	0.98	1857.21
D8	0.99	2851.99
D9	0.98	1995.66
D10	0.98	1821.83
D11	0.98	1908.38
D12	0.99	1882.04
Mean±SD	0.98±0.004	2317.35±658.45
IA1	0.64	3394.07
IA2	0.77	3068.99
IA3	0.7	1620.8
IA4	0.71	2441.2
IA5	0.95	6151.6
IB1	0.98	1616.15
IB2	0.98	2262.31
IB3	0.95	1905.61
IC1	0.81	1995.32
IC2	0.9	2893.34
IC3	0.88	2827.5
IC4	0.77	2121.82
IC5	0.98	1686.11
IC6	0.99	3021.38
ID1	0.99	4814.07
ID2	0.98	2195.78
ID3	0.99	2741.11
ID4	0.98	1852.8
Mean±SD	0.89±0.12	2700.55±1168.69

Table S6 Phyla, genera and species showing significant differences between the domestic and imported IF samples. P-value was adjusted by Benjamini-Hochberg method.

Taxonomy	Relative contribution (%)		Median, range (%)		P-value
	Domestic IF	Imported IF	Domestic IF	Imported IF	
Phyla					
Tenericutes	0.252	0.208	0,0-0.889	0-1.219	0.002
Planctomycetes	0.005	0.001	0,0-0.033	0-0.016	0.042
Genera					
Lactococcus	48.291	27.916	49.953,37.823-54.509	32.911,7.481-54.415	0.026
Anoxybacillus	4.325	3.57	3.642,2.238-8.637	0.381,0.07-39.7	0.043
Acinetobacter	3.036	0.884	2.47,1.918-4.949	0.648,0.047-2.338	0.001
Leuconostoc	1.602	0.28	1.263,0.72-3.367	0.232,0.07-0.6	0.000
Klebsiella	1.006	0.142	0.953,0.318-1.948	0.037,0-1.117	0.001
Petrobacter	0.704	0.031	0.97,0-1.446	0.021,0-0.146	0.039
Deinococcus	0.617	0.01	0.524,0.087-1.299	0,0-0.11	0.000
Citrobacter	0.361	0.026	0.267,0.116-0.72	0,0-0.164	0.000
Enterobacter	0.312	0.039	0.217,0-0.68	0,0-0.261	0.017
Enterococcus	0.158	1.23	0.135,0-0.707	0.575,0-8.189	0.043
Burkholderia	0.157	0.001	0.16,0.032-0.254	0,0-0.016	0.000
Gallionella	0.063	0.003	0.041,0-0.331	0,0-0.044	0.013
Kurthia	0.062	0	0.047,0-0.225	0,0-0	0.001
Atopostipes	0.028	0.006	0.024,0-0.065	0,0-0.044	0.026
rc4-4	0.027	0.003	0.024,0-0.1	0,0-0.039	0.018
Species					
Lactococcus lactis	27.784	8.659	25.45,14.855-41.022	5.478,1.961-48.873	0.025
Anoxybacillus kestanbolensis	2.589	3.052	1.913,1.274-6.473	0.255,0.017-19.582	0.049
Acinetobacter baumannii	2.099	0.453	1.835,1.36-3.432	0.11,0-1.583	0.001
Anoxybacillus flavithermus	1.595	1.709	1.386,0.819-2.951	0.135,0-14.887	0.017
Leuconostoc lactis	1.3	0.076	0.981,0.424-3.109	0.088,0-0.469	0.001
Klebsiella pneumoniae	0.823	0.09	0.796,0.289-1.461	0.019,0-0.395	0.001
Petrobacter succinatimandens	0.704	0.028	0.97,0-1.446	0.021,0-0.146	0.044
Deinococcus geothermalis	0.615	0.006	0.524,0.087-1.299	0,0-0.057	0
Lactococcus chungangensis	0.492	0.127	0.533,0.16-0.782	0.234,0.035-0.542	0.044
Acinetobacter junii	0.402	0.009	0.31,0.02-0.889	0,0-0.061	0
Leuconostoc mesenteroides	0.21	0.054	0.195,0.12-0.347	0.087,0-0.209	0.027
Klebsiella oxytoca	0.183	0.091	0.155,0.018-0.487	0,0-0.756	0.017
Burkholderia multivorans	0.157	0.002	0.16,0.032-0.254	0,0-0.016	0
Pseudomonas citronellolis	0.096	0	0.067,0.015-0.254	0,0-0	0
Enterobacter hormaechei	0.07	0.004	0.031,0-0.2	0,0-0.02	0.004
Kurthia gibsonii	0.06	0	0.047,0-0.2	0,0-0	0.002
Bacillus fumarioli	0.053	0	0.04,0-0.125	0,0-0	0
Acinetobacter schindleri	0.052	0.008	0.043,0-0.181	0,0-0.044	0.017
Aeromonas hydrophila	0.045	0.002	0.021,0-0.251	0,0-0.02	0.017
Enterobacter aerogenes	0.037	0.002	0.027,0-0.14	0,0-0.02	0.005
Atopostipes suicloacalis	0.028	0.009	0.024,0-0.065	0,0-0.044	0.032
Pseudomonas mosselii	0.025	0	0.009,0-0.136	0,0-0	0.036
Achromobacter spanius	0.02	0	0.007,0-0.096	0,0-0	0.036

Table S7 The relative abundances (in percentage) of prevalent bacteria at genus level and whey protein nitrogen index (WPNI) value of samples

Bacteria	Domestic IF	Imported IF			
		Subgroup 1	Subgroup 2	Subgroup 3	Subgroup 4
Bacillus	8.75	1.33	13.44	8.35	16.38
Lactobacillus	1	3.13	6.23	6.69	0.63
Streptococcus	9.49	65.79	13.27	35.11	3.42
WPNI	6.54±0.57	6.01±0.73	3.58±0.79	5.4±3.59	1.99±2.66

Remarks: WPNI value represents as mean ± standard deviation.

Table S8 Bacterial counts in infant formula

Sample	Total Bacteria Count	Coliforms Count	*Salmonella* Count	*Staphylococcus aureus* Count	*Enterobacter sakazakii* Count
	cfu/g	cfu/g	cfu/g	cfu/g	cfu/g
D1	40±42.43	nd	nd	nd	nd
D2	70±14.14	nd	nd	nd	nd
D3	60±28.28	nd	nd	nd	nd
D4	45±21.21	nd	nd	nd	nd
D5	50±42.43	nd	nd	nd	nd
D6	80±14.14	nd	nd	nd	nd
D7	95±7.07	nd	nd	nd	nd
D8	80±14.14	nd	nd	nd	nd
D9	60±42.43	nd	nd	nd	nd
D10	90±0	nd	nd	nd	nd
D11	50±14.14	nd	nd	nd	nd
D12	75±7.07	nd	nd	nd	nd
IA1	95±7.07	nd	nd	nd	nd
IA2	140±14.14	nd	nd	nd	nd
IA3	nd	nd	nd	nd	nd
IA4	30±42.43	nd	nd	nd	nd
IA5	10±14.14	nd	nd	nd	nd
IB1	85±35.36	nd	nd	nd	nd
IB2	30±14.14	nd	nd	nd	nd
IB3	135±35.36	nd	nd	nd	nd
IC1	165±21.21	nd	nd	nd	nd
IC2	35±7.07	nd	nd	nd	nd
IC3	135±7.07	nd	nd	nd	nd
IC4	140±14.14	nd	nd	nd	nd
IC5	110±0	nd	nd	nd	nd
IC6	nd	nd	nd	nd	nd
ID1	135±21.21	nd	nd	nd	nd
ID2	160±14.14	nd	nd	nd	nd
ID3	110±84.85	nd	nd	nd	nd
ID4	45±21.21	nd	nd	nd	nd

nd: not detecable

The viable counts for the target bacteria in samples were performed with two dilution gradient (10^{-1} and 10^{-2}) in duplicate and are presented as mean ± standard deviation