

## **Variation in human milk composition is related to differences in milk and infant fecal microbial communities**

Figure S1: Relative abundances of the initial top 25 bacterial genera in milk before and after prevalence-based filtering

Figure S2: Milk and infant fecal microbiome beta diversities and most abundant taxa

Figure S3: Differences in the alpha and beta diversities of milk and infant fecal community state types

Figure S4: HMO composition

Table S1: Selected cohort characteristics

Table S2: Milk microbial community state type (lactotype) characteristics

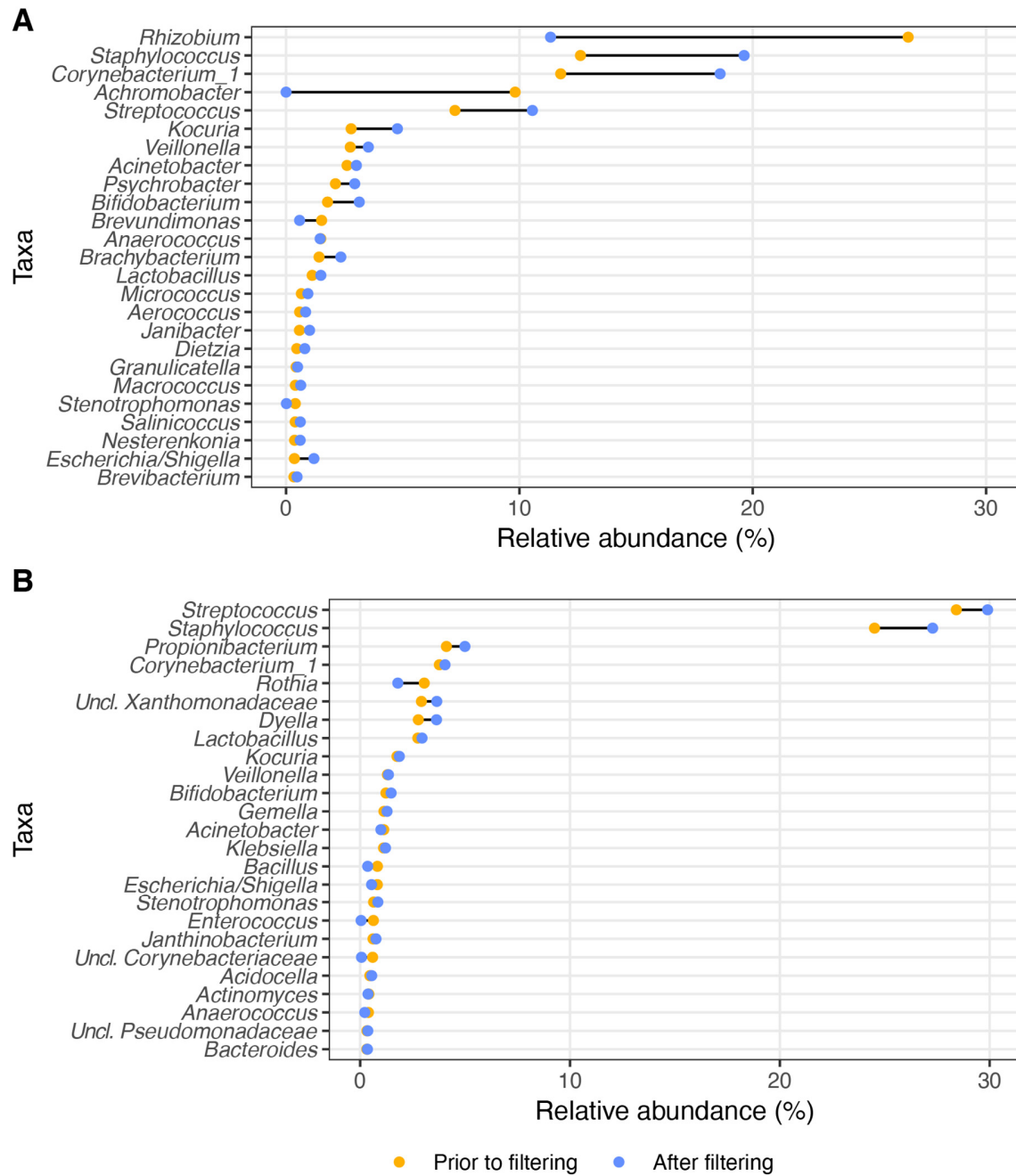
Table S3: Infant fecal microbial community state type (enterotype) characteristics

Table S4: Indicator taxa of the microbial lactotypes

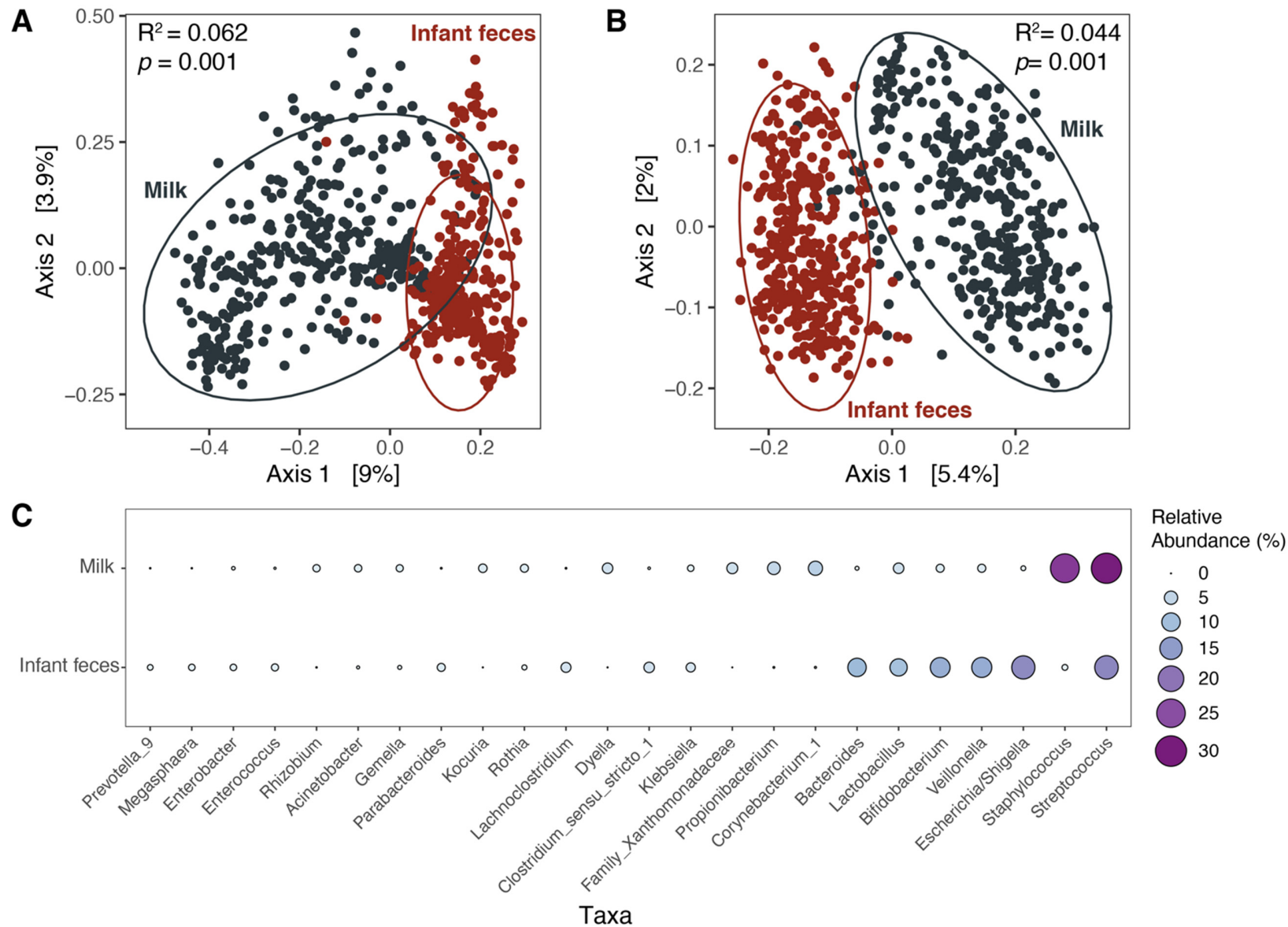
Table S5: Indicator taxa of the infant microbial enterotypes

Table S6: HMO concentrations and ratios among microbial lactotypes

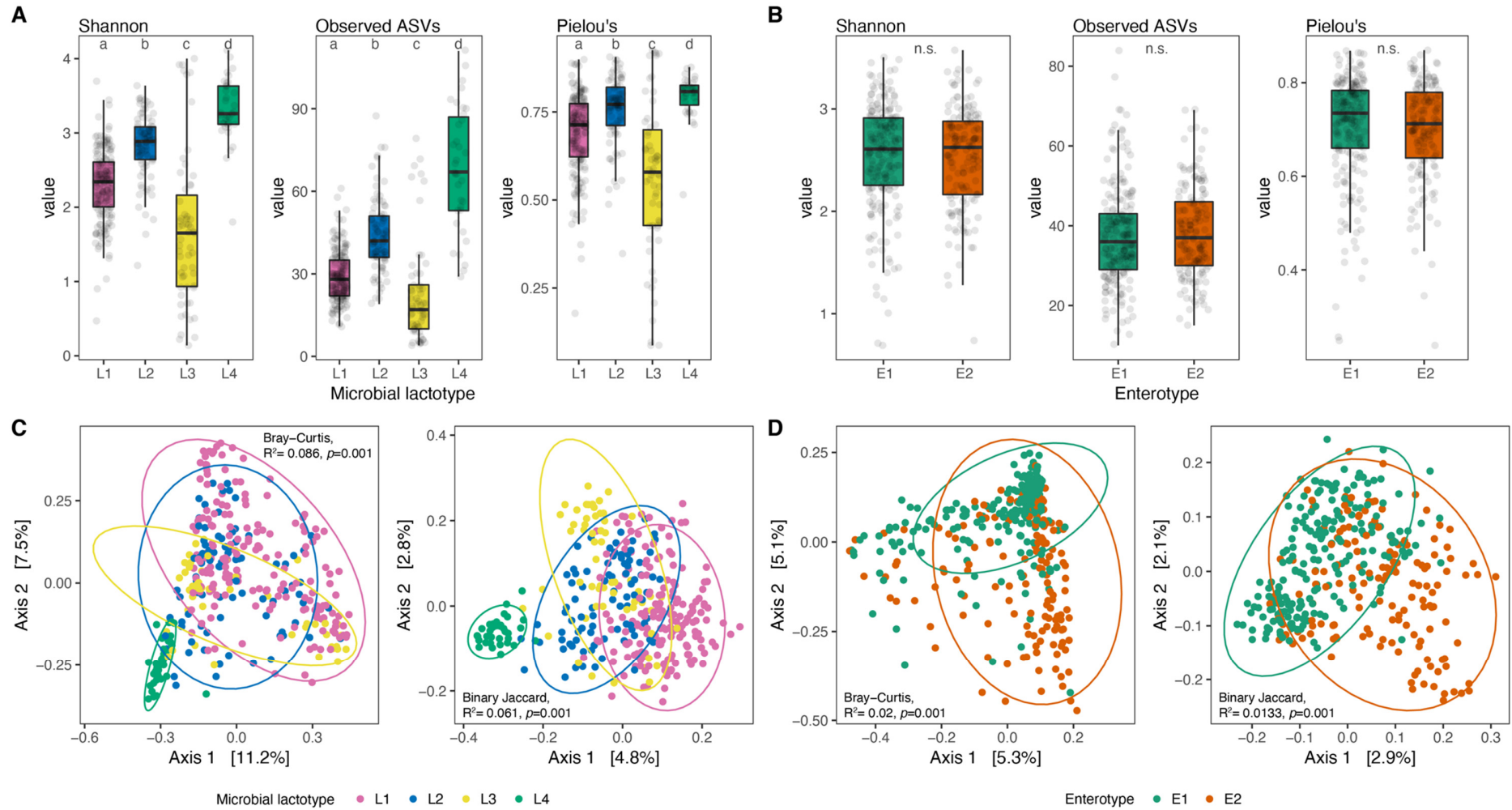
Table S7: HMO concentrations and ratios between enterotypes



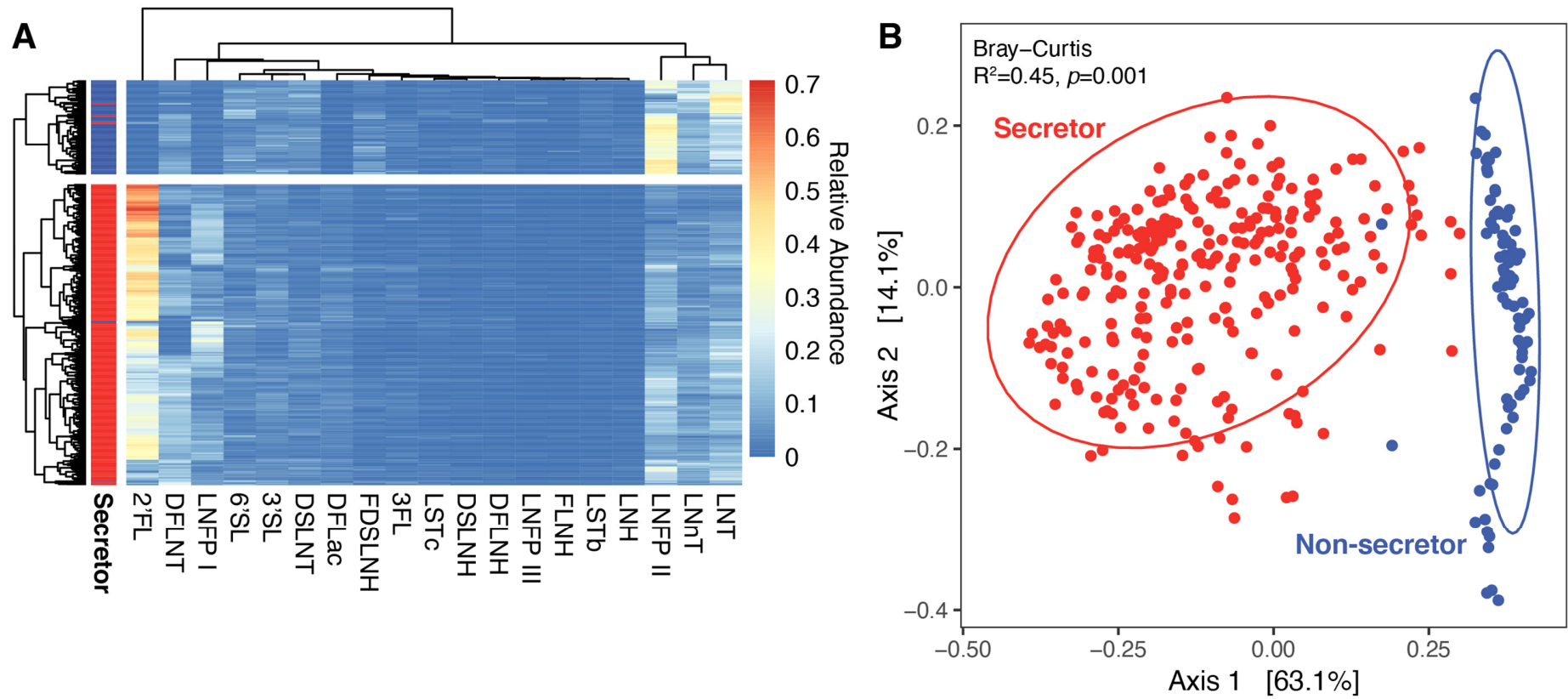
**Figure S1.** Relative abundances of the initial top 25 bacterial genera in milk before and after prevalence-based filtering. **(A)** Rural Ethiopia cohort and **(B)** all other. For the ETR milk samples, 580 of the initial 2,511 ASVs were validated to have statistical support as non-contaminants. For the remaining population cohort samples, 1,761 of the initial 8,964 ASVs were validated to have statistical support as non-contaminants. In general, there were marginal differences in the relative abundance of the most abundant genera (e.g., *Staphylococcus* and *Streptococcus*). Overall, most ASVs marked as contaminants in milk came from very low abundant genera (i.e., less than 0.001% across all milk samples). Only two of the initially most abundant taxa in milk were observed to have reductions in abundance > 10% (*Achromobacter* and *Rhizobium* in the ETR cohort). The reduction of *Rhizobium* abundance in the ETR cohort was attributed to the removal of a single *Rhizobium* ASV, although another abundant and prevalent *Rhizobium* ASV in the ETR samples not found in the respective negative controls was retained. Within the ETR samples the initial top 25 genera represented ~91% of all genera (from 458 genera) and in the decontam-filtered samples the top 25 genera represented ~92% of all genera (from 137 genera). Similarly, in the remaining population cohorts the initial top 25 genera represented ~86% of all genera (from 983 genera) and in the decontam-filtered samples the top 25 genera represented ~92% of all genera (from 334 genera).



**Figure S2.** Milk and infant fecal microbiome beta diversities and most abundant taxa. **(A)** Microbial community structure (Bray-Curtis). **(B)** Microbial community membership (binary Jaccard). Differences between sample types were tested using PERMANOVA as implemented in vegan, with  $R^2$  and  $p$  values listed. Ellipses represent the 95% confidence ellipses. **(C)** Bubble plot showing the most abundant taxa in milk and infant feces.



**Figure S3.** Differences in the alpha and beta diversities of milk and infant fecal community state types. The alpha and beta diversities of milk (**A,C**) and infant feces (**B,D**) were assessed and differences among and between community state types tested. Alpha diversity of milk (**A**) and infant feces was (**B**) assessed by computing Shannon diversity, observed ASVs, and Pielou's evenness metrics, and differences in these metrics was tested using the Kruskal-Wallis test, followed by Dunn's test (in milk samples) and the Mann-Whitney test (infant fecal). The beta diversities of milk (**C**) and infant feces (**D**) were assessed using Bray-Curtis and binary Jaccard metrics, with differences in community state types tested using PERMANOVA as implemented in vegan. Letters in panels **A** and **B** represent groups that statistically differ from one another ( $p < 0.05$ ); n.s., not significant. Ellipses in panels **C** and **D** represent the 95% confidence ellipses.



**Figure S4.** HMO composition. **(A)** Heatmap of the relative abundances of the 19 HMOs that represent the majority of HMOs present in milk. Maternal secretor status is denoted on the left-hand side (secretors, red; non-secretors, blue). Samples and HMOs are hierarchically clustered. **(B)** Multidimensional scaling (MDS) of HMO profiles based on Bray-Curtis distance. Samples are colored by maternal secretor status, and PERMANOVA  $R^2$  and  $p$  values are given. Ellipses represent 95% confidence ellipses.

**Table S1. Selected cohort characteristics**

Characteristic	Population												<i>p</i>
	All (n=357)	ETR (n=40)	ETU (n=26)	GBR (n=37)	GBU (n=36)	GN (n=28)	KE (n=41)	PE (n=42)	SP (n=36)	SW (n=21)	USC (n=12)	USW (n=38)	
Maternal age (y) <sup>1</sup>	27.4±6.1	24.6±5.1	22.2±3.5	27.1±7.4	26.9±5.0	27.4±5.6	25.3±5.2	26.6±6.4	34.5±3.5	30.1±4.9	30.6±4.7	29.1±5.1	<0.001
Time postpartum (d) <sup>2</sup>	64.6±21.9	70.9±31.9	58.3±15.3	64.6±16.6	61.6±18.1	59±20.3	72.9±23.9	60.3±17	72.3±24.8	48.8±19.2	59.1±19.9	68.1±16	<0.001
Parity (n)	2.4±1.9	3.5±2.1	1.6±1.1	4.2±3.2	3.3±2	2.1±1	2.5±1.4	2±1.0	1.3±0.7	1.5±0.7	1.8±0.7	1.8±1.1	<0.001
Body mass index (kg/m <sup>2</sup> ) <sup>3</sup>	24.2±4.6	21.3±2.8	22.1±3.2	21.4±2.9	23.1±3.3	24.6±4.2	23.7±3.7	28±5.4	23.3±3.5	25.7±4.3	29±4.5	26.9±5.3	<0.001
Vaginal delivery, n (%) <sup>4</sup>	303 (86)	39 (100)	26 (100)	37 (100)	35 (97)	24 (89)	32 (80)	22 (52)	33 (92)	17 (81)	8 (67)	30 (79)	<0.001
Infant sex, Female, n (%) <sup>5</sup>	174 (49)	17 (44)	12 (46)	16 (44)	21 (58)	12 (43)	23 (56)	23 (55)	17 (47)	9 (43)	3 (27)	21 (55)	0.73
Infant weight-for-length z-score <sup>6</sup>	0.1±0.1	-0.3±1.0	-0.6±1.5	0.5±1.2	-0.1±1.1	-0.2±1.4	1.4±2.2	0.6±1.3	-0.3±1.1	-0.4±1.0	0.7±2.9	-1.0±1.1	<0.001
Exclusively breastfeeding, n (%) <sup>7</sup>	212 (60)	38 (95)	23 (89)	36 (97)	19 (53)	8 (29)	15 (37)	13 (31)	23 (64)	9 (43)	6 (50)	22 (60)	<0.001

**Footnote:** Categorical data are given as number of participants and, in parentheses, percent of total. Continuous data are provided as means ± standard deviation; *p* values were calculated from Kruskal-Wallis test for continuous data and Chi-squared test for categorical data. Infant weight-for-length z-scores were based on the 2006 WHO growth reference. <sup>1</sup>, missing values for 3 dyads: 2 in GBR and 1 in GBU; <sup>2</sup>, missing values for 1 dyad in GBR; <sup>3</sup>, missing values for 7 dyads: 1 from GN, 2 from KE, 4 from USW; <sup>4</sup>, missing values for 3 dyads: 1 in ETR, GN, and KE; <sup>5</sup>, missing values for 3 dyads: 1 in ETR, GBR, and USC; <sup>6</sup>, missing values for 10 dyads: 1 in ETR/GBR/GBU KE, 4 in USC, and 2 USW; <sup>7</sup>, missing values for 1 dyad in USW.

Table S2. Milk microbial community state type (lactotype) characteristics						
Characteristic	Microbial Lactotype				<i>p</i>	FDR <i>p</i>
	L1 (n=178)	L2 (n=85)	L3 (n=59)	L4 (n=35)		
Maternal age (y) <sup>1</sup>	28.2±5.8	26.1±6.7	28.9±5.9	24.2±4.4	<0.001	0.002
Time postpartum (d) <sup>2</sup>	61.8±20.5	69.1±19.8	62.1±18.8	71.8±33.6	0.030	0.045
Parity (n)	2.0±1.4	3.0±2.5	2.2±1.4	3.4±1.9	<0.001	0.002
Maternal body mass index (kg/m <sup>2</sup> ) <sup>3</sup>	25.5±4.8	22.8±4.2	23.9±3.9	21.3±2.9	<0.001	0.002
Maternal secretor status (secretor), n (%)	147 (83)	68 (80)	38 (64)	21 (60)	0.002	0.004
Vaginal delivery, n (%) <sup>4</sup>	146 (82)	73 (87)	50 (86)	34 (100)	0.053	0.060
Infant sex, Female, n (%) <sup>5</sup>	88 (50)	45 (54)	27 (46)	14 (41)	0.612	0.612
Infant weight-for-length z-score <sup>6</sup>	0.0±1.6	0.4±1.6	0.0±1.3	-0.3±1.1	0.053	0.060
Exclusively breastfeeding, n (%) <sup>7</sup>	99 (56)	54 (64)	25 (42)	34 (97)	<0.001	0.002

**Footnote:** Categorical data are given as number of participants and, in parentheses, percent of total. Continuous data are provided as means ± standard deviation; *p* values were calculated from Kruskal-Wallis test for continuous data and Chi-squared test for categorical data. Infant weight-for-length z-scores were based on the 2006 WHO growth reference. <sup>1</sup>, missing values for 3 dyads: 2 in GBR and 1 in GBU; <sup>2</sup>, missing values for 1 dyad in GBR; <sup>3</sup>, missing values for 7 dyads: 1 from GN, 2 from KE, 4 from USW; <sup>4</sup>, missing values for 3 dyads: 1 in ETR, GN, and KE; <sup>5</sup>, missing values for 3 dyads: 1 in ETR, GBR, and USC; <sup>6</sup>, missing values for 10 dyads: 1 in ETR/GBR/GBU KE, 4 in USC, and 2 USW; <sup>7</sup>, missing values for 1 dyad in USW.

**Table S3. Infant fecal microbial community state type (enterotype) characteristics**

Characteristic	Microbial enterotype			
	E1 (n=207)	E2 (n=150)	<i>p</i>	FDR <i>p</i>
Maternal age (y) <sup>1</sup>	28.1±6.2	26.6±5.9	0.022	0.040
Time postpartum (d) <sup>2</sup>	66±23.3	62±19.6	0.202	0.260
Parity (n)	2.2±1.7	2.8±2.0	<0.001	0.009
Maternal body mass index (kg/m <sup>2</sup> ) <sup>3</sup>	24.8±4.9	23.3±4.0	0.003	0.012
Maternal secretor status (secretor), n (%)	155 (75)	119 (79)	0.392	0.441
Vaginal delivery, n (%) <sup>4</sup>	170 (83)	132 (89)	0.182	0.260
Infant sex, Female, n (%) <sup>5</sup>	97 (48)	77 (51)	0.551	0.551
Infant weight-for-length z-score <sup>6</sup>	-0.1±1.7	0.2±1.4	0.004	0.012
Exclusively breastfeeding, n (%) <sup>7</sup>	112 (54)	102 (69)	0.009	0.020

**Footnote:** Categorical data are given as number of participants and, in parentheses, percent of total. Continuous data are provided as means ± standard deviation; *p* values were calculated from Mann-Whitney test for continuous data and Chi-squared test for categorical data. Infant weight-for-length z-scores were based on the 2006 WHO growth reference. <sup>1</sup>, missing values for 3 dyads: 2 in GBR and 1 in GBU; <sup>2</sup>, missing values for 1 dyad in GBR; <sup>3</sup>, missing values for 7 dyads: 1 from GN, 2 from KE, 4 from USW; <sup>4</sup>, missing values for 3 dyads: 1 in ETR, GN, and KE; <sup>5</sup>, missing values for 3 dyads: 1 in ETR, GBR, and USC; <sup>6</sup>, missing values for 10 dyads: 1 in ETR/GBR/GBU KE, 4 in USC, and 2 USW; <sup>7</sup>, missing values for 1 dyad in USW.



**Table S4. Indicator taxa of the microbial lactotypes**

Taxa	Microbial lactotype	indval	<i>p</i>	frequency	FDR <i>p</i>
Family Xanthomonadaceae	L1	0.54	0.001	235	0.006
<i>Dyella</i>	L1	0.48	0.001	242	0.006
<i>Janthinobacterium</i>	L1	0.41	0.001	185	0.006
<i>Streptococcus</i>	L1	0.41	0.001	348	0.006
<i>Acidocella</i>	L1	0.34	0.001	178	0.006
<i>Flavobacterium</i>	L1	0.22	0.001	73	0.006
<i>Aeromonas</i>	L1	0.34	0.002	144	0.011
<i>Rothia</i>	L1	0.28	0.003	155	0.015
<i>Fluviicola</i>	L1	0.09	0.006	20	0.028
Family Caulobacteraceae	L1	0.10	0.014	22	0.049
Family Clostridiaceae 1	L1	0.11	0.02	23	0.064
<i>Ralstonia</i>	L1	0.07	0.023	17	0.071
<i>Yersinia</i>	L1	0.20	0.025	104	0.075
Phylum Parcubacteria	L1	0.09	0.029	26	0.084
<i>Burkholderia</i>	L1	0.08	0.039	27	0.104
<i>Fodinicola</i>	L1	0.07	0.048	16	0.124
<i>Hydrotaea</i>	L1	0.07	0.058	19	0.142
<i>Bradyrhizobium</i>	L1	0.08	0.089	29	0.210
<i>Morganella</i>	L1	0.07	0.103	25	0.240
<i>Clostridium sensu stricto</i> 18	L1	0.07	0.128	21	0.283
<i>Clostridium sensu stricto</i> 9	L1	0.04	0.131	10	0.286
Family Bacillaceae	L1	0.05	0.134	15	0.286
hgcl clade	L1	0.03	0.134	6	0.286
<i>Alpinimonas</i>	L1	0.04	0.156	8	0.316
<i>Sediminibacterium</i>	L1	0.03	0.168	8	0.330
<i>Cytophaga</i>	L1	0.03	0.177	5	0.333
<i>Acidovorax</i>	L1	0.05	0.204	19	0.353
<i>Limnohabitans</i>	L1	0.05	0.221	18	0.377
<i>Candidatus Flaviluna</i>	L1	0.02	0.228	4	0.387
<i>Achromobacter</i>	L1	0.02	0.231	4	0.390
<i>Acidibacter</i>	L1	0.03	0.25	8	0.409
Phylum SM2F11	L1	0.02	0.263	4	0.424
<i>Azorhizobium</i>	L1	0.02	0.264	4	0.424
Family Microbacteriaceae	L1	0.02	0.264	4	0.424
<i>Kingella</i>	L1	0.02	0.276	4	0.439
<i>Candidatus Rhodoluna</i>	L1	0.03	0.282	13	0.445
<i>Pseudarcicella</i>	L1	0.03	0.312	12	0.484
Family Pseudomonadaceae	L1	0.09	0.326	69	0.504
Phylum Bacteroidetes	L1	0.03	0.329	7	0.506

<i>Candidatus Planktoluna</i>	L1	0.02	0.365	3	0.554
PRD01a011B	L1	0.02	0.392	3	0.587
<i>Pantoea</i>	L1	0.04	0.393	14	0.587
<i>Schlegelella</i>	L1	0.03	0.399	12	0.594
<i>Phenylobacterium</i>	L1	0.02	0.412	3	0.610
Phylum Proteobacteria	L1	0.02	0.431	3	0.628
<i>Rhodococcus</i>	L1	0.02	0.454	9	0.646
<i>Rheinheimera</i>	L1	0.02	0.462	4	0.650
<i>Mesorhizobium</i>	L1	0.02	0.466	8	0.652
<i>Propionivibrio</i>	L1	0.02	0.481	5	0.666
<i>Candidatus Planktophila</i>	L1	0.03	0.508	12	0.671
Order GR-WP33-30	L1	0.02	0.508	4	0.671
Family NS11-12 marine group	L1	0.02	0.51	4	0.671
<i>Ewingella</i>	L1	0.01	0.6	5	0.766
<i>Cellulomonas</i>	L1	0.01	0.607	2	0.766
<i>Dechloromonas</i>	L1	0.01	0.607	2	0.766
<i>Nubsella</i>	L1	0.01	0.607	2	0.766
<i>Mangroviflexus</i>	L1	0.01	0.611	2	0.766
<i>Gemella</i>	L1	0.18	0.612	163	0.766
Phylum TM6	L1	0.01	0.612	2	0.766
<i>Marinomonas</i>	L1	0.01	0.629	2	0.782
Family Comamonadaceae	L1	0.01	0.637	2	0.784
<i>Helicobacter</i>	L1	0.01	0.641	2	0.786
<i>Gordonia</i>	L1	0.01	0.646	2	0.789
Phylum Candidate division SR1	L1	0.01	0.649	4	0.789
<i>Caulobacter</i>	L1	0.01	0.65	2	0.789
Family Holophagaceae	L1	0.01	0.661	2	0.800
Family Rhodobiaceae	L1	0.01	0.678	3	0.815
<i>Paludibacter</i>	L1	0.01	0.691	2	0.821
<i>Thauera</i>	L1	0.01	0.691	2	0.821
<i>Tolumonas</i>	L1	0.01	0.696	3	0.823
<i>Legionella</i>	L1	0.01	0.712	2	0.839
<i>Candidatus Aquiluna</i>	L1	0.01	0.721	3	0.842
<i>Romboutsia</i>	L1	0.01	0.725	6	0.844
<i>Clostridium sensu stricto</i> 13	L1	0.01	0.734	3	0.850
<i>Hyphomicrobium</i>	L1	0.01	0.737	5	0.850
<i>Sphingorhabdus</i>	L1	0.01	0.742	3	0.852
<i>Tepidimonas</i>	L1	0.01	0.751	2	0.860
Lachnospiraceae UCG-001	L1	0.01	0.765	2	0.867
<i>Haemophilus</i>	L1	0.04	0.767	33	0.867
<i>Pseudomonas</i>	L1	0.10	0.784	93	0.881
<i>Herbaspirillum</i>	L1	0.01	0.836	6	0.922

<i>Tepidiphilus</i>	L1	0.01	0.866	3	0.947
<i>Alcaligenes</i>	L1	0.01	0.892	5	0.969
<i>Scardovia</i>	L1	0.01	0.924	4	0.998
<i>Cloacibacterium</i>	L1	0.01	0.951	12	1.000
Phylum WCHB1-60	L1	0.01	0.953	3	1.000
<i>Azotobacter</i>	L1	0.01	0.979	4	1.000
<i>Bordetella</i>	L1	0.01	1	1	1.000
<i>Candidatus Alysiosphaera</i>	L1	0.01	1	1	1.000
Class WCHB1-32	L1	0.01	1	1	1.000
Family Bacteroidales S24-7 group	L1	0.01	1	1	1.000
Family DSSF69	L1	0.01	1	1	1.000
Family Gemmatimonadaceae	L1	0.01	1	1	1.000
<i>Geodermatophilus</i>	L1	0.01	1	1	1.000
<i>Pelosinus</i>	L1	0.01	1	1	1.000
<i>Serratia</i>	L1	0.01	1	1	1.000
<i>Sorangium</i>	L1	0.01	1	1	1.000
<i>Sulfuricurvum</i>	L1	0.01	1	1	1.000
Family KCM-B-15	L1	0.01	1	2	1.000
Class Bacilli	L1	0.01	1	2	1.000
Family Paenibacillaceae	L1	0.00	1	2	1.000
Family Nocardiodiaceae	L1	0.00	1	2	1.000
<i>Paracoccus</i>	L2	0.31	0.001	69	0.006
<i>Microvirga</i>	L2	0.14	0.001	13	0.006
<i>Mobilicoccus</i>	L2	0.13	0.001	11	0.006
Family Intrasporangiaceae	L2	0.18	0.002	21	0.011
Family Sphingomonadaceae	L2	0.12	0.002	11	0.011
<i>Nocardioides</i>	L2	0.15	0.003	22	0.015
<i>Marmoricola</i>	L2	0.09	0.003	10	0.015
<i>Propionibacterium</i>	L2	0.39	0.004	275	0.019
<i>Saccharopolyspora</i>	L2	0.09	0.006	10	0.028
<i>Altererythrobacter</i>	L2	0.06	0.007	5	0.032
<i>Georgenia</i>	L2	0.06	0.008	5	0.035
<i>Piscicoccus</i>	L2	0.09	0.011	15	0.041
<i>Serinicoccus</i>	L2	0.07	0.011	7	0.041
Order JG30-KF-CM45	L2	0.05	0.013	6	0.046
<i>Turicibacter</i>	L2	0.07	0.015	11	0.050
<i>Propioniciclava</i>	L2	0.06	0.023	11	0.071
<i>Massilia</i>	L2	0.06	0.023	8	0.071
<i>Atopobium</i>	L2	0.13	0.025	48	0.075
<i>Thermomonas</i>	L2	0.05	0.026	4	0.077
Family Planococcaceae	L2	0.04	0.027	3	0.080
<i>Rubellimicrobium</i>	L2	0.05	0.028	4	0.082

Family Rhodobacteraceae	L2	0.05	0.032	8	0.090
<i>Streptomyces</i>	L2	0.05	0.033	8	0.092
<i>Sporosarcina</i>	L2	0.04	0.036	3	0.098
<i>Actinomyces</i>	L2	0.15	0.042	82	0.111
Family Familyl	L2	0.05	0.045	4	0.118
<i>Blastococcus</i>	L2	0.05	0.046	4	0.120
<i>Agrococcus</i>	L2	0.05	0.048	4	0.124
<i>Aureimonas</i>	L2	0.04	0.049	3	0.124
<i>Lysobacter</i>	L2	0.04	0.049	3	0.124
<i>Aquitalea</i>	L2	0.05	0.05	10	0.126
<i>Tessaracoccus</i>	L2	0.05	0.051	11	0.128
<i>Actinopolyspora</i>	L2	0.03	0.062	4	0.150
<i>Peptoniphilus</i>	L2	0.07	0.102	24	0.239
<i>Empedobacter</i>	L2	0.05	0.122	14	0.275
<i>Singulisphaera</i>	L2	0.03	0.124	6	0.278
<i>Yimella</i>	L2	0.02	0.131	2	0.286
<i>Sphingomonas</i>	L2	0.05	0.133	17	0.286
<i>Pandoraea</i>	L2	0.02	0.133	2	0.286
<i>Phycoccus</i>	L2	0.02	0.137	2	0.291
<i>Flavisolibacter</i>	L2	0.02	0.138	2	0.291
<i>Erythrobacter</i>	L2	0.02	0.141	2	0.294
<i>Nitrosomonas</i>	L2	0.02	0.141	2	0.294
<i>Pontibacter</i>	L2	0.03	0.145	6	0.299
Class TA18	L2	0.02	0.145	2	0.299
<i>Pedobacter</i>	L2	0.06	0.146	20	0.299
<i>Bdellovibrio</i>	L2	0.03	0.156	8	0.316
Class Thermomicrobia	L2	0.02	0.159	2	0.321
Mycobacterium	L2	0.02	0.166	2	0.330
Phylum Gracilibacteria	L2	0.02	0.168	4	0.330
Class Thermoleophilia	L2	0.02	0.169	2	0.330
<i>Nocardiopsis</i>	L2	0.02	0.17	2	0.330
<i>Salinimicrobium</i>	L2	0.02	0.17	2	0.330
<i>Acidiphilium</i>	L2	0.02	0.171	2	0.330
<i>Bhargavaea</i>	L2	0.02	0.171	2	0.330
<i>Ornithinococcus</i>	L2	0.02	0.173	2	0.332
Family Micrococcaceae	L2	0.02	0.176	2	0.333
<i>Peptostreptococcus</i>	L2	0.05	0.178	13	0.333
<i>Psychrobacillus</i>	L2	0.02	0.178	2	0.333
<i>Defluviicoccus</i>	L2	0.02	0.18	2	0.334
<i>Isoptericola</i>	L2	0.02	0.181	2	0.334
Family 0319-6M6	L2	0.02	0.182	2	0.334
<i>Gaiella</i>	L2	0.02	0.182	2	0.334

<i>Mogibacterium</i>	L2	0.02	0.183	2	0.334
<i>Filibacter</i>	L2	0.02	0.185	2	0.334
Family Micromonosporaceae	L2	0.02	0.187	2	0.336
<i>Tetrasphaera</i>	L2	0.04	0.189	11	0.338
<i>Citricoccus</i>	L2	0.02	0.193	2	0.342
Class Gitt-GS-136	L2	0.02	0.195	2	0.344
<i>Cellulosilyticum</i>	L2	0.02	0.2	2	0.351
Order Sphingobacteriales	L2	0.02	0.208	2	0.358
<i>Paenibacillus</i>	L2	0.02	0.237	4	0.396
<i>Variovorax</i>	L2	0.06	0.24	30	0.398
<i>Anoxybacillus</i>	L2	0.02	0.267	4	0.427
Order Obscuribacterales	L2	0.03	0.295	8	0.462
Family Cryomorphaceae	L2	0.01	0.428	2	0.626
<i>Aggregatibacter</i>	L2	0.02	0.434	4	0.630
<i>Micromonospora</i>	L2	0.01	0.445	2	0.641
Family MN 122.2a	L2	0.01	0.457	2	0.648
<i>Ezakiella</i>	L2	0.01	0.46	3	0.650
<i>Noviherbaspirillum</i>	L2	0.01	0.467	2	0.652
Family JG34-KF-161	L2	0.01	0.486	1	0.671
<i>Ensifer</i>	L2	0.01	0.492	1	0.671
<i>Dermacoccus</i>	L2	0.01	0.496	1	0.671
<i>Xanthomonas</i>	L2	0.01	0.499	1	0.671
<i>Bryocella</i>	L2	0.01	0.499	2	0.671
<i>Propionimicrobium</i>	L2	0.01	0.502	1	0.671
Order Ardenticatenales	L2	0.01	0.506	1	0.671
<i>Sanguibacter</i>	L2	0.01	0.511	1	0.671
Family MIZ14	L2	0.01	0.512	1	0.671
Family Rhodothermaceae	L2	0.01	0.512	1	0.671
<i>Yaniella</i>	L2	0.01	0.522	1	0.682
<i>Finegoldia</i>	L2	0.05	0.533	25	0.692
<i>Roseomonas</i>	L2	0.02	0.59	8	0.757
Family Flavobacteriaceae	L2	0.02	0.615	10	0.767
<i>Alicyclophilus</i>	L2	0.02	0.635	7	0.784
<i>Halomonas</i>	L2	0.03	0.637	20	0.784
<i>Sphaerotilus</i>	L2	0.01	0.676	4	0.815
<i>Oxalophagus</i>	L2	0.01	0.692	4	0.821
<i>Citrobacter</i>	L2	0.02	0.718	15	0.841
<i>Dolosigranulum</i>	L2	0.02	0.738	14	0.850
<i>Undibacterium</i>	L2	0.01	0.757	2	0.864
<i>Collinsella</i>	L2	0.01	0.779	2	0.878
Order PeM15	L2	0.01	0.788	4	0.882
<i>Megamonas</i>	L2	0.01	0.79	3	0.882

<i>Aquamicrobium</i>	L2	0.01	0.804	2	0.895
Family Bradyrhizobiaceae	L2	0.01	0.873	2	0.952
<i>Microvirgula</i>	L2	0.01	0.988	8	1.000
<i>Haematobacter</i>	L2	0.01	0.994	5	1.000
<i>Solitalea</i>	L2	0.01	1	2	1.000
Family 480-2	L2	0.01	1	3	1.000
<i>Alishewanella</i>	L2	0.01	1	3	1.000
<i>Roseateles</i>	L2	0.01	1	3	1.000
<i>Oribacterium</i>	L2	0.01	1	2	1.000
<i>Dialister</i>	L2	0.00	1	2	1.000
<i>Rhizobacter</i>	L2	0.00	1	2	1.000
<i>Klebsiella</i>	L3	0.40	0.001	36	0.006
<i>Lactobacillus</i>	L3	0.39	0.001	150	0.006
<i>Escherichia/Shigella</i>	L3	0.29	0.001	47	0.006
<i>Bacteroides</i>	L3	0.22	0.001	27	0.006
<i>Campylobacter</i>	L3	0.17	0.001	13	0.006
<i>Parabacteroides</i>	L3	0.12	0.001	13	0.006
<i>Paucisalibacillus</i>	L3	0.08	0.004	6	0.019
<i>Sphingobium</i>	L3	0.07	0.01	9	0.041
<i>Ochrobactrum</i>	L3	0.06	0.013	7	0.046
<i>Gluconobacter</i>	L3	0.08	0.015	7	0.050
Order Clostridiales	L3	0.05	0.015	3	0.050
Family Enterobacteriaceae	L3	0.11	0.017	31	0.055
Family Rhizobiaceae	L3	0.03	0.023	2	0.071
<i>Akkermansia</i>	L3	0.05	0.024	3	0.073
<i>Tyzzarella 3</i>	L3	0.03	0.03	2	0.086
<i>Tatumella</i>	L3	0.07	0.031	9	0.088
<i>Proteus</i>	L3	0.03	0.035	2	0.097
<i>Megasphaera</i>	L3	0.05	0.036	4	0.098
Family Lachnospiraceae	L3	0.03	0.037	2	0.099
<i>Prevotella</i>	L3	0.05	0.11	13	0.253
Order Sphingomonadales	L3	0.03	0.126	4	0.281
<i>Lachnoclostridium</i>	L3	0.04	0.191	9	0.340
<i>Enterobacter</i>	L3	0.14	0.203	75	0.353
<i>Solobacterium</i>	L3	0.03	0.216	5	0.370
<i>Nostoc</i>	L3	0.02	0.235	1	0.395
<i>Porphyrobacter</i>	L3	0.02	0.238	1	0.396
<i>Capnocytophaga</i>	L3	0.02	0.253	2	0.412
Family Saprospiraceae	L3	0.02	0.277	1	0.439
<i>Negativicoccus</i>	L3	0.02	0.284	2	0.446
<i>Filifactor</i>	L3	0.02	0.309	2	0.481
<i>Weissella</i>	L3	0.05	0.353	29	0.541

<i>Holdemanella</i>	L3	0.01	0.365	2	0.554
<i>Eubacterium</i>	L3	0.01	0.369	2	0.556
<i>Phylum SHA-109</i>	L3	0.01	0.416	2	0.614
Order Verrucomicrobiales	L3	0.01	0.428	2	0.626
<i>Stenotrophomonas</i>	L3	0.15	0.441	97	0.638
<i>Prevotella</i> 9	L3	0.02	0.453	5	0.646
<i>Parvimonas</i>	L3	0.02	0.469	3	0.652
<i>Fusobacterium</i>	L3	0.02	0.534	10	0.692
<i>Clostridium sensu stricto</i> 1	L3	0.04	0.54	32	0.698
<i>Actinobacillus</i>	L3	0.01	0.688	3	0.821
<i>Staphylococcus</i>	L3	0.27	0.714	352	0.839
<i>Pelomonas</i>	L3	0.01	0.83	5	0.919
Family Anaerolineaceae	L3	0.01	0.848	2	0.933
<i>Polynucleobacter</i>	L3	0.01	0.866	5	0.947
<i>Bacillus</i>	L3	0.06	0.9	47	0.975
<i>Macrococcus</i>	L4	0.81	0.001	38	0.006
<i>Brachybacterium</i>	L4	0.80	0.001	67	0.006
<i>Aerococcus</i>	L4	0.68	0.001	35	0.006
<i>Janibacter</i>	L4	0.66	0.001	48	0.006
<i>Psychrobacter</i>	L4	0.65	0.001	45	0.006
<i>Nesterenkonia</i>	L4	0.62	0.001	36	0.006
<i>Corynebacterium</i> 1	L4	0.60	0.001	259	0.006
<i>Arthrobacter</i>	L4	0.57	0.001	38	0.006
<i>Rhizobium</i>	L4	0.56	0.001	37	0.006
<i>Brevibacterium</i>	L4	0.56	0.001	46	0.006
<i>Facklamia</i>	L4	0.53	0.001	27	0.006
<i>Anaerococcus</i>	L4	0.51	0.001	76	0.006
<i>Kocuria</i>	L4	0.51	0.001	157	0.006
<i>Salinicoccus</i>	L4	0.47	0.001	23	0.006
<i>Jeotgalicoccus</i>	L4	0.46	0.001	16	0.006
<i>Micrococcus</i>	L4	0.42	0.001	97	0.006
<i>Veillonella</i>	L4	0.38	0.001	191	0.006
<i>Bifidobacterium</i>	L4	0.34	0.001	172	0.006
<i>Delftia</i>	L4	0.33	0.001	29	0.006
Family Staphylococcaceae	L4	0.31	0.001	11	0.006
<i>Ornithinimicrobium</i>	L4	0.31	0.001	53	0.006
<i>Microbacterium</i>	L4	0.31	0.001	60	0.006
<i>Granulicatella</i>	L4	0.31	0.001	72	0.006
<i>Kytococcus</i>	L4	0.30	0.001	13	0.006
<i>Lactococcus</i>	L4	0.30	0.001	14	0.006
<i>Globicatella</i>	L4	0.30	0.001	13	0.006
<i>Brevundimonas</i>	L4	0.29	0.001	45	0.006

<i>Dietzia</i>	L4	0.29	0.001	65	0.006
<i>Leuconostoc</i>	L4	0.28	0.001	30	0.006
Phylum Saccharibacteria	L4	0.27	0.001	38	0.006
<i>Olivibacter</i>	L4	0.20	0.001	7	0.006
<i>Planomicrobium</i>	L4	0.20	0.001	7	0.006
<i>Sphingobacterium</i>	L4	0.17	0.001	17	0.006
<i>Nosocomiicoccus</i>	L4	0.17	0.001	6	0.006
<i>Pediococcus</i>	L4	0.17	0.001	6	0.006
<i>Enterococcus</i>	L4	0.15	0.001	24	0.006
<i>Alkalibacterium</i>	L4	0.14	0.001	8	0.006
Family Carnobacteriaceae	L4	0.14	0.001	5	0.006
<i>Solibacillus</i>	L4	0.14	0.001	5	0.006
<i>Raoultella</i>	L4	0.12	0.001	9	0.006
<i>Aliicoccus</i>	L4	0.11	0.001	4	0.006
Order Micrococcales	L4	0.11	0.001	6	0.006
<i>Demequina</i>	L4	0.09	0.001	3	0.006
<i>Duganella</i>	L4	0.09	0.001	3	0.006
<i>Deinococcus</i>	L4	0.15	0.002	17	0.011
<i>Acetobacter</i>	L4	0.12	0.002	8	0.011
<i>Porphyromonas</i>	L4	0.11	0.002	16	0.011
<i>Clostridium sensu stricto</i> 12	L4	0.10	0.002	6	0.011
<i>Luteimonas</i>	L4	0.10	0.003	10	0.015
<i>Rahnella</i>	L4	0.09	0.003	3	0.015
<i>Comamonas</i>	L4	0.12	0.004	22	0.019
<i>Lautropia</i>	L4	0.08	0.004	5	0.019
<i>Promicromonospora</i>	L4	0.06	0.006	2	0.028
<i>Leifsonia</i>	L4	0.06	0.008	2	0.035
<i>Zhihengliuella</i>	L4	0.06	0.008	2	0.035
<i>Exiguobacterium</i>	L4	0.07	0.009	7	0.039
<i>Dysgonomonas</i>	L4	0.06	0.01	2	0.041
Family Brucellaceae	L4	0.06	0.01	2	0.041
<i>Paenalcaligenes</i>	L4	0.06	0.01	2	0.041
<i>Pseudoalteromonas</i>	L4	0.06	0.01	2	0.041
<i>Pseudobutyrvibrio</i>	L4	0.06	0.01	2	0.041
Family Aerococcaceae	L4	0.06	0.011	2	0.041
Family Dermabacteraceae	L4	0.06	0.011	2	0.041
<i>Fastidiosipila</i>	L4	0.06	0.011	2	0.041
<i>Oceanitalea</i>	L4	0.06	0.011	2	0.041
<i>Salana</i>	L4	0.06	0.011	2	0.041
<i>Curtobacterium</i>	L4	0.05	0.011	3	0.041
<i>Marinococcus</i>	L4	0.06	0.012	2	0.044
<i>Marinilactibacillus</i>	L4	0.06	0.013	2	0.046



<i>Planococcus</i>	L4	0.06	0.013	2	0.046
<i>Tropicimonas</i>	L4	0.06	0.013	2	0.046
<i>Actinotalea</i>	L4	0.06	0.015	2	0.050
<i>Neisseria</i>	L4	0.11	0.016	35	0.053
<i>Methylobacterium</i>	L4	0.08	0.016	17	0.053
<i>Peptoclostridium</i>	L4	0.07	0.017	11	0.055
<i>Flaviflexus</i>	L4	0.06	0.017	2	0.055
<i>Chryseomicrobium</i>	L4	0.06	0.029	12	0.084
<i>Erysipelatoclostridium</i>	L4	0.05	0.037	7	0.099
<i>Alloprevotella</i>	L4	0.08	0.053	22	0.132
<i>Aquabacterium</i>	L4	0.04	0.055	4	0.136
<i>Knoellia</i>	L4	0.04	0.061	8	0.149
<i>Leptotrichia</i>	L4	0.04	0.067	5	0.161
<i>Atopostipes</i>	L4	0.03	0.071	4	0.170
<i>Acinetobacter</i>	L4	0.26	0.077	156	0.183
<i>Gardnerella</i>	L4	0.06	0.107	20	0.247
<i>Ignavigranum</i>	L4	0.03	0.111	4	0.253
<i>Bergeyella</i>	L4	0.07	0.114	22	0.259
<i>Prevotella 7</i>	L4	0.06	0.178	26	0.333
<i>Agromyces</i>	L4	0.03	0.184	5	0.334
<i>Moraxella</i>	L4	0.12	0.203	66	0.353
<i>Pseudonocardia</i>	L4	0.02	0.245	3	0.404
<i>Devosia</i>	L4	0.02	0.25	6	0.409
<i>Corynebacterium</i>	L4	0.04	0.366	15	0.554
Family Neisseriaceae	L4	0.05	0.452	33	0.646
<i>Intestinibacter</i>	L4	0.04	0.504	26	0.671
<i>Abiotrophia</i>	L4	0.02	0.506	5	0.671
Family Corynebacteriaceae	L4	0.03	0.553	17	0.712
<i>Chryseobacterium</i>	L4	0.11	0.76	72	0.865
Family Halomonadaceae	L4	0.01	0.818	7	0.908

**Table S5. Indicator taxa of the infant microbial enterotypes**

Taxa	Microbial enterotype	indval	<i>p</i>	frequency	FDR <i>p</i>
<i>Bacteroides</i>	E1	0.82	0.001	262	0.017
<i>Lachnoclostridium</i>	E1	0.56	0.001	148	0.017
<i>Clostridium sensu stricto</i> 1	E1	0.44	0.001	128	0.017
<i>Parabacteroides</i>	E1	0.32	0.001	88	0.017
<i>Erysipelatoclostridium</i>	E1	0.27	0.001	68	0.017
<i>Enterococcus</i>	E1	0.45	0.002	188	0.023
Family Enterobacteriaceae	E1	0.20	0.002	67	0.023
<i>Citrobacter</i>	E1	0.16	0.002	38	0.023
<i>Peptoclostridium</i>	E1	0.15	0.002	35	0.023
<i>Ruminiclostridium</i> 5	E1	0.10	0.002	26	0.023
Erysipelotrichaceae Incertae Sedis	E1	0.09	0.002	20	0.023
<i>Enterobacter</i>	E1	0.24	0.003	77	0.031
<i>Escherichia/Shigella</i>	E1	0.56	0.004	329	0.039
<i>Flavonifractor</i>	E1	0.09	0.005	23	0.045
<i>Alistipes</i>	E1	0.06	0.006	13	0.053
<i>Blautia</i>	E1	0.11	0.009	26	0.072
<i>Dorea</i>	E1	0.07	0.011	17	0.085
<i>Phascolarctobacterium</i>	E1	0.05	0.015	10	0.113
<i>Haemophilus</i>	E1	0.17	0.022	62	0.162
Family Ruminococcaceae	E1	0.06	0.024	16	0.172
<i>Hungatella</i>	E1	0.04	0.031	8	0.216
<i>Raoultella</i>	E1	0.09	0.04	31	0.259
<i>Anaeroglobus</i>	E1	0.03	0.04	7	0.259
<i>Tyzzerella</i> 4	E1	0.04	0.053	10	0.328
<i>Faecalibacterium</i>	E1	0.03	0.066	6	0.396
<i>Negativicoccus</i>	E1	0.11	0.108	46	0.554
<i>Anaerostipes</i>	E1	0.03	0.108	8	0.554
<i>Morganella</i>	E1	0.04	0.115	11	0.579
<i>Bilophila</i>	E1	0.03	0.124	10	0.613
<i>Varibaculum</i>	E1	0.04	0.133	11	0.646
<i>Akkermansia</i>	E1	0.06	0.139	19	0.652
<i>Dysgonomonas</i>	E1	0.05	0.139	14	0.652
<i>Sutterella</i>	E1	0.10	0.143	35	0.659
<i>Succinivibrio</i>	E1	0.02	0.185	4	0.733
<i>Butyricimonas</i>	E1	0.02	0.186	4	0.733
<i>Megasphaera</i>	E1	0.13	0.193	64	0.739
<i>Lactococcus</i>	E1	0.06	0.193	23	0.739
<i>Eggerthella</i>	E1	0.04	0.207	17	0.782
<i>Terrisporobacter</i>	E1	0.01	0.231	3	0.861

<i>Subdoligranulum</i>	E1	0.01	0.236	3	0.867
<i>Catabacter</i>	E1	0.01	0.25	3	0.894
[ <i>Eubacterium</i> ] <i>hallii</i> group	E1	0.01	0.255	3	0.894
Family Bacteroidales S24-7 group	E1	0.01	0.261	3	0.894
<i>Parascardovia</i>	E1	0.01	0.262	3	0.894
<i>Epulopiscium</i>	E1	0.01	0.263	3	0.894
<i>Eubacterium</i>	E1	0.04	0.347	15	0.993
<i>Intestinibacter</i>	E1	0.03	0.355	15	0.993
[ <i>Eubacterium</i> ] <i>coprostanoligenes</i> group	E1	0.01	0.494	2	0.993
Lachnospiraceae Incertae Sedis	E1	0.01	0.494	2	0.993
<i>Microbacterium</i>	E1	0.01	0.502	2	0.993
<i>Anaerotruncus</i>	E1	0.01	0.504	2	0.993
<i>Barnesiella</i>	E1	0.01	0.507	2	0.993
<i>Gordonibacter</i>	E1	0.01	0.507	2	0.993
<i>Aeromonas</i>	E1	0.01	0.51	2	0.993
Ruminococcaceae UCG-014	E1	0.01	0.513	2	0.993
Christensenellaceae R-7 group	E1	0.01	0.515	2	0.993
<i>Providencia</i>	E1	0.01	0.517	2	0.993
<i>Acidovorax</i>	E1	0.01	0.521	2	0.993
<i>Comamonas</i>	E1	0.01	0.521	2	0.993
<i>Hyphomicrobium</i>	E1	0.01	0.521	2	0.993
<i>Salmonella</i>	E1	0.01	0.522	2	0.993
<i>Syntrophococcus</i>	E1	0.01	0.535	2	1.000
<i>Odoribacter</i>	E1	0.01	0.553	5	1.000
<i>Collinsella</i>	E1	0.02	0.568	9	1.000
<i>Moraxella</i>	E1	0.01	0.612	3	1.000
Lachnospiraceae UCG-004	E1	0.01	0.693	7	1.000
<i>Propionibacterium</i>	E1	0.05	0.699	26	1.000
<i>Leuconostoc</i>	E1	0.03	0.699	18	1.000
<i>Parasutterella</i>	E1	0.01	0.706	4	1.000
<i>Prevotella</i> 9	E1	0.03	0.708	17	1.000
<i>Acidocella</i>	E1	0.01	0.742	3	1.000
<i>Scardovia</i>	E1	0.01	0.747	6	1.000
<i>Fusobacterium</i>	E1	0.04	0.754	22	1.000
<i>Acinetobacter</i>	E1	0.04	0.755	21	1.000
<i>Catenibacterium</i>	E1	0.02	0.765	7	1.000
<i>Clostridium sensu stricto</i> 13	E1	0.01	0.765	3	1.000
<i>Aerococcus</i>	E1	0.01	0.772	5	1.000
<i>Trabulsiella</i>	E1	0.01	0.81	6	1.000
Family Clostridiaceae 1	E1	0.01	0.856	3	1.000
<i>Paucisalibacillus</i>	E1	0.01	0.857	5	1.000
<i>Actinobacillus</i>	E1	0.00	0.858	3	1.000

<i>Lactonifactor</i>	E1	0.01	0.879	4	1.000
<i>Finegoldia</i>	E1	0.07	0.884	38	1.000
<i>Solobacterium</i>	E1	0.01	0.925	5	1.000
Family Bifidobacteriaceae	E1	0.01	0.933	4	1.000
<i>Peptoniphilus</i>	E1	0.06	0.958	43	1.000
<i>Anaerococcus</i>	E1	0.05	0.959	37	1.000
<i>Kluyvera</i>	E1	0.02	0.973	12	1.000
<i>Aerosphaera</i>	E1	0.00	1	1	1.000
<i>Aggregatibacter</i>	E1	0.00	1	1	1.000
<i>Ameyamaea</i>	E1	0.00	1	1	1.000
<i>Anaerosalibacter</i>	E1	0.00	1	1	1.000
<i>Anaerosporobacter</i>	E1	0.00	1	1	1.000
<i>Aquabacterium</i>	E1	0.00	1	1	1.000
<i>Bradyrhizobium</i>	E1	0.00	1	1	1.000
<i>Caulobacter</i>	E1	0.00	1	1	1.000
Class Actinobacteria	E1	0.00	1	1	1.000
Class Alphaproteobacteria	E1	0.00	1	1	1.000
Class Mollicutes	E1	0.00	1	1	1.000
<i>Clostridium sensu stricto</i> 18	E1	0.00	1	1	1.000
<i>Clostridium sensu stricto</i> 2	E1	0.00	1	1	1.000
<i>Clostridium sensu stricto</i> 9	E1	0.00	1	1	1.000
<i>Coprobacter</i>	E1	0.00	1	1	1.000
<i>Devosia</i>	E1	0.00	1	1	1.000
<i>Dyella</i>	E1	0.00	1	1	1.000
Erysipelotrichaceae UCG-006	E1	0.00	1	1	1.000
<i>Facklamia</i>	E1	0.00	1	1	1.000
Family 11-24	E1	0.00	1	1	1.000
Family Bacteroidales RF16 group	E1	0.00	1	1	1.000
Family Enterococcaceae	E1	0.00	1	1	1.000
Family Hyphomicrobiaceae	E1	0.00	1	1	1.000
Family Leptotrichiaceae	E1	0.00	1	1	1.000
Family Planococcaceae	E1	0.00	1	1	1.000
Family Pseudomonadaceae	E1	0.00	1	1	1.000
Family Rhodobacteraceae	E1	0.00	1	1	1.000
Family Sphingomonadaceae	E1	0.00	1	1	1.000
<i>Flavisolibacter</i>	E1	0.00	1	1	1.000
<i>Geobacillus</i>	E1	0.00	1	1	1.000
<i>Gluconobacter</i>	E1	0.00	1	1	1.000
<i>Helicobacter</i>	E1	0.00	1	1	1.000
<i>Intestinimonas</i>	E1	0.00	1	1	1.000
<i>Johnsonella</i>	E1	0.00	1	1	1.000
<i>Kingella</i>	E1	0.00	1	1	1.000

<i>Kocuria</i>	E1	0.00	1	1	1.000
<i>Lachnoclostridium</i> 5	E1	0.00	1	1	1.000
<i>Leptotrichia</i>	E1	0.00	1	1	1.000
<i>Massilia</i>	E1	0.00	1	1	1.000
<i>Megamonas</i>	E1	0.00	1	1	1.000
<i>Novosphingobium</i>	E1	0.00	1	1	1.000
Order Gastranaerophilales	E1	0.00	1	1	1.000
Order Micrococcales	E1	0.00	1	1	1.000
Order Mollicutes RF9	E1	0.00	1	1	1.000
<i>Oribacterium</i>	E1	0.00	1	1	1.000
<i>Paludibacter</i>	E1	0.00	1	1	1.000
<i>Paraprevotella</i>	E1	0.00	1	1	1.000
<i>Patulibacter</i>	E1	0.00	1	1	1.000
<i>Pediococcus</i>	E1	0.00	1	1	1.000
Phylum Bacteroidetes	E1	0.00	1	1	1.000
Phylum SM2F11	E1	0.00	1	1	1.000
Phylum TM6	E1	0.00	1	1	1.000
<i>Pigmentiphaga</i>	E1	0.00	1	1	1.000
<i>Polynucleobacter</i>	E1	0.00	1	1	1.000
Prevotellaceae NK3B31 group	E1	0.00	1	1	1.000
<i>Pseudoclavibacter</i>	E1	0.00	1	1	1.000
<i>Roseomonas</i>	E1	0.00	1	1	1.000
<i>Ruminiclostridium</i>	E1	0.00	1	1	1.000
Ruminococcaceae UCG-004	E1	0.00	1	1	1.000
Ruminococcaceae UCG-005	E1	0.00	1	1	1.000
<i>Sarcina</i>	E1	0.00	1	1	1.000
<i>Selenomonas</i> 3	E1	0.00	1	1	1.000
<i>Streptomyces</i>	E1	0.00	1	1	1.000
<i>Tepidimicrobium</i>	E1	0.00	1	1	1.000
<i>Thalassospira</i>	E1	0.00	1	1	1.000
<i>Trueperella</i>	E1	0.00	1	1	1.000
<i>Tyzzerella</i>	E1	0.00	1	1	1.000
[ <i>Ruminococcus</i> ] <i>gauvreauii</i> group	E1	0.00	1	2	1.000
<i>Brevibacterium</i>	E1	0.00	1	2	1.000
<i>Brevundimonas</i>	E1	0.00	1	2	1.000
<i>Mogibacterium</i>	E1	0.00	1	4	1.000
<i>Rhizobium</i>	E1	0.00	1	2	1.000
[ <i>Eubacterium</i> ] <i>nodatum</i> group	E1	0.00	1	3	1.000
<i>Alloscardovia</i>	E1	0.00	1	2	1.000
Family Prevotellaceae	E1	0.00	1	4	1.000
Family Methylophilaceae	E1	0.00	1	2	1.000
<i>Murdochella</i>	E1	0.00	1	2	1.000

<i>Bacillus</i>	E1	0.00	1	2	1.000
<i>Macrococcus</i>	E1	0.00	1	2	1.000
<i>Fusicatenibacter</i>	E1	0.00	1	2	1.000
<i>Desulfovibrio</i>	E1	0.00	1	2	1.000
<i>Streptococcus</i>	E2	0.81	0.001	352	0.017
<i>Bifidobacterium</i>	E2	0.66	0.001	318	0.017
<i>Lactobacillus</i>	E2	0.63	0.001	295	0.017
<i>Gemella</i>	E2	0.60	0.001	138	0.017
<i>Rothia</i>	E2	0.53	0.001	135	0.017
<i>Staphylococcus</i>	E2	0.52	0.001	223	0.017
<i>Atopobium</i>	E2	0.31	0.001	68	0.017
<i>Granulicatella</i>	E2	0.30	0.001	59	0.017
<i>Prevotella</i>	E2	0.27	0.001	75	0.017
<i>Tyzzerella</i> 3	E2	0.22	0.001	34	0.017
Order Lactobacillales	E2	0.09	0.001	13	0.017
<i>Corynebacterium</i> 1	E2	0.21	0.002	72	0.023
<i>Gardnerella</i>	E2	0.06	0.002	10	0.023
<i>Actinomyces</i>	E2	0.28	0.003	117	0.031
<i>Porphyromonas</i>	E2	0.10	0.004	24	0.039
<i>Dolosigranulum</i>	E2	0.05	0.005	9	0.045
<i>Lachnoanaerobaculum</i>	E2	0.04	0.007	9	0.060
<i>Peptostreptococcus</i>	E2	0.11	0.009	29	0.072
<i>Fastidiosipila</i>	E2	0.03	0.04	4	0.259
<i>Ezakiella</i>	E2	0.08	0.044	25	0.278
<i>Candidatus Rhodoluna</i>	E2	0.02	0.067	3	0.396
Phylum Firmicutes	E2	0.02	0.07	3	0.402
Family Coriobacteriaceae	E2	0.03	0.071	7	0.402
<i>Mitsuokella</i>	E2	0.02	0.077	3	0.427
Class Bacilli	E2	0.03	0.085	6	0.462
<i>Prevotella</i> 6	E2	0.04	0.091	12	0.485
<i>Flavobacterium</i>	E2	0.03	0.148	8	0.671
<i>Pseudomonas</i>	E2	0.02	0.156	5	0.696
<i>Thermomonas</i>	E2	0.01	0.167	2	0.709
<i>Holdemanella</i>	E2	0.06	0.168	22	0.709
<i>Weissella</i>	E2	0.06	0.171	19	0.709
<i>Paracoccus</i>	E2	0.01	0.172	2	0.709
<i>Sphingomonas</i>	E2	0.01	0.172	2	0.709
<i>Sphingobacterium</i>	E2	0.01	0.18	2	0.731
<i>Olsenella</i>	E2	0.02	0.245	7	0.889
<i>Senegalimassilia</i>	E2	0.02	0.28	5	0.940
Family Flavobacteriaceae	E2	0.01	0.308	4	0.993
<i>Psychrobacter</i>	E2	0.01	0.311	4	0.993

<i>Proteus</i>	E2	0.04	0.352	16	0.993
<i>Allisonella</i>	E2	0.01	0.355	3	0.993
<i>Klebsiella</i>	E2	0.19	0.374	114	0.993
<i>Stenotrophomonas</i>	E2	0.03	0.384	14	0.993
<i>Sneathia</i>	E2	0.01	0.395	1	0.993
<i>Bdellovibrio</i>	E2	0.01	0.4	1	0.993
<i>Rhodococcus</i>	E2	0.01	0.407	1	0.993
<i>Abiotrophia</i>	E2	0.01	0.408	1	0.993
<i>Ottowia</i>	E2	0.01	0.409	1	0.993
<i>Taibaiella</i>	E2	0.01	0.409	1	0.993
<i>Fluviicola</i>	E2	0.01	0.411	1	0.993
<i>Sphingopyxis</i>	E2	0.01	0.411	1	0.993
<i>Limnohabitans</i>	E2	0.01	0.417	1	0.993
<i>Candidatus Planktophila</i>	E2	0.01	0.418	1	0.993
<i>Olivibacter</i>	E2	0.01	0.418	1	0.993
<i>Parapedobacter</i>	E2	0.01	0.418	1	0.993
<i>[Eubacterium] brachy</i> group	E2	0.01	0.419	1	0.993
<i>Methylobacterium</i>	E2	0.01	0.42	1	0.993
Family Family XIII	E2	0.01	0.426	1	0.993
<i>Haloferula</i>	E2	0.01	0.426	1	0.993
<i>Ochrobactrum</i>	E2	0.01	0.426	1	0.993
<i>Azorhizobium</i>	E2	0.01	0.427	1	0.993
<i>Pseudacidovorax</i>	E2	0.01	0.427	1	0.993
<i>Kurthia</i>	E2	0.01	0.428	1	0.993
<i>Achromobacter</i>	E2	0.01	0.429	1	0.993
<i>Brachybacterium</i>	E2	0.01	0.429	1	0.993
Family Microbacteriaceae	E2	0.01	0.43	1	0.993
<i>Robinsoniella</i>	E2	0.01	0.43	1	0.993
<i>Cruoricaptor</i>	E2	0.01	0.432	1	0.993
Class Clostridia	E2	0.01	0.433	1	0.993
Family Peptostreptococcaceae	E2	0.02	0.438	5	0.993
<i>Niabella</i>	E2	0.01	0.439	1	0.993
<i>Weeksella</i>	E2	0.01	0.439	1	0.993
<i>Bordetella</i>	E2	0.01	0.441	1	0.993
<i>Rhodopseudomonas</i>	E2	0.01	0.441	1	0.993
<i>Arthrobacter</i>	E2	0.01	0.443	1	0.993
Class WCHB1-32	E2	0.01	0.451	1	0.993
<i>Romboutsia</i>	E2	0.01	0.456	1	0.993
<i>Hafnia</i>	E2	0.01	0.468	3	0.993
<i>Prevotella 7</i>	E2	0.02	0.469	6	0.993
Class Gammaproteobacteria	E2	0.01	0.477	3	0.993
Order Bacteroidales	E2	0.02	0.481	7	0.993

Order Clostridiales	E2	0.06	0.49	26	0.993
<i>Acetobacter</i>	E2	0.03	0.518	11	0.993
<i>Delftia</i>	E2	0.02	0.588	7	1.000
Family Corynebacteriaceae	E2	0.02	0.598	10	1.000
<i>Prevotella 2</i>	E2	0.01	0.613	7	1.000
Phylum Saccharibacteria	E2	0.04	0.642	19	1.000
<i>Dermabacter</i>	E2	0.01	0.665	4	1.000
<i>Dialister</i>	E2	0.08	0.732	46	1.000
<i>Parvimonas</i>	E2	0.03	0.734	15	1.000
<i>Pseudarcicella</i>	E2	0.01	0.743	2	1.000
<i>Alloprevotella</i>	E2	0.00	0.749	2	1.000
Phylum Proteobacteria	E2	0.01	0.754	2	1.000
<i>Ureaplasma</i>	E2	0.01	0.763	2	1.000
<i>Mobiluncus</i>	E2	0.00	0.763	2	1.000
<i>Propionimicrobium</i>	E2	0.01	0.781	2	1.000
<i>Acidaminococcus</i>	E2	0.02	0.814	8	1.000
<i>Peptococcus</i>	E2	0.01	0.881	4	1.000
<i>Campylobacter</i>	E2	0.07	0.929	41	1.000
<i>Veillonella</i>	E2	0.45	0.96	323	1.000
<i>Chryseobacterium</i>	E2	0.01	0.961	6	1.000
Family Lachnospiraceae	E2	0.06	0.991	42	1.000
<i>Neisseria</i>	E2	0.00	1	4	1.000
Family Veillonellaceae	E2	0.00	1	3	1.000



**Table S6. HMO concentrations and ratios among microbial lactotypes**

HMO	Microbial lactotype				<i>p</i>	FDR <i>p</i>
	L1	L2	L3	L4		
2'FL	4745±3294 <sup>a</sup>	3315±2742 <sup>b</sup>	3031±3360 <sup>bc</sup>	2134±2444 <sup>c</sup>	1.33E-07	1.13E-06
3FL	212±200	153±127	174±194	200±146	6.43E-02	7.54E-02
LNnT	825±489 <sup>a</sup>	1006±543 <sup>b</sup>	843±618 <sup>a</sup>	870±366 <sup>ab</sup>	7.82E-03	1.33E-02
3'SL	541±293	472±251	514±239	427±220	2.50E-02	3.40E-02
DFLac	338±266 <sup>a</sup>	338±258 <sup>a</sup>	318±303 <sup>a</sup>	160±170 <sup>b</sup>	1.33E-03	2.51E-03
6'SL	497±357 <sup>a</sup>	451±214 <sup>a</sup>	614±458 <sup>a</sup>	368±397 <sup>b</sup>	3.10E-04	8.11E-04
LNT	1508±1041	1648±980	1629±1229	1371±835	2.85E-01	2.93E-01
LNFP I	1132±1009	1140±1197	1138±1262	879±1071	1.22E-01	1.33E-01
LNFP II	1644±1101 <sup>ab</sup>	1810±1228 <sup>a</sup>	1328±993 <sup>b</sup>	1729±1057 <sup>ab</sup>	3.97E-02	5.00E-02
LNFP III	67±94 <sup>a</sup>	31±41 <sup>b</sup>	47±37 <sup>a</sup>	44±55 <sup>ab</sup>	1.08E-03	2.17E-03
LSTb	92±68	93±60	99±83	90±44	8.65E-01	8.65E-01
LSTc	142±121 <sup>a</sup>	132±74 <sup>a</sup>	174±135 <sup>a</sup>	100±118 <sup>b</sup>	4.08E-04	9.92E-04
DFLNT	1249±819 <sup>a</sup>	939±766 <sup>b</sup>	969±891 <sup>b</sup>	701±759 <sup>b</sup>	3.71E-05	1.58E-04
LNH	98±76	84±63	88±72	69±52	4.67E-02	5.67E-02
DSLNT	420±301 <sup>ab</sup>	540±370 <sup>c</sup>	441±276 <sup>ac</sup>	317±189 <sup>b</sup>	1.04E-03	2.17E-03
FLNH	48±52 <sup>a</sup>	29±29 <sup>a</sup>	46±66 <sup>a</sup>	4±3 <sup>b</sup>	4.84E-11	1.64E-09
DFLNH	134±129	106±109	96±86	88±99	2.33E-02	3.40E-02
FDSLNH	220±208 <sup>ab</sup>	239±185 <sup>a</sup>	215±221 <sup>ab</sup>	166±200 <sup>b</sup>	3.03E-02	3.97E-02
DSLNH	99±94 <sup>a</sup>	108±78 <sup>a</sup>	108±91 <sup>a</sup>	49±46 <sup>b</sup>	2.43E-04	7.51E-04
Total HMOs	14011±3736 <sup>a</sup>	12634±3439 <sup>b</sup>	11871±4558 <sup>b</sup>	9768±3863 <sup>c</sup>	3.71E-08	4.21E-07
Small HMOs	5995±3409 <sup>a</sup>	4391±2767 <sup>b</sup>	4333±3481 <sup>b</sup>	3130±2349 <sup>b</sup>	3.21E-07	2.18E-06
Modified lactose	238310±31136 <sup>a</sup>	241837±37969 <sup>a</sup>	225019±27337 <sup>b</sup>	236339±27814 <sup>ab</sup>	5.35E-03	9.58E-03
Type 1 HMOs	4796±2036	5230±2038	4635±2112	4385±1679	8.00E-02	9.06E-02
Type 2 HMOs	1034±548	1169±578	1063±660	1015±440	1.25E-01	1.33E-01
α-1-2-fucosylated HMOs	5877±4005 <sup>a</sup>	4455±3611 <sup>b</sup>	4169±4049 <sup>bc</sup>	3013±3426 <sup>c</sup>	1.05E-05	5.08E-05
terminal α-2-6-sialylated HMOs	638±445 <sup>a</sup>	582±265 <sup>a</sup>	788±552 <sup>a</sup>	469±479 <sup>b</sup>	1.69E-04	5.74E-04
internal α-2-6-sialylated HMOs	511±342 <sup>a</sup>	633±415 <sup>b</sup>	540±328 <sup>ab</sup>	406±213 <sup>a</sup>	8.97E-03	1.45E-02
terminal α-2-3-sialylated HMOs	961±423 <sup>a</sup>	1012±466 <sup>a</sup>	955±400 <sup>a</sup>	744±341 <sup>b</sup>	1.48E-02	2.29E-02
HMO-bound Sia	2749±1188 <sup>a</sup>	2921±1131 <sup>a</sup>	2928±1238 <sup>a</sup>	2049±1021 <sup>b</sup>	2.87E-04	8.11E-04
HMO-bound Fuc	11511±4221 <sup>a</sup>	9485±3568 <sup>b</sup>	8745±5240 <sup>bc</sup>	7056±3826 <sup>c</sup>	8.67E-09	1.47E-07
HMO-bound Sia/total HMO	0.21±0.1 <sup>a</sup>	0.24±0.09 <sup>b</sup>	0.27±0.13 <sup>b</sup>	0.22±0.09 <sup>ab</sup>	4.57E-04	1.04E-03
HMO-bound Fuc/total HMO	0.81±0.17 <sup>a</sup>	0.74±0.17 <sup>b</sup>	0.69±0.25 <sup>b</sup>	0.7±0.19 <sup>b</sup>	2.55E-06	1.45E-05
HMO-bound Fuc/HMO-bound Sia	4.94±2.62 <sup>a</sup>	3.72±1.86 <sup>b</sup>	3.55±2.52 <sup>b</sup>	4.19±2.92 <sup>ab</sup>	6.31E-05	2.38E-04

**Footnote:** Concentrations are given as nmol/mL; mean ± sd. *P* values were calculated from Kruskal-Wallis test (followed by Dunn's post hoc test; letters denote significance groups, *p* < 0.05). 2'-fucosyllactose (2'FL), 3-fucosyllactose (3FL), lacto-N-neotetraose (LNnT), 3'-sialyllactose (3'SL), difucosyllactose (DFLac), 6'-sialyllactose (6'SL), lacto-N-tetraose (LNT), lacto-N-fucopentaose (LNFP) I, LNFP II, LNFP III, sialyl-LNT (LST) b, LSTc, difucosyllacto-LNT (DFLNT), lacto-N-hexaose (LNH), disialyllacto-N-tetraose (DSLNT), fucosyllacto-N-hexaose (FLNH), difucosyllacto-N-hexaose (DFLNH), fucodisialyllacto-lacto-N-hexaose (FDSLNH) and disialyllacto-N-hexaose (DSLNH); small HMOs (2'FL, 3FL, 3'SL, 6'SL, and DFLac), modified lactose (small HMOs and lactose), type 1 HMOs (LNT, LNFP I, LNFP II, LSTb, and DSLNT), type 2 HMOs (LNnT, LNFP III, and LSTc), α-1-2-fucosylated HMOs (2'FL

and LNFP I), terminal  $\alpha$ -2-6-sialylated HMOs (6'SL and LSTc), internal  $\alpha$ -2-6-sialylated HMOs (DSLNT and LSTb), terminal  $\alpha$ -2-3-sialylated HMOs (3'SL and DSLNT), ratio of HMO-bound sialic acid (Sia) to total HMOs (HMO-bound Sia/total HMOs), ratio of HMO-bound fucose (Fuc) to total HMOs (HMO-bound Fuc/total HMOs), and ratio of the ratio of HMO-bound Fuc to HMO-bound Sia (HMO-bound Fuc/HMO-bound Sia).

**Table S7. HMO concentrations and ratios between microbial enterotypes**

HMO	Enterotype			
	E1	E2	<i>p</i>	FDR <i>p</i>
2'FL	3921±3314	3789±3125	6.96E-01	7.88E-01
3FL	213±200	160±144	8.74E-03	4.78E-02
LNnT	821±501	950±535	6.29E-03	4.28E-02
3'SL	539±286	468±241	9.84E-03	4.78E-02
DFLac	310±278	328±253	4.08E-01	6.60E-01
6'SL	502±386	480±316	5.10E-01	6.86E-01
LNT	1515±1078	1594±992	2.02E-01	4.02E-01
LNFP I	994±979	1271±1242	7.64E-02	2.16E-01
LNFP II	1655±1120	1618±1118	6.11E-01	7.42E-01
LNFP III	63±88	39±45	7.58E-02	2.16E-01
LSTb	92±72	95±59	2.31E-01	4.13E-01
LSTc	133±125	151±99	2.94E-03	3.34E-02
DFLNT	1128±808	1002±860	5.13E-02	1.94E-01
LNH	87±64	94±80	8.88E-01	8.93E-01
DSLNT	398±288	502±333	5.30E-04	1.80E-02
FLNH	42±55	34±40	4.64E-01	6.86E-01
DFLNH	124±123	106±106	2.48E-01	4.22E-01
FDSLNH	219±212	218±195	8.93E-01	8.93E-01
DSLNH	96±94	100±78	1.74E-01	3.92E-01
Total HMOs	12852±4192	12997±3829	7.68E-01	8.16E-01
Small HMOs	5174±3441	4897±3173	5.01E-01	6.86E-01
Modified lactose	236468±33410	237231±31015	5.24E-01	6.86E-01
Type 1 HMOs	4654±1959	5079±2095	6.74E-02	2.16E-01
Type 2 HMOs	1018±560	1139±569	1.23E-02	5.23E-02
α1-2-fucosylated HMOs	4914±3997	5060±3958	6.84E-01	7.88E-01
terminal α-2-6-sialylated HMOs	635±479	630±383	1.85E-01	3.92E-01
internal α-2-6-sialylated HMOs	490±330	597±375	1.91E-03	3.25E-02
terminal α-2-3-sialylated HMOs	937±424	970±432	7.18E-01	7.88E-01
HMO-bound Sia	2692±1237	2833±1118	8.69E-02	2.18E-01
HMO-bound Fuc	10231±4725	10001±4120	5.52E-01	6.95E-01
HMO-bound Sia/total HMO	0.23±0.11	0.23±0.09	4.55E-01	6.86E-01
HMO-bound Fuc/total HMO	0.77±0.2	0.75±0.18	8.99E-02	2.18E-01
HMO-bound Fuc/HMO-bound Sia	4.59±2.86	4.01±1.97	2.13E-01	4.02E-01

**Footnote:** Concentrations are given as nmol/mL; mean ± sd. 2'-fucosyllactose (2'FL), 3-fucosyllactose (3FL), lacto-N-neotetraose (LNnT), 3'-sialyllactose (3'SL), difucosyllactose (DFLac), 6'-sialyllactose (6'SL), lacto-N-tetraose (LNT), lacto-N-fucopentaose (LNFP) I, LNFP II, LNFP III, sialyl-LNT (LST) b, LSTc, difucosyllacto-LNT (DFLNT), lacto-N-hexaose (LNH), disialyllacto-N-tetraose (DSLNT), fucosyllacto-N-hexaose (FLNH), difucosyllacto-N-hexaose (DFLNH), fucodisialyllacto-lacto-N-hexaose (FDSLNH) and disialyllacto-N-hexaose (DSLNH); small HMOs (2'FL, 3FL,

3'SL, 6'SL, and DFLac), modified lactose (small HMOs and lactose), type 1 HMOs (LNT, LNFP I, LNFP II, LSTb, and DSLNT), type 2 HMOs (LNnT, LNFP III, and LSTc),  $\alpha$ -1-2-fucosylated HMOs (2'FL and LNFP I), terminal  $\alpha$ -2-6-sialylated HMOs (6'SL and LSTc), internal  $\alpha$ -2-6-sialylated HMOs (DSLNT and LSTb), terminal  $\alpha$ -2-3-sialylated HMOs (3'SL and DSLNT), ratio of HMO-bound sialic acid (Sia) to total HMOs (HMO-bound Sia/total HMOs), ratio of HMO-bound fucose (Fuc) to total HMOs (HMO-bound Fuc/total HMOs), and ratio of the ratio of HMO-bound Fuc to HMO-bound Sia (HMO-bound Fuc/HMO-bound Sia).