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University College Cork, Ireland
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SUPPLEMENTARY INFORMATION

The Composition of Human Milk and Infant Faecal Microbiota Over the First Three Months of Life: A Pilot Study

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Supplementary Table S1: Relative abundance (%) of the core microbiota at genus level and remaining taxa for each mother, M1 – M10, at week 1, 3, 6 and 12.

* = Sample not collected.

	M1-W1	M1-W3*	M1-W6	M1-W12
Core	**68.52**		**78.41**	**67.25**
Telmatobacter				0.37
Iamia				0.26
Actinomyces				0.08
Atopobium				0.14
Mycobacterium				0.33
Humicoccus				0.14
Brevibacterium				0.02
Dermacoccus				0.13
Rhodoluna	0.20			
Microbacterium	0.58			0.17
Kocuria	0.52			0.01
Nesterenkonia	1.85			
Bacteroides	0.55			
Cloacibacterium	0.07		0.11	
Corynebacterium			0.18	
Rhodococcus			0.06	
Micrococcus				0.31
Nocardioides				0.16
Propionibacterium			0.03	0.66
Chitinophagaceae uncultured				0.29
Pseudonocardia				0.13
Patulibacter				0.53
Prevotella				0.19
Alistipes				0.07
Chryseobacterium				3.58
Pedobacter	0.13		0.50	2.15

Sphingobacterium	0.07			
Candidate division OD1 uncultured	2.12		1.53	1.35
Candidate division OP11 uncultured			0.33	0.19
Candidate division TM7 uncultured	0.19		0.35	0.15
Bacillus	3.43			
Anaerolineaceae uncultured			0.10	
Chloroflexi uncultured			0.77	0.05
Cyanobacteria uncultured			1.22	0.58
Fibrobacteraceae uncultured				0.23
Anoxybacillus			0.57	0.39
Gemella	0.05			
Aerococcus	1.81			
Exiguobacterium				0.37
Planomicrobium				0.02
Leuconostoc				0.26
Granulicatella	0.09			
Lactococcus	0.40		0.11	0.08
Anaerococcus				0.37
Finegoldia				1.65
Helcococcus				0.02
Peptoniphilus				0.52
Anaerostipes				0.65
Coprococcus				0.66
Lachnospiraceae Incertae Sedis				1.00
Lachnospiraceae uncultured	0.24			1.08
Roseburia			0.66	
Fastidiosipila				0.14
Dialister				0.37
Veillonella	3.72		0.01	0.01
Fusobacterium	1.01			
Erysipelotrichaceae Incertae Sedis			0.48	2.16
Devosia			1.20	
Aminobacter			0.01	
Ochrobactrum	0.82		0.01	
Phyllobacterium			0.53	
Phyllobacteriaceae uncultured			0.29	
Leptotrichia/Sneathia				0.30
Rhizobium			2.49	2.79
Paracoccus			0.60	
Methylobacterium	0.17			
Rhodospirillaceae uncultured				0.57
Sphingomonas	0.33			1.16
Achromobacter	1.84		3.01	0.41
Ralstonia	0.01		3.22	0.88
Acidovorax	4.13		0.32	0.52
Aquabacterium	0.09			
Curvibacter			0.74	0.22
Limnohabitans	0.01		0.01	0.14
Massilia	2.28			
Pseudorhodoferax				0.18

Comamonadaceae uncultured			0.19	0.07
Undibacterium	0.39		0.07	
Methylophilaceae uncultured	0.02			
Nitrosococcus			0.83	
Bilophila				0.28
0319-6G20 uncultured				0.17
Shewanella				0.16
Citrobacter	0.21		0.13	0.17
Erwinia			0.01	
Escherichia-Shigella				0.16
Haemophilus			0.17	0.06
Acinetobacter	0.63		0.41	0.31
Pseudoxanthomonas	1.87			
Chthoniobacter	0.12			
Enhydrobacter				0.24
Akkermansia				0.26

	M2-W1	**M2-W3**	**M2-W6**	**M2-W12**
Core	**85.06**	**81.10**	**83.93**	**50.02**
Corynebacterium	0.09		0.12	
Leifsonia	0.15			
Bryobacter				0.10
Iamia				0.25
Actinomyces				0.16
Microbacterium	0.51			0.04
Micrococcus				0.30
Sphingobacterium	0.01			
Rothia				0.32
Propionibacterium		0.31		0.23
Yaniella			0.03	
Prevotella				0.13
Chryseobacterium				1.13
Pedobacter			2.65	0.56
Candidate division OD1 uncultured	0.98	1.44	2.49	1.34
Candidate division OP11 uncultured				0.31
Cyanobacteria uncultured	0.04			
Gemella				
Cyanobacteria uncultured				0.49
Anoxybacillus		0.10		0.14
Enterococcus	1.96	3.28		
Blautia		0.10		
Coprococcus			0.09	
Abiotrophia				0.05
Facklamia				0.55
Granulicatella				0.30
Lachnospiraceae Incertae Sedis	1.41	0.95	0.08	0.01
Lachnospiraceae uncultured		0.21		0.47
Peptostreptococcaceae Incertae Sedis	0.56			

Ruminococcus		1.39		
Erysipelotrichaceae Incertae Sedis	0.13	0.40		
Selenomonas				0.10
Veillonella				1.46
Fusobacterium				0.01
Leptotrichia/Sneathia				0.09
Ochrobactrum	0.01	0.01		0.27
Bosea			0.05	
Devosia	0.02		0.01	0.47
Methylobacterium				
Phyllobacterium	1.76	1.99		0.90
Phyllobacteriaceae uncultured		0.10		
Rhizobium	0.65	2.24	3.19	2.38
Paracoccus				0.02
Sphingobium				1.27
Sphingomonas	0.79		0.08	0.34
Ralstonia		0.43	1.59	1.40
Achromobacter	0.17	0.74		1.23
Burkholderia	0.01			0.13
Acidovorax	0.14	0.47	0.34	
Curvibacter				0.04
Limnohabitans	0.02	0.82	1.27	0.60
Pelomonas		0.09		
Polaromonas				0.10
Pseudorhodoferax		0.02	0.04	0.02
Comamonadaceae uncultured		0.01	0.01	0.09
Massilia		1.67		
Undibacterium	0.17	0.10	0.74	
Neisseria				0.72
Citrobacter	0.04	0.30	0.20	0.08
Escherichia-Shigella	0.01	0.06	2.58	
Actinobacillus				0.11
Haemophilus				0.10
Acinetobacter		0.03		31.70
Akkermansia			0.38	

	M3-W1	**M3-W3**	**M3-W6**	**M3-W12**
Core	**64.54**	**90.17**	**60.97**	**80.62**
Gardnerella	0.01	0.03		
Corynebacterium		0.06		
Yaniella		0.10		
Marmoricola		0.01		
Blastococcus			0.58	
Agrococcus			0.09	
Leifsonia			0.16	
Rhodococcus				1.12
Microbacterium			0.20	0.08
Propionibacterium	0.02	0.06	0.63	
Bacteroides	4.50		1.00	

Mucilaginibacter	2.56			
Chryseobacterium				3.36
Cloacibacterium		0.23		
Prevotella			1.30	
env.OPS 17 uncultured			1.07	
Pedobacter	3.95	0.48	3.12	1.36
Candidate division OD1 uncultured	1.89	0.04	1.50	1.66
Candidate division OP11 uncultured			0.84	
Candidate division TM7 uncultured	0.26		0.65	
Chloroflexi uncultured	0.31	0.01	0.78	
Cyanobacteria uncultured	1.50		0.64	0.16
Bacillus	1.27		1.19	
Anoxybacillus		0.35		
Gemella		2.16		0.53
Alkalibacterium		0.12		
Granulicatella		0.03		
Planomicrobium			2.00	0.01
Carnobacterium			0.28	
Enterococcus		0.12	0.71	
Blautia		0.01	0.52	
Lachnospiraceae Incertae Sedis	0.01	0.03	1.25	2.25
Lachnospiraceae uncultured			0.01	0.03
Peptostreptococcaceae Incertae Sedis			0.25	
Peptostreptococcaceae uncultured			0.05	
Faecalibacterium	2.61		1.39	
Subdoligranulum	4.12		0.03	
Ruminococcaceae uncultured	3.93		0.02	
Phyllobacterium	0.10	0.15		
Veillonella		1.48		
Erysipelotrichaceae *Incertae Sedis*		0.07	0.53	
Gemmatimonas		0.01	0.28	0.26
Rhizobium	1.55	0.23		
Rhodospirillaceae uncultured	1.19			
Planctomycetaceae uncultured			0.88	
Devosia			0.26	0.30
Methylobacterium			0.67	0.65
Geminicoccus			0.48	
Erythrobacteraceae uncultured			0.75	
Rhizobium			3.13	2.18
Sphingobium			0.30	0.01
Sphingomonas			0.75	
Sphingopyxis			0.46	
Paracoccus		0.06	2.46	
Achromobacter		0.03	1.41	2.57
Ralstonia	1.15	0.31	1.84	3.10
Acidovorax		0.01		
Limnohabitans	0.02		0.19	0.83
Pseudorhodoferax				0.06
Comamonadaceae uncultured	0.04			0.36
Collimonas				0.79

Massilia				
Undibacterium	2.55			0.18
Polaromonas		0.01	0.37	
Comamonadaceae uncultured			0.04	
Aquaspirillum		0.01		
Neisseria		0.13		
Bdellovibrio	0.05	0.01	0.02	
Bilophila			1.42	
Azovibrio				0.33
Syntrophorhabdus				0.21
Citrobacter	0.07	1.55	0.16	0.10
Serratia			0.01	
Aquicella			0.35	
Escherichia-Shigella	0.01	0.06		
Piscirickettsia	0.36			
Pseudofulvimonas	0.06			
Acinetobacter		0.67	0.37	
Lysobacter			0.44	

	M4-W1	**M4-W3**	**M4-W6**	**M4-W12**
Core	**82.89**	**78.72**	**87.75**	**74.24**
Corynebacterium	1.01			
Mycobacterium	0.07			
Actinomyces			0.01	0.12
Atopobium			0.20	
Rhodococcus			0.24	
Collinsella				0.04
Leucobacter				0.38
Microbacterium	0.01	0.01	0.45	0.10
Chitinophagaceae uncultured	0.99			
Rothia				0.65
Yaniella				0.37
Propionibacterium			0.13	0.43
Solirubrobacter				0.10
Alistipes				0.09
S24-7 uncultured				0.49
Capnocytophaga				0.57
Chryseobacterium				1.84
Wautersiella				0.12
Pedobacter	0.98	0.08	0.03	1.16
Sphingobacterium	0.17			0.01
Candidate division OD1 uncultured	0.28	0.11	1.07	1.50
Candidate division TM7 uncultured	0.03			
Chloroflexi uncultured				0.17
Cyanobacteria uncultured	0.36		0.16	
Anoxybacillus				0.86
Gemella	3.50	0.48	1.15	0.06
Trichococcus	0.04			

Enterococcus	0.58		0.12	0.12
Anaerostipes				0.15
Coprococcus				0.87
Lachnospiraceae Incertae Sedis			0.33	2.78
Lachnospiraceae uncultured	0.24		0.48	0.77
Peptostreptococcaceae Incertae Sedis	0.17			
Selenomonas				0.59
Veillonella	0.13	0.52	1.84	4.03
Erysipelotrichaceae Incertae Sedis	0.13			0.14
Ochrobactrum	1.04			
Devosia	0.01			
Methylobacterium	0.01			
Phyllobacterium	0.08			
Phyllobacteriaceae uncultured	0.47			
Planctomycetaceae uncultured			0.48	
Gemmatimonas				0.09
Rhodopseudomonas				0.28
Rhizobium	0.69	0.04	0.55	0.77
Paracoccus	0.09			1.05
Sphingobium		0.11		
Sphingomonas				0.22
Achromobacter	0.64	0.04	0.01	1.31
Ralstonia	1.32	0.11	0.90	0.97
Acidovorax		0.08	0.21	0.68
Comamonas				0.11
Limnohabitans	0.01		0.32	0.61
Pseudorhodoferax				0.03
Comamonadaceae uncultured	0.01		0.27	0.09
Undibacterium	0.01		0.52	0.06
Methylophilaceae uncultured		0.12	0.61	
Azospira			0.65	
Sandaracinaceae uncultured				0.21
Shewanella				0.32
Citrobacter	1.25	0.76	0.09	0.07
Erwinia		0.05	0.74	
Escherichia-Shigella	0.16		0.01	0.40
Haemophilus	0.01			
Acinetobacter	0.01	18.64	0.50	1.06
Enhydrobacter			0.02	

	M5-W1	**M5-W3**	**M5-W6***	**M5-W12**
Core	**85.66**	**73.43**		**73.80**
Corynebacterium	0.01			
Rhodococcus	0.19			
Leifsonia	0.03			
Atopobium		0.11		
Leucobacter		0.12		

Microbacterium		0.04		0.11
Yaniella		0.27		
Propionibacterium	0.03	0.07		
Bergeyella		0.22		
Kocuria				0.64
Chryseobacterium				3.36
Pedobacter	0.22	0.75		4.86
Candidate division OD1 uncultured	2.63	0.07		0.31
Chloroflexi uncultured		0.05		
Cyanobacteria uncultured	0.46			0.11
Anoxybacillus		0.13		0.53
Gemella	1.75	3.32		
Granulicatella	0.22	1.24		
Enterococcus	0.03	0.20		
Bacillus				2.57
Lachnospiraceae Incertae Sedis	0.44	0.12		1.00
Lachnospiraceae uncultured	0.24	0.04		
Veillonella	0.72	13.54		0.01
Erysipelotrichaceae Incertae Sedis	0.01	0.06		
Gemmatimonas		1.06		
Ochrobactrum	0.18	0.12		0.05
Devosia	0.06			0.61
Phyllobacterium				1.65
Phyllobacteriaceae uncultured	0.01			
Methylobacterium		0.33		
Albibacter		0.06		
Rhizobium	0.60	0.45		2.27
Rhodospirillaceae uncultured	0.57			0.36
Paracoccus		0.03		
Novosphingobium		0.12		
Achromobacter	0.01	0.19		0.26
Ralstonia	0.88	0.27		2.73
Acidovorax	2.01	0.01		1.88
Delftia	0.01			
Curvibacter		0.01		
Limnohabitans	0.02	0.03		0.01
Pelomonas		0.05		
Comamonadaceae uncultured	0.04	0.04		0.19
Undibacterium				0.34
Neisseria		0.11		0.16
Bilophila				0.19
Citrobacter	0.13	0.03		0.41
Escherichia-Shigella	0.01	0.13		0.01
Haemophilus	0.18	0.79		0.01
Piscirickettsia				0.25
Acinetobacter	0.58			

	M6-W1	**M6-W3**	**M6-W6**	**M6-W12**

Core	**83.05**	**84.97**	**79.89**	**74.05**
Chloracidobacterium	0.07			
Actinomyces	0.01			
Rhodococcus	0.02			
Kocuria	0.31			
Leifsonia		0.01		
Microbacterium		0.09		
Rothia		0.05		
Microthrix				0.20
Yaniella				0.53
Propionibacterium	0.02	0.02		0.01
Bacteroides	0.02			
Rikenellaceae uncultured				0.04
Chryseobacterium				2.95
Leifsonia			0.14	
Pedobacter	0.60	0.46	1.77	2.01
Candidate division OD1 uncultured	0.08	0.31	3.40	3.35
Candidate division TM7 uncultured			0.02	1.67
Cyanobacteria uncultured	0.01	0.01		0.26
Anoxybacillus	0.87		0.39	2.39
Gemella	1.45	9.00	0.01	
Granulicatella	0.01			
Enterococcus	0.03	0.40	0.06	
Lachnospiraceae Incertae Sedis	0.37	0.12		1.12
Lachnospiraceae uncultured		0.04	0.15	0.23
Roseburia	0.12			
Veillonella	1.61	0.52	0.01	0.01
Gemmatimonas	0.01			
Caulobacter	0.09			
Devosia	0.01	0.26	1.23	
Methylobacterium	0.01	0.21		
Aminobacter	0.74			
Erysipelotrichaceae Incertae Sedis				0.08
Ochrobactrum				0.53
Phyllobacterium		0.26	0.43	0.01
Phyllobacteriaceae uncultured	0.10	0.08		
Rhizobium	0.14	0.39	1.68	3.80
Paracoccus	0.13		2.79	
Rhodospirillaceae uncultured	0.17			
Achromobacter	0.14	0.65	4.31	1.06
Ralstonia	0.90	0.12	2.38	0.50
Acidovorax	0.01	0.04	0.01	0.82
Curvibacter	0.34			0.14
Delftia	0.01			0.01
Limnohabitans	0.03		0.02	0.14
Schlegelella			0.37	
Comamonadaceae uncultured	0.07		0.15	
Massilia	0.01			
Pseudorhodoferax		0.26		0.01

Bdellovibrio			0.59	
Massilia				0.25
Citrobacter	0.04	0.01	0.12	0.17
Erwinia				0.01
Escherichia-Shigella	0.02			0.14
Haemophilus	0.48	0.62		
Silanimonas				0.55
Lysobacter		0.15		
Sinobacteraceae uncultured	0.29			
Akkermansia	0.09			

	M7-W1	**M7-W3**	**M7-W6**	**M7-W12**
Core	**87.09**	**84.87**	**85.80**	**82.72**
Bacteroides	0.02			
S24-7 uncultured	0.28			
Gardnerella			0.01	
Corynebacterium		0.27	1.19	
Agrococcus				0.01
Leifsonia				0.11
Microbacterium				0.48
Yaniella		0.08		0.47
Alpinimonas			0.96	
Rhodoluna			0.43	
Microbacterium			0.10	
Propionibacterium			0.05	0.28
Bacteroides				0.01
Chryseobacterium				2.98
Pedobacter	2.67	0.35	0.04	2.19
Candidate division OD1 uncultured	0.48	1.01	3.01	0.40
Cyanobacteria uncultured				0.18
Gemella			0.01	
Granulicatella			0.02	0.46
Enterococcus	1.49	2.51	0.13	
Anaerostipes	0.11			
Blautia		2.54		0.18
Lachnospiraceae Incertae Sedis	0.54	0.01		0.67
Lachnospiraceae uncultured	1.55	2.10		0.14
Erysipelotrichaceae Incertae Sedis		0.01		
Caulobacter		0.01		
Ochrobactrum		0.01		
Devosia	0.59	0.12		
Oscillibacter				0.28
Veillonella			0.03	3.08
Erysipelotrichaceae Incertae Sedis				0.26
Devosia				0.48
Phyllobacterium	1.93	0.72	0.07	0.10
Phyllobacteriaceae uncultured			0.15	

Rhizobium	0.11	0.36		0.24
Rhodospirillaceae uncultured		0.06	1.27	
Paracoccus				0.22
Achromobacter	0.26	1.01	1.39	1.17
Ralstonia	0.03	1.10	1.94	2.53
Acidovorax	0.22	0.57	0.86	0.61
Limnohabitans	1.20		0.04	0.62
Pseudorhodoferax	0.02		0.15	0.03
Delftia		0.01		
Comamonadaceae uncultured		0.05	0.10	0.10
Undibacterium	0.01	0.26	0.55	
Methylophilaceae uncultured	0.48			
Citrobacter		0.32	0.14	0.33
Sinobacteraceae uncultured		0.13		
Erwinia				0.01
Escherichia-Shigella	0.01		0.01	0.81
Akkermansia			0.01	
Acinetobacter				0.37

	M8-W1	**M8-W3**	**M8-W6**	**M8-W12**
Core	**81.07**	**81.71**	**75.92**	**80.93**
Corynebacterium			0.01	
Agrococcus			0.01	
Microbacterium	0.31		0.61	
Yaniella	0.30			
Bacteroides	0.04			
Parabacteroides	0.05			
Lacibacter	0.01			
Actinomyces		0.11		
Propionibacterium		0.29		
Chryseobacterium				5.47
Pedobacter	0.11	1.93	4.38	1.16
Candidate division OD1 uncultured	2.35	0.86	0.96	1.11
Candidate division TM7 uncultured		0.02		
Cyanobacteria uncultured			2.52	
Anoxybacillus		1.12		
Bacillus	0.01	0.91		
Gemella	0.45	2.06	1.41	
Carnobacterium				0.37
Enterococcus	1.43	6.32		0.44
Blautia	2.16	0.07		0.17
Coprococcus		0.01		
Lachnospiraceae Incertae Sedis	0.64	0.02		1.42
Lachnospiraceae uncultured	1.90	0.02		
Peptostreptococcaceae Incertae Sedis		0.01		
Peptostreptococcaceae uncultured		0.12		
Veillonella		0.17		0.48
Erysipelotrichaceae Incertae Sedis	1.98	0.24		0.20

Caulobacter	0.05			
Phyllobacteriaceae uncultured				0.08
Rhizobium	1.91	0.26		0.98
Achromobacter	0.98	0.08		
Granulicatella			1.21	
Bosea				0.09
Ochrobactrum			0.75	0.22
Devosia			1.91	1.46
Sphingomonas			2.71	0.33
Derxia				0.51
Ralstonia	1.03	0.36	0.17	1.13
Acidovorax	0.88	0.01	0.01	0.83
Curvibacter				0.09
Limnohabitans	1.07	0.17	3.01	2.35
Neisseriaceae uncultured	0.12			
Pseudorhodoferax			0.11	0.08
Comamonadaceae uncultured			0.02	0.14
Undibacterium		0.13	0.50	0.40
Methylophilaceae uncultured				0.10
Kingella				1.52
Neisseria				0.12
Bdellovibrio				1.33
0319-6G20 uncultured				0.41
Sulfurimonas				0.41
Citrobacter	0.27	0.01	0.07	0.13
Escherichia-Shigella	0.11	0.08		
Pantoea	0.16			
Legionella				0.29
Aggregatibacter				0.11
Haemophilus				0.13
Acinetobacter		0.01		0.12

	M9-W1	**M9-W3**	**M9-W6**	**M9-W12**
CORE	**67.65**	**66.54**	**90.42**	**70.87**
Actinomyces			0.06	
Gardnerella			0.01	
Collinsella			0.02	
Rhodococcus			0.01	0.18
Leifsonia			0.17	0.27
Yaniella			0.13	
Microbacterium		0.16		0.37
Rothia				0.48
Propionibacterium	0.05	1.29		0.90
Bacteroides	4.42	0.01		
Prevotella				0.15
Chryseobacterium				1.19
Ferruginibacter				0.24
Chitinophagaceae uncultured				0.92

Pedobacter	0.79	10.29		0.28
Candidate division OD1 uncultured	0.13	0.12	1.11	4.08
Candidate division SR1 uncultured				0.50
Candidate division TM7 uncultured				0.01
Chloroflexi uncultured		1.03		
Anoxybacillus				0.02
Gemella	1.21			0.63
Enterococcus		0.10	0.01	0.71
Clostridium		0.04		
Blautia				1.14
Lachnospiraceae Incertae Sedis	0.02	0.07		1.81
Lachnospiraceae uncultured				0.12
Subdoligranulum			0.01	
Rhodopseudomonas			0.05	
Selenomonas				0.17
Veillonella				2.77
Erysipelotrichaceae Incertae Sedis				0.83
Ochrobactrum	0.01		0.01	0.40
Devosia	0.01	0.37		
Methylobacterium	0.01	0.53		
Albibacter	0.01			
Aminobacter	0.01		0.10	
Phyllobacterium		0.47	0.39	1.49
Phyllobacteriaceae uncultured			0.41	
Rhizobium		2.43	0.96	3.69
Paracoccus			0.42	
Rhodospirillaceae uncultured				0.13
Sphingomonas		1.16	0.59	1.37
Achromobacter		1.42	3.62	0.74
Ralstonia		1.35	0.06	1.38
Acidovorax	0.02	0.04		0.10
Undibacterium	0.02			
Limnohabitans		1.47	0.03	0.55
Pelomonas				0.48
Pseudorhodoferax		3.26		0.02
Comamonadaceae uncultured		0.17	0.01	0.08
Massilia		1.00		
Undibacterium		0.82	0.18	
Bdellovibrio		0.98	0.52	
Citrobacter	0.01	0.33	0.09	0.19
Erwinia		0.04	0.01	
Escherichia-Shigella	0.02	3.29	0.45	0.01
Serratia			0.01	
Haemophilus	24.13	0.01		
Acinetobacter				0.35

	M10-W1	**M10-W3**
Core	**91.15**	**63.79**

Gardnerella	0.01	
Leifsonia	0.11	
Corynebacterium		10.27
Brevibacterium		0.52
Agrococcus		0.01
Alpinimonas		0.01
Rhodoluna		0.01
Leucobacter		0.31
Microbacterium	0.18	0.21
Marmoricola	0.09	
Propionibacterium		1.03
Fluviicola		0.44
Bergeyella		0.06
Hydrotalea		0.41
Pedobacter	1.09	0.89
Candidate division OD1 uncultured	0.20	0.24
Candidate division TM7 uncultured		0.09
Chloroflexi uncultured		0.01
Cyanobacteria uncultured		0.01
Gemella		2.74
Enterococcus	0.38	0.77
Lactococcus		0.43
Lachnospiraceae Incertae Sedis	0.02	0.05
Lachnospiraceae uncultured		0.13
Veillonella	2.64	1.20
Phyllobacterium		
Rhizobium	0.51	
Erythrobacteraceae uncultured	0.05	
Erysipelotrichaceae Incertae Sedis		0.38
Devosia		0.01
Achromobacter	0.04	0.17
Burkholderia	0.01	
Alcaligenes		0.24
Ralstonia	0.54	0.46
Acidovorax	0.35	0.17
Curvibacter		0.01
Limnohabitans	0.01	0.13
Comamonadaceae uncultured	0.01	
Undibacterium	0.21	0.40
Bdellovibrio		0.01
Aeromonadaceae uncultured		4.37
Marinobacter		0.44
Pseudoalteromonas		2.64
Citrobacter	0.10	0.09
Haemophilus	0.09	
Escherichia-Shigella		0.66
Halomonas		2.23

Supplementary Table S2: Relative abundance (%) of the core microbiota at genus level and remaining taxa for each infant, M1 – M10, at week 1, 3, 6 and 12.

* = Breast milk sample not collected.

	F1-W1	F1-W3	F1-W6	F1-W12
Actinobaculum	0.00	0.00	0.00	0.01
Actinomyces	0.00	0.00	0.00	0.73
Bifidobacterium	2.08	46.90	35.75	6.85
Gardnerella	18.04	5.85	7.48	9.82
Eggerthella	0.00	0.00	0.00	0.01
Corynebacterium	0.01	0.00	0.00	0.00
Rhodococcus	0.03	0.00	0.00	0.00
Rothia	0.01	0.04	0.05	0.00
Propionibacterium	0.00	0.00	0.00	0.00
Bacteroides	5.47	0.01	0.01	0.01
Parabacteroides	10.75	0.27	0.41	17.10
Prevotella	0.00	0.00	0.01	0.00
Gemella	0.06	0.00	0.01	0.02
Staphylococcus	41.82	15.52	10.78	0.04
Enterococcus	0.42	0.71	1.11	2.60
Lactobacillus	0.25	3.95	5.80	1.30
Lactococcus	0.02	0.00	0.00	0.00
Streptococcus	10.78	11.81	36.80	0.50
Lachnospiraceae Incertae Sedis	10.02	0.29	0.41	22.97
Peptostreptococcaceae Incertae Sedis	0.00	0.01	0.00	0.00
Veillonella	0.00	0.02	0.01	10.33
Erysipelotrichaceae Incertae Sedis	0.01	0.00	0.00	0.00
Citrobacter	0.12	0.00	0.00	0.08
Enterobacter	0.05	0.02	0.00	0.72
Erwinia	0.00	0.01	0.00	0.03

Escherichia-Shigella	0.04	14.56	0.62	26.81
Haemophilus	0.00	0.00	0.74	0.02

	F2-W1	**F2-W3**	**F2-W6**	**F2-W12**
Actinomyces	0.00	0.02	0.02	0.03
Bifidobacterium	24.51	46.39	20.34	19.79
Gardnerella	0.00	0.01	0.01	0.01
Atopobium	0.00	0.01	0.00	0.01
Corynebacterium	0.00	0.03	0.01	0.00
Rhodococcus	0.01	0.04	0.21	0.10
Rothia	0.03	0.02	0.01	0.04
Bacteroides	0.00	0.01	0.01	0.06
Candidate division TM7 uncultured	0.00	0.00	0.00	0.11
Gemella	0.09	0.01	0.01	0.07
Staphylococcus	8.87	0.52	0.01	0.02
Dolosigranulum	0.00	0.02	0.01	0.01
Enterococcus	0.17	0.27	2.15	10.62
Lactobacillus	1.38	0.84	0.01	0.01
Streptococcus	2.58	5.84	0.27	3.75
Clostridium	0.00	11.02	1.67	2.13
Peptostreptococcaceae Incertae Sedis	0.00	1.48	1.30	0.04
Flavonifractor	0.00	0.00	0.00	1.21
Veillonella	5.87	8.60	12.52	14.84
Erysipelotrichaceae Incertae Sedis	0.00	0.00	0.00	1.30
Citrobacter	43.40	10.82	28.51	4.92
Enterobacter	12.37	13.51	32.33	6.59
Erwinia	0.15	0.11	0.27	1.03
Escherichia-Shigella	0.01	0.01	0.27	29.45
Haemophilus	0.51	0.37	0.04	0.06

	F3-W1	**F3-W3**	**F3-W6**	**F3-W12***
Bifidobacterium	0.02	23.07	8.59	
Gardnerella	0.01	0.00	0.02	
Atopobium	0.00	0.00	0.04	
Eggerthella	0.00	0.00	0.11	
Gordonibacter	0.00	0.00	0.00	
Corynebacterium	0.00	0.04	0.00	
Rothia	0.06	0.16	0.07	
Bacteroides	0.00	0.01	44.88	
Prevotella	0.00	0.00	0.02	

Gemella	0.01	0.01	0.07	
Staphylococcus	41.47	6.65	0.35	
Dolosigranulum	0.00	0.01	0.00	
Enterococcus	3.31	0.06	0.01	
Lactobacillus	0.00	20.50	11.18	
Streptococcus	21.78	18.53	6.36	
Clostridium	5.17	14.50	0.00	
Sarcina	0.62	0.04	0.00	
Lachnospiraceae Incertae Sedis	0.00	0.00	5.23	
Veillonella	2.13	4.30	19.91	
Erysipelotrichaceae Incertae Sedis	25.34	11.80	3.07	
Enterobacter	0.00	0.01	0.02	
Escherichia-Shigella	0.01	0.01	0.03	
Haemophilus	0.05	0.26	0.01	

	F4-W1	**F4-W3**	**F4-W6**	**F4-W12**
Actinobaculum	0.00	0.00	0.23	0.03
Actinomyces	0.00	0.46	2.15	2.76
Bifidobacterium	9.53	17.18	7.16	20.99
Gardnerella	5.86	20.26	4.76	0.96
Scardovia	0.00	0.00	0.07	0.04
Atopobium	0.00	0.00	0.12	0.01
Collinsella	0.59	0.18	1.41	5.02
Eggerthella	0.00	0.15	1.40	0.15
Corynebacterium	0.00	0.00	0.00	0.01
Rothia	0.01	0.00	0.00	0.01
Propionibacterium	0.00	0.00	0.26	0.09
Bacteroides	0.00	0.01	0.01	0.01
Porphyromonas	0.00	0.04	0.00	0.00
Prevotella	0.00	0.08	0.00	0.00
Gemella	0.02	0.01	0.00	0.00
Staphylococcus	1.55	0.23	0.06	0.08
Dolosigranulum	0.00	0.00	0.01	0.00
Enterococcus	1.06	0.38	3.43	3.66
Lactobacillus	0.02	1.33	10.02	7.55
Streptococcus	0.85	1.02	1.82	0.22
Clostridium	0.00	0.00	0.00	1.93
Anaerococcus	0.00	0.02	0.01	0.61
Finegoldia	0.01	0.02	0.02	0.61
Peptoniphilus	0.00	0.00	0.00	0.25
Coprococcus	0.00	0.00	0.00	0.54
Peptostreptococcaceae Incertae Sedis	0.00	0.00	0.00	0.44
Negativicoccus	0.00	0.01	0.00	0.00
Veillonella	42.81	37.09	37.73	21.04

Erysipelotrichaceae Incertae Sedis	0.00	0.00	0.00	0.01
Citrobacter	0.00	0.00	0.02	0.00
Enterobacter	0.00	0.01	0.07	0.00
Erwinia	0.00	0.00	0.01	0.00
Escherichia-Shigella	37.66	21.47	29.22	32.73
Haemophilus	0.00	0.00	0.01	0.00

	F5-W1	**F5-W3**	**F5-W6**	**F5-W12**
Actinomyces	0.43	0.00	0.00	0.07
Bifidobacterium	9.42	5.34	6.97	11.22
Gardnerella	0.01	10.29	24.23	27.60
Scardovia	0.00	0.00	0.00	0.03
Atopobium	0.00	0.00	0.08	0.04
Collinsella	0.17	0.00	0.00	0.00
Eggerthella	0.11	0.00	0.00	0.00
Corynebacterium	0.00	0.02	0.15	0.02
Rhodococcus	0.00	0.00	0.00	0.01
Rothia	0.01	0.00	0.23	0.05
Bacteroides	8.15	0.00	0.01	0.01
Parabacteroides	4.69	0.00	0.00	0.00
Prevotella	0.00	0.00	0.00	0.04
Gemella	0.18	0.09	0.18	0.06
Staphylococcus	11.48	2.73	6.47	0.08
Granulicatella	0.08	0.01	0.10	0.00
Enterococcus	1.58	0.00	0.01	1.40
Lactobacillus	0.01	0.02	0.00	0.00
Streptococcus	22.37	24.10	30.78	13.40
Peptoniphilus	0.00	0.00	0.00	0.01
Lachnospiraceae Incertae Sedis	2.48	0.00	0.00	0.01
Veillonella	3.37	15.07	6.82	1.67
Erysipelotrichaceae Incertae Sedis	0.00	0.00	0.01	0.01
Enterobacter	0.00	0.00	0.01	0.02
Erwinia	0.00	0.01	0.01	0.00
Escherichia-Shigella	35.20	42.17	23.71	44.23
Haemophilus	0.23	0.12	0.21	0.01

	F6-W1	**F6-W3**	**F6-W6**	**F6-W12**
Actinomyces	0.00	0.00	0.00	0.01
Bifidobacterium	0.13	0.08	0.26	0.21
Gardnerella	27.91	29.77	48.29	35.20
Eggerthella	0.00	0.00	0.00	0.29
Corynebacterium	0.00	0.00	0.00	0.01
Rhodococcus	0.00	0.00	0.00	0.73

Rothia	0.03	0.05	0.04	0.00
Propionibacterium	0.00	0.00	0.04	0.07
Bacteroides	0.01	0.01	0.00	0.00
Elizabethkingia	0.00	0.00	0.01	0.00
Gemella	0.18	0.17	0.10	0.00
Staphylococcus	7.49	21.27	4.62	0.09
Enterococcus	0.01	0.01	6.94	1.29
Lactobacillus	59.81	45.31	30.06	4.44
Streptococcus	0.97	0.38	2.18	0.22
Clostridium	0.00	0.00	0.05	0.29
Peptostreptococcaceae Incertae Sedis	0.02	0.00	0.01	0.44
Veillonella	0.20	0.01	0.03	1.39
Erysipelotrichaceae Incertae Sedis	0.01	0.00	0.00	4.05
Citrobacter	0.00	0.00	4.85	1.06
Enterobacter	0.00	0.00	2.21	49.07
Erwinia	0.00	0.00	0.03	1.04
Escherichia-Shigella	0.02	0.02	0.05	0.06
Haemophilus	3.20	2.92	0.23	0.03

	F7-W1	**F7-W3**	**F7-W6**	**F7-W12**
Actinomyces	0.00	0.20	0.00	0.06
Bifidobacterium	41.74	34.67	32.28	43.47
Gardnerella	8.97	12.16	4.05	0.21
Atopobium	0.00	0.00	0.01	0.03
Corynebacterium	0.01	0.06	0.01	0.01
Rothia	0.00	1.40	0.00	0.00
Bacteroides	0.02	0.01	0.01	0.00
Elizabethkingia	0.00	0.00	0.01	0.00
Gemella	0.01	0.01	0.00	0.02
Staphylococcus	32.83	15.31	0.63	0.69
Dolosigranulum	0.01	0.06	0.01	0.01
Enterococcus	0.02	0.00	0.01	5.30
Lactobacillus	0.03	0.01	0.12	1.46
Streptococcus	16.19	17.11	14.46	28.56
Clostridium	0.01	16.51	0.00	0.45
Peptostreptococcaceae Incertae Sedis	0.00	0.00	0.00	0.18
Veillonella	0.02	0.01	48.08	1.68
Erysipelotrichaceae Incertae Sedis	0.01	0.00	0.00	0.00
Enterobacter	0.00	0.01	0.01	0.00
Escherichia-Shigella	0.03	2.00	0.19	17.77
Haemophilus	0.03	0.01	0.00	0.00

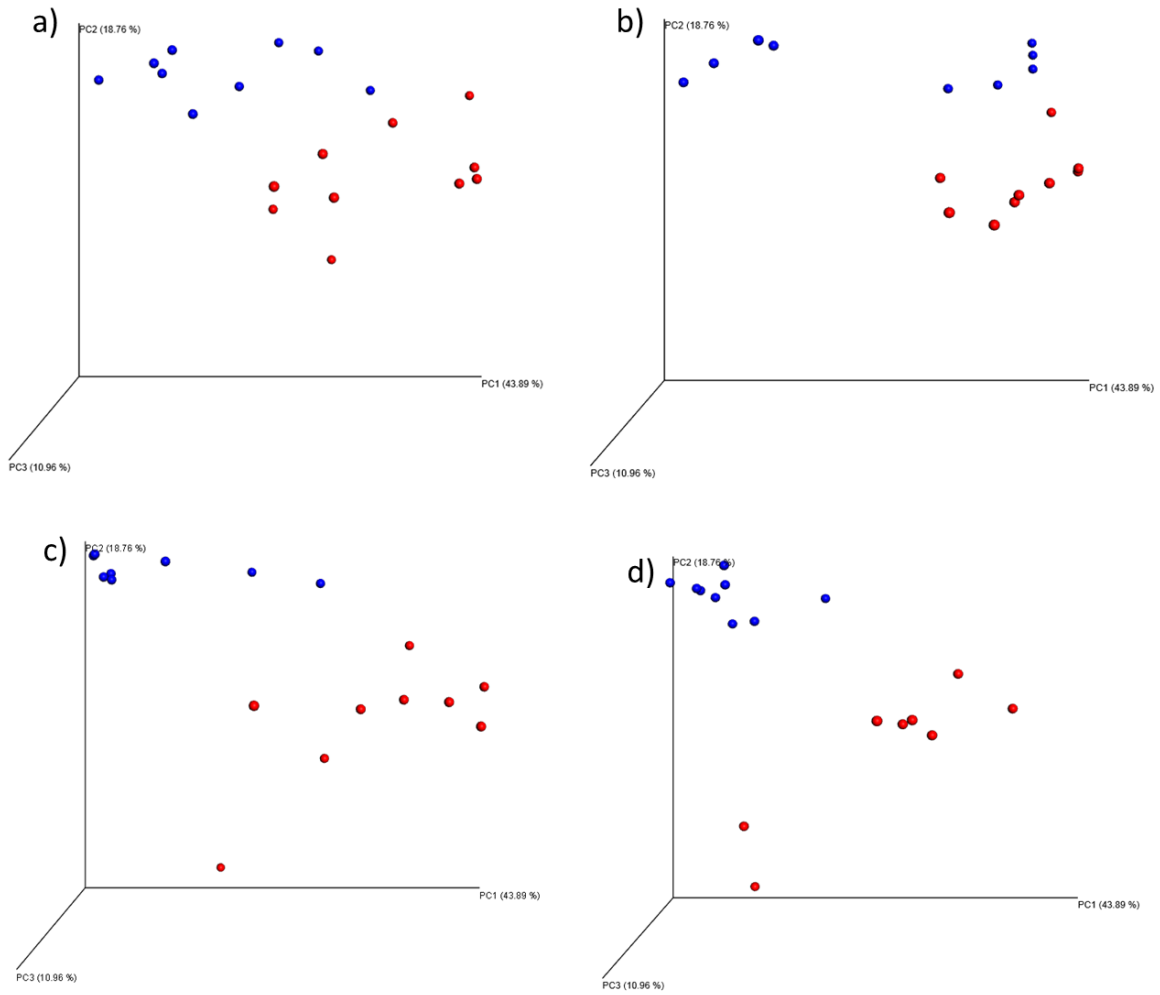
	F8-W1	**F8-W3**	**F8-W6**	**F8-W12**

Actinomyces	0.00	0.00	0.00	0.02
Bifidobacterium	7.72	2.24	2.62	8.01
Gardnerella	40.72	14.37	5.45	8.88
Eggerthella	0.00	0.00	0.00	0.14
Corynebacterium	0.01	0.00	0.00	0.00
Rhodococcus	0.00	0.00	0.00	0.01
Rothia	0.01	0.01	0.03	0.01
Propionibacterium	0.00	0.00	0.00	0.02
Bacteroides	0.03	0.07	16.04	43.01
Elizabethkingia	0.00	0.00	0.00	0.01
Gemella	0.06	0.02	0.00	0.01
Staphylococcus	30.43	0.34	0.00	0.10
Dolosigranulum	0.00	0.01	0.00	0.00
Enterococcus	0.00	0.08	0.51	10.83
Lactobacillus	0.01	0.01	0.15	2.60
Streptococcus	14.71	0.36	0.15	0.24
Clostridium	0.00	0.00	0.15	0.01
Coprococcus	0.00	0.00	0.03	0.00
Lachnospiraceae Incertae Sedis	0.00	0.00	0.03	0.26
Peptostreptococcaceae Incertae Sedis	0.00	0.00	0.00	0.88
Veillonella	2.16	67.31	63.52	10.03
Citrobacter	0.00	0.01	0.00	0.03
Enterobacter	0.00	0.00	0.03	0.69
Erwinia	0.00	0.00	0.00	0.06
Escherichia-Shigella	3.89	15.13	11.28	14.13
Haemophilus	0.23	0.02	0.00	0.00

	F9-W1	**F9-W3**	**F9-W6**	**F9-W12**
Actinomyces	0.42	0.05	0.17	1.10
Bifidobacterium	0.02	0.01	0.03	0.00
Gardnerella	0.00	0.01	0.00	0.00
Eggerthella	0.00	0.00	0.02	0.02
Corynebacterium	0.00	0.00	0.01	0.00
Rothia	0.00	0.00	0.00	0.08
Propionibacterium	0.00	0.00	0.26	0.00
Bacteroides	0.01	0.01	0.00	0.01
Gemella	0.06	0.16	0.00	0.00
Staphylococcus	11.76	7.06	0.67	0.05
Dolosigranulum	0.00	0.00	0.00	0.01
Enterococcus	0.00	0.00	0.00	0.04
Lactobacillus	0.01	0.01	0.54	0.21
Streptococcus	27.51	57.78	40.35	0.98
Clostridium	0.00	13.27	15.35	1.02
Sarcina	0.00	0.02	0.01	0.00

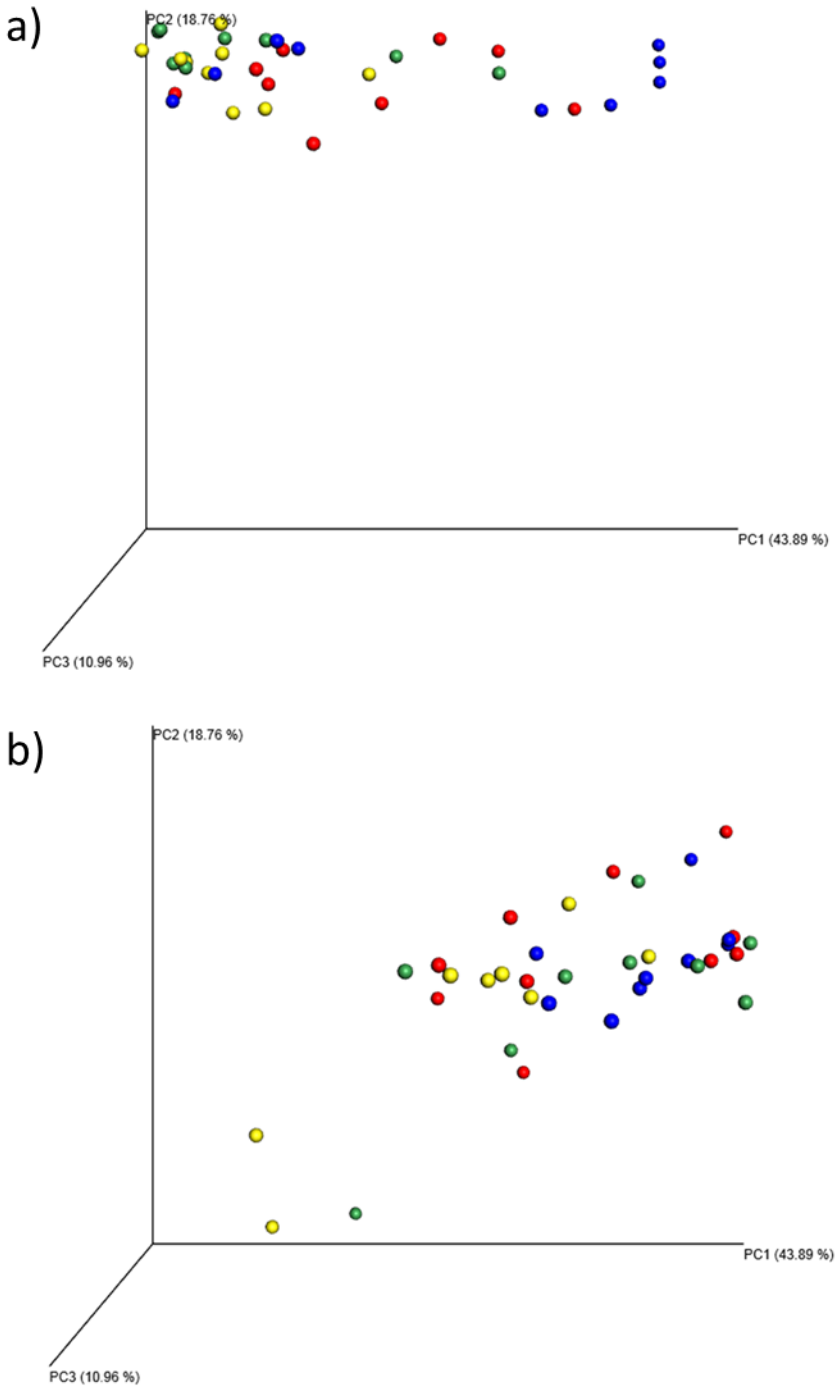
Anaerococcus	0.00	0.00	0.00	0.00
Finegoldia	0.00	0.00	0.00	0.00
Peptoniphilus	0.00	0.24	0.12	0.00
Coprococcus	0.00	0.00	0.00	0.00
Lachnospiraceae Incertae Sedis	0.00	0.00	16.78	32.09
Peptostreptococcaceae Incertae Sedis	0.00	0.04	1.33	0.10
Flavonifractor	0.00	0.00	0.00	0.00
Ruminococcaceae Incertae Sedis	0.00	0.00	0.00	0.00
Megasphaera	0.00	0.08	1.27	0.56
Negativicoccus	0.00	2.35	0.36	0.15
Phascolarctobacterium	0.00	0.00	0.00	0.00
Veillonella	27.18	11.26	15.92	22.80
Erysipelotrichaceae Incertae Sedis	0.00	0.00	0.00	0.00
Citrobacter	0.00	0.00	0.00	0.20
Enterobacter	0.00	0.00	0.00	0.04
Erwinia	0.00	0.00	0.00	0.00
Escherichia-Shigella	0.02	0.02	0.01	0.01
Haemophilus	32.79	7.32	6.54	0.03
Akkermansia	0.00	0.00	0.00	39.49

	F10-W1	**F10-W3**	**F10-W6***	**F10-W12***
Bifidobacterium	1.62	6.14		
Gardnerella	0.00	0.02		
Eggerthella	0.00	0.02		
Corynebacterium	0.01	0.09		
Rhodococcus	0.00	0.01		
Rothia	0.01	0.01		
Bacteroides	0.01	0.01		
Elizabethkingia	0.02	0.00		
Flavobacterium	0.01	0.00		
Gemella	0.01	0.00		
Staphylococcus	1.38	3.06		
Dolosigranulum	0.00	0.01		
Enterococcus	0.48	0.01		
Lactobacillus	0.00	0.01		
Streptococcus	0.73	1.60		
Clostridium	0.47	0.01		
Lachnospiraceae Incertae Sedis	0.01	6.76		
Veillonella	52.83	3.24		
Erysipelotrichaceae Incertae Sedis	0.01	1.42		
Enterobacter	0.00	0.01		
Escherichia-Shigella	41.18	77.36		
Haemophilus	1.15	0.14		



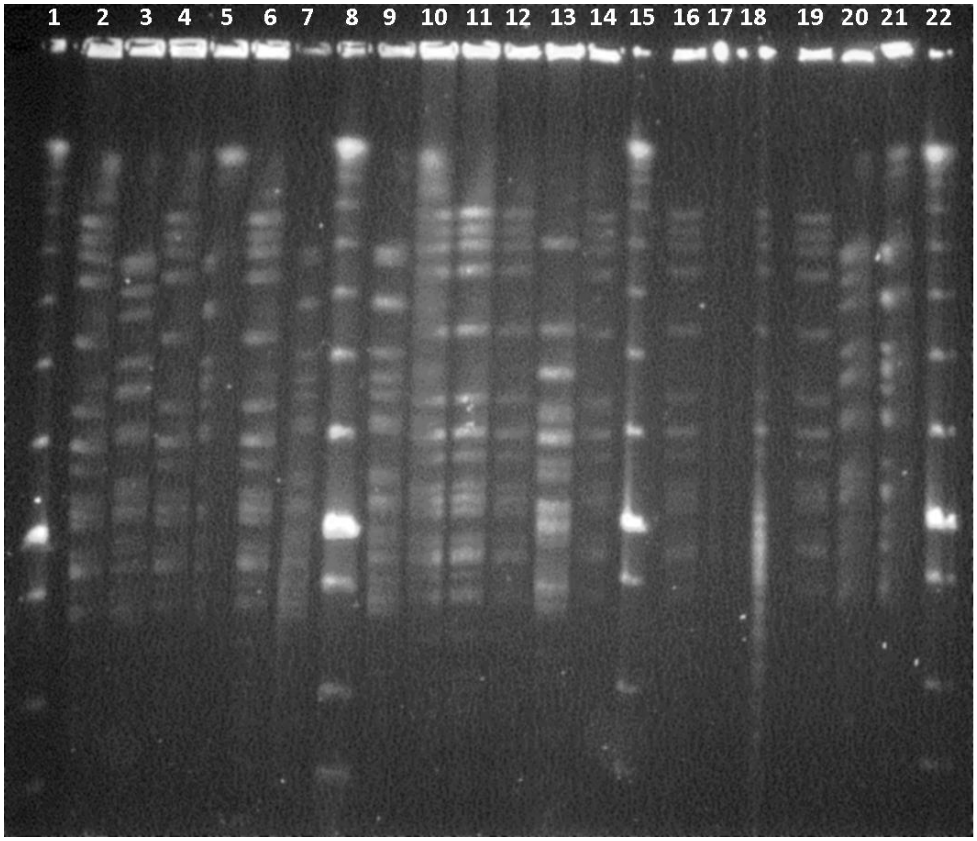
Supplementary Figure S1:

Principal coordinates analysis of Weighted UniFrac values between milk (blue) and faecal (red) samples over time with the axes scaled by the percentage of the variance that they contain. a) Week 1, b) Week 3, c) Week 6 and d) Week 12.



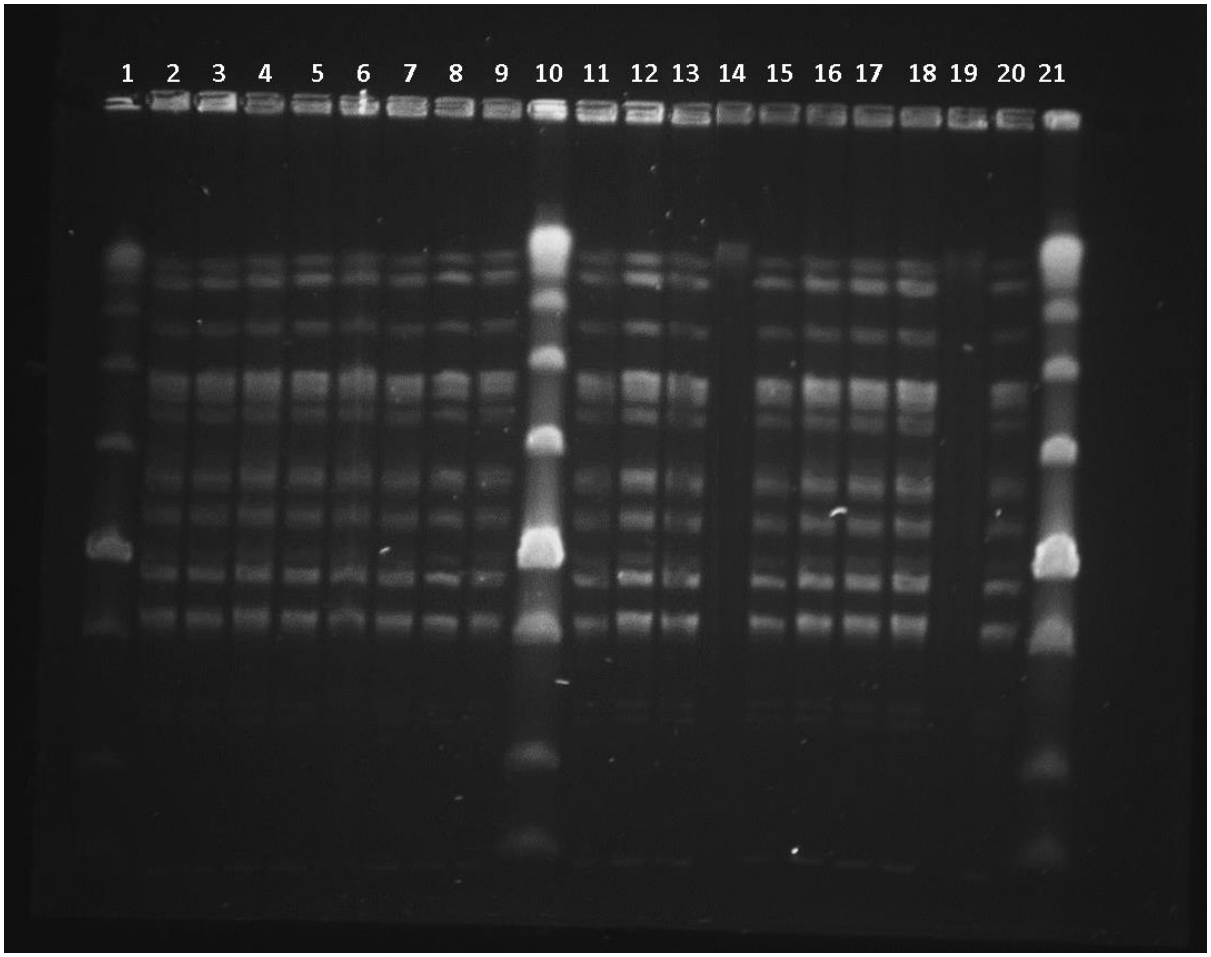
Supplementary Figure S2:

Principal coordinates analysis of Weighted UniFrac values between a) milk samples over time and b) faecal samples over time, with the axes scaled by the percentage of the variance that they contain. Red = Week 1, Blue = Week 3, Green = Week 6 and Yellow = Week 12.



Supplementary Figure S3:

Un-edited image of pulse-field gel electrophoresis patterns of XbaI-digested genomic DNA of *B. breve* isolates from human milk and infant faeces. Lanes 1, 8 and 15 contain a low molecular weight marker; Lanes 2, 4, 6 10 and 11 contain isolates from breast-milk; Lanes 12, 14, 16 and 19 contain isolates from infant faeces.



Supplementary Figure S4:

Un-edited image of pulse-field gel electrophoresis patterns of ApaI-digested genomic DNA of *L. plantarum* isolates from human milk and infant faeces. Lanes 1, 10 and 21 contain a low molecular weight marker; Lanes 2-9 contain isolates from breast-milk; Lanes 11-20 contain isolates from infant faeces.