Table S1. Detection frequency (%) of taxa identified by HOMIM microarray in exclusively formula or exclusively breastfed, three-month-old infants. Taxa are identified by species name or by their Human Oral Taxon (HOT) (www.homd.org) number if unnamed, or by cluster group. Clusters are indicated by superscript numbers, with targeted taxa in the footnote. Differences between groups are shown as p-values from Chi^2 test and logisitic regression after adjustment for mode of delivery. P-value adjustment for false discovery rates indicates differences with p-values <0.005 as statistically significant.

					p-value	
Phylum	**Bacteria**	**Probe ID**	**Formula fed**	**Breast -fed**	**Chi^2 test**	**Logistic regression**
Firmicutes/Bacilli	*Streptococcus* Cluster I[1]	AB98	100.0	75.0	0.012	0.998
	Streptococcus Cluster II[2]	Q59	57.1	100.0	0.000	0.997
	Streptococcus Cluster III[3]	Q65	81.0	100.0	0.003	0.997
	Streptococcus anginosus/gordonii	F49	0.0	6.8	0.221	0.998
	*Streptococcus anginosus/intermedius**	AB82, Q62	92.2	100.0	0.145	0.997
	*Streptococcus australis**	AB83, U50	52.4	86.4	0.003	0.05[D,BF]
	*Streptococcus constellatus/intermedius**	AB77, F48	0.0	18.2	0.037	0.998
	*Streptococcus cristatus**	AD88, AD89	57.1	40.9	0.220	0.192
	Streptococcus infantis/Streptococcus sp. HOT 065	Y74	76.2	54.5	0.093	0.092
	Streptococcus mitis bv 2/*Streptococcus* sp. HOT 069	Q64	61.9	88.6	0.012	0.021
	*Streptococcus mutans**	AC57, X04	0.0	6.8	0.221	0.998
	Streptococcus oralis/Streptococcus sp. HOT 064	F46	100.0	100.0	1.000	-
	Streptococcus parasanguinis I and II*	AB05, R17	100.0	90.9	0.154	0.998
	Streptococcus salivarius/Streptococcus sp. HOT 067	E34	52.4	56.8	0.736	0.972
	Streptococcus sanguinis	AB78, AB75	9.5	9.1	0.955	0.508
	Streptococcus sp. HOT 070/071	N20	23.3	6.8	0.051	0.896
	Gemella haemolysans	K63	100.0	93.2	0.221	0.998
	Gemella morbillorum	K64	9.5	31.8	0.051	0.198[D]
	Gemella sanguinis	AB17	0.0	2.3	0.486	0.998
	Granulicatella adiacens/elegans	W81	57.1	15.9	0.001	0.002
	Granulicatella adiacens	AB30	42.9	13.6	0.009	0.015
	*Granulicatella elegans**	AB29, AB28	47.6	31.8	0.217	0.030 [D,#]
	Lactobacillus Cluster I[4]	W94	23.8	45.5	0.093	0.804[D]
Firmicutes/Clostridia	*Eubacterium yurii*	W84	0.0	6.8	0.221	0.998
	Eubacterium saburreum	W21	0.0	6.8	0.221	0.998
	Lachnospiraceae [G-1] sp. HOT 082 (Eubacterium saburreum)	AB50	9.1	2.3	0.280	0.548
	Catonella morbi/Catonella sp. HOT 164	O56	0.0	6.8	0.221	0.998
	*Parvimonas micra**	V05, L97	4.8	11.4	0.390	0.749
	Dialister pneumosintes	X78	0.0	2.3	0.486	0.998
	Megasphaera micronuciformis	AA57	4.8	0.0	0.145	0.997
	Megasphaera sp. HOT 123	AD11	28.6	0.0	0.000	0.897
	Selenomonas Cluster I[5]	AC13	0.0	2.3	0.486	0.998
	Selenomonas infelix/Selenomonas sp. HOT 126/481	O54	4.8	15.9	0.201	0.226
	Selenomonas noxia	AC04	0.0	2.3	0.486	0.998

	Selenomonas sputigena	AB04	4.8	2.3	0.587	0.900
	*Solobacterium moorei**	AC01, AC02	61.9	2.3	0.000	0.003[D,FF]
	Veillonella atypica/parvula	Q67	100.0	86.8	0.076	0.998
	*Veillonella atypica**	W88, W04	100.0	54.4	0.000	0.998[D]
	Veillonella sp. EF509966 (intestinal isolate)	AD63-C	23.8	47.7	0.066	0.240
	Veillonella parvula	AC37, M04	90.5	77.3	0.199	0.115
	Veillonella sp. HOT 780	AD02	95.2	34.1	0.000	0.001
	Veillonellaceae [G-1] sp. HOT 155	AB58	0.0	2.3	0.486	0.998
	Veillonellaceae [G1] sp. HOT 135/148	W86	0.0	2.3	0.614	0.998
Actinobacteria	*Actinomyces* Cluster I[6]	AB35	0.0	18.2	0.037	0.998
	Actinomyces Cluster II[7]	AC99	23.8	4.5	0.019	0.054
	Actinomyces gerencseriae	E46	33.3	88.6	0.000	0.000
	Actinomyces sp. HOT 175	P91	9.5	2.3	0.193	0.494
	Corynebacterium matruchotii	AB96	0.0	4.5	0.321	0.998
	*Rothia mucilaginosa**	AB62, AB63	61.9	52.3	0.465	0.648
	Rothia dentocariosa/mucilaginosa	E52	52.4	61.4	0.492	0.630
	Propionibacterium propionicum	AB71	0.0	4.5	0.321	0.998
	Bifidobacterium animalis ss. *animalis /lactis*	AC27	4.8	11.4	0.390	0.998
	Atopobium parvulum	X29	4.0	0.0	0.145	0.997
	Slackia exigua	AB52	47.6	43.2	0.736	0.120[D]
Fusobacterium	*Fusobacterium nucleatum ss. animalis/nucleatum*	AE01	33.9	29.5	0.757	0.776
	Fusobacterium periodonticum	R20	23.8	6.8	0.051	0.169
	Leptotrichia buccalis/goodfellowii/Sneathia sanguinegens	AA45	57.1	13.6	0.000	0.007[D,BF]
	*Leptotrichia hofstadii**	AA58, Y55	14.3	2.3	0.059	0.240
	Leptotrichia sp. HOT 215	AA59	4.8	0.0	0.145	0.997
Bacterioidetes	*Bacteroidetes* phylum*	X57, K76	0.0	4.5	0.321	0.998
	Porphyromonas catoniae/Porphyromonas sp. HOT 279	N95	9.5	0.0	0.038	0.997
	Porphyromonas endodontalis	W78	4.8	0.0	0.145	0.997
	Tannerella forsythia	X56	9.5	0.0	0.038	0.997
	Prevotella Cluster I[8]	Y65	0.0	6.8	0.221	0.998
	Prevotella Cluster IV[9]	AA44	33.3	2.3	0.000	0.014
	Prevotella loescheii/Prevotella sp. HOT 472	Y64	0.0	6.8	0.221	0.998
	Prevotella melaninogenica/histicola	T81	28.6	2.3	0.001	0.025
	Prevotella nigrescens	W40	0.0	4.5	0.321	0.998
	Prevotella multisaccharivorax	AC59	19.0	0.0	0.003	0.997
	Prevotella sp. HOT 308	Q94	4.8	0.0	0.145	0.997
	Capnocytophaga granulosa/Capnocytophaga sp. HOT 326	AA89	0.0	6.8	0.221	0.998
	Capnocytophaga sputigena	W46	4.8	4.5	0.969	0.656
Proteobacteriuma	*Kingella oralis*	AA77	47.6	4.5	0.000	0.004
	Kingella oralis and *Neisseria*	O86	47.6	2.3	0.000	0.003
	Neisseria Cluster I[10]	Y60	4.8	0.0	0.145	0.997
	Neisseria elongata	AA75	0.0	4.5	0.321	0.998
	Neisseria flavescens	AA76	42.9	0.0	0.000	0.997
	Neisseria gonorrhoea/ polysaccharea	O76	33.3	0.0	0.000	0.998
	Lautropia mirabilis	X44	33.3	2.3	0.000	0.021

	Cardiobacterium hominis	O97	0.0	9.1	0.154	0.998
	Pseudomonas Cluster I[11]	O96	9.5	6.8	0.702	0.761
	Aggregatibacter segnis/Aggregatibacter sp. HOT 512*	AA78, P05	0.0	2.3	0.486	0.998
	Aggregatibacter actinomycetemcomitans	P02	14.3	0.0	0.010	0.997
	Haemophilus parainfluenzae	W79	57.1	34.1	0.078	0.321[D]
	Haemophilus sp. HOT 035/ 036*	AA97, X31	66.7	13.6	0.000	0.001[D,FF]
	Campylobacter Cluster I[12]	T87	9.5	11.4	0.823	0.972
	Campylobacter concisus	O46	9.5	4.5	0.435	0.885
	*Campylobacter concisus/rectus**	X36, T86	38.1	15.9	0.047	0.065
	*Campylobacter gracilis**	Q04, X34	9.5	11.4	0.823	0.442
	*Campylobacter showae**	W36, X35	0.0	6.8	0.221	0.998
TM7	*TM7* [G-1] sp. HOT 347/349*	Y77, W85	47.6	6.8	0.000	0.007
	TM7 [G-5] sp. HOT 356/437*	O32, AC48	0.0	2.3	0.486	0.998
Synergistes	*Synergistes* [G-3] sp. HOT359	AC53	9.5	0.0	0.038	0.997

1) *Streptococcus* Cluster I (probe AB98) targets *S. mitis* biovar 2, *S. peroris*, *S. pneumonia, Streptococcus* sp. HOT 423.
2) *Streptococcus* Cluster II (probe Q59) targets *S. salivarius*, *S. sanguinis*, *Streptococcus* sp. HOT 070/071
3) *Streptococcus* Cluster III (probe Q65) targets *S. salivarius*, *S. sanguinis*, *S. sinensis, S. sobrinus.*
4) *Lactobacillus* Cluster I (probe W94) targets *L. casei*, *L. paracasei, L. rhamnosus.*
5) *Selenomonas* Cluster I (probe AC13) targets *S. infelix*, *Selenomonas* sp. HOT 126/479/481.
6) *Actinomyces* Cluster I (probe AB35) targets *A. meyeri*, *A. odontolyticus, A. oricola, A. naeslundii IIviscosus.*
7) *Actinomyces* Cluster II (probe AC99) targets *A. meyeri*, *A. odontolyticus, Actinomyces* sp. HOT 180/181.
8) *Prevotella* Cluster I (probe Y65) targets *P. loescheii*, *Prevotella* sp. HOT 317/472/Y65
9) *Prevotella* Cluster IV (probe AA44) targets *P. loescheii, P. nigrescens*, *P. pallens, Prevotella* sp. HOT 782.
10) *Neisseria* Cluster I (probe Y60): *N. gonorrhoeae, N. meningitidis, N. polysaccharea.*
11) *Pseudomonas* Cluster I (probe O96) targets *P. aeruginosa*, *P. fluorescens*, *P. pseudoalcaligenes*, *P. otitidis.*
12) *Campylobacter* Cluster I (probe T87) targets *C. curvus*, *C. rectus, C. showae.*

* Two or more different probes with positive signals for the same species were combined

D) Species detection was independently associated with mode of delivery.

BF) Species detection prevalence was higher in breastfed than formula fed infants in both vaginally and Caesarean section delivered infants when analyse separately in mode of delivery strata

FF) Species detection prevalence was higher in formula fed than breastfed infants in both vaginally and Caesarean section delivered infants when analysed separately in mode of delivery strata

\# Species detection was more prevalent in formula fed vaginally delivered infants, but more prevalent in breastfed Caesarean section delivered infants when analysed separately in mode of delivery strata