Supplemental Information

SUBJECTS AND METHODS

• Nutritional Assessment

Breastfeeding was characterized by using World Health Organization criteria.[45] Weight was measured to the nearest 10 g (Salter 914 electronic scale; Fairmont, MN). Recumbent length was measured to the nearest tenth of a centimeter by using a sliding scale produced locally. Birth weight was measured by hospital staff by using a different scale to the nearest 50 g.

• TI

Ultrasound was performed by using a Just Vision 400 with PVF-745v probe (Toshiba; Tochigi, Japan) to derive the volume-related TI.[46]

• Blood Leukocytes

Heparinized venous blood was collected at 6 and 15 weeks. A complete blood count with differential was performed on blood diluted 1:5 with EDTA-isotonic saline (Sysmex XT1800i; Diamond Diagnostics, Holliston, MA). Concentrations of naive and memory/activated CD4 and CD8 T cells were determined by using Multitest reagents, Trucount tubes, a FACSCalibur flow cytometer, and CellQuest Pro software (BD Biosciences, San Jose, CA).

• Vaccine-Specific T-cell SI

The flow cytometric assay of specific cell-mediated immune response in activated whole blood (FASCIA) method[47–49] was used to measure the SI after 6 days of culture of peripheral blood mononuclear cells at 37°C in 5% CO_2 in medium containing 10% heat-inactivated autologous plasma plus the T-cell mitogen SEB (Toxin Technologies, Sarasota, FL) as a positive control, diluent as a negative control, or 1 of 4 vaccine antigens: PPD from *Mycobacterium bovis*, the organism used in the BCG vaccine (NIBSC; Potters Bar, United Kingdom); purified and inactivated polio virus types 1, 2, and 3 (Sanofi-Pasteur, Lyon, France); HBV surface antigen (adw subtype, recombinant; Fitzgerald, Acton, MA); or TT (NIBSC). Lymphoblasts were identified with forward/side scatter, memory/activated T cells by expression of CD3, CD4, CD8, and CD45RO. Dead cells were excluded by using a viability dye. Flow analysis was performed with a FACSAria III and FacsDiva software (BD Biosciences) and data analysis with FlowJo software (TreeStar, Ashland, OR) to calculate the SI as the ratio of memory/activated T-cell blasts in cultures with stimulation relative to the negative control.

• Antibody in Lymphocyte Supernatant Assay

The assay was performed essentially as described.[50] Commercial ELISA kits were used to measure IgG specific for TT (The Binding Site, San Diego, CA), polio virus (Fitzgerald), and HBV (Diasorin, Stillwater, MN) in the supernatant of peripheral blood mononuclear cells cultured for 48 hours at 37°C in 5% CO_2 in medium containing 10% fetal bovine serum at a density of 1×10^7 per mL.

• PPD-DTH Skin-Test Response

The area of induration was measured 48 hours after intradermal injection of 0.1 mL tuberculin, a PPD from a human strain of *Mycobacterium tuberculosis* (1.0 TU; Span Diagnostics Ltd, Gujarat, India) on the flexor surface of the forearm.

• Characterization of Microbiota by DNA Sequence Analysis

Stool DNA was extracted by using a fecal DNA kit (Zymo Research, Irvine, CA). Mixed-template amplicons were amplified from this DNA by using the F515-R806 (V4) segment of the bacterial 16S rRNA gene modified to contain an adapter region for sequencing on the Illumina MiSEQ platform and a unique barcode sequence to enable multiplexing of up to ~1500 samples in a single sequencing run.[51] Raw data were demultiplexed, quality-filtered, and analyzed by using the open-source software Quantitative Insights Into Microbial Ecology (QIIME).[52,53] All samples produced useful data. The median number of complete V4 sequence reads per sample was 37 883 with only 1 sample $<$15 000. Operational taxonomic units were assigned by using the QIIME implementation of UCLUST[54] and a threshold of 97% pairwise identity.

• Identification of *Bifidobacterium* Species

A *Bifidobacterium*-specific T-RFLP assay was performed as described.[44] Briefly, DNA was amplified by PCR by using primers NBIF-F and NBIF-R (Supplemental Table 4), purified and cut with restriction enzymes AluI and HaeIII, fragment sizes were determined on an ABI 3100 analyzer (Applied Biosystems, Carlsbad, CA) for comparison with expected sizes. The results used are for the HaeIII fragments, which are consistent with the AluI results.

• Differentiation of *B longum* Subspecies *infantis* and *longum*

DNA was amplified by PCR by using a mixture containing 0.5 μL of 10 μM stock of each of 3 primers, FWD_BL_BI, REV_BL and REV_BI (Supplemental Table 4): 12.5 μL GoTaq Green Master Mix (Promega, Madison, WI), 1 μL of 25 mM $MgCl_2$, 1 μL of template DNA, and 9 μL of nuclease free water. Cycling conditions were 95°C for 2 minutes, 30 cycles of 95°C for 1 minute, 54°C for 1 minute, and 72°C for 30 seconds, followed by a 72°C extension for 5 minutes. PCR products were purified by using the QIAquick PCR purification kit (Qiagen, Valencia, CA) and diluted 1:10 for analysis (1.5 μL) by capillary electrophoresis on an ABI 3100 genetic analyzer. The HEX fluorophore on the primer common to both subspecies allowed detection and differentiation of the amplicon sizes unique to *B longum* subspecies *longum* and *B longum* subspecies *infantis,* and an approximate quantification of the abundance of each amplicon based on peak area. The samples were analyzed with PeakScanner 1.0 software (Applied Biosyste).

• Quantification of *Bifidobacterium* by PCR

Total bacteria and *Bifidobacterium* 16S rDNA copy number per gram of stool were measured by qPCR. SYBR green and TaqMan qPCR assays were performed on a 7500 Fast Real-Time PCR system (Applied Biosystems) with primers specific for bacteria and the genus *Bifidobacterium* (Supplemental Table 4). Universal Bacteria SYBR green assays contained 10 μL 2×Takara SYBR Premix Ex TaqII master mix (Clontech, Mountain View, CA), 6 μL water, 200 nM forward and reverse primers (Uni334F and Uni514R), and 1 μL genomic DNA. Each *Bifidobacterium*-specific TaqMan assay contained 10 μL 2×TaqMan Universal PCR master mix (Applied Biosystems), 3.75 μL water, 300 nM forward and reverse primers (Bif F and Bif R), 150 nM *Bifidobacterium*-specific probe (Bif P), and 2.5 μL genomic DNA. Cycling conditions and primer sequences are described in Supplemental Table 4. Each sample was assayed in triplicate with a nontemplate control for each plate.

RESULTS

• Vaccine Responses at 15 Weeks

All 4 vaccines stimulate T-cell responses, with CD4 T-cells being important for all of the vaccines and CD8 responses also being expected for OPV and BCG vaccines. Responses to the BCG and TT vaccines were higher than responses to OPV and HBV (Supplemental Fig 9). The OPV responses were low overall but positive ($>$1.0 SI) in 44% (18 of 41) of subjects. Vaccine-specific IgG responses were also assessed for OPV, TT, and HBV, whereas the DTH skin-test response to PPD antigen was used to evaluate the BCG response. The median (interquartile range) OPV-IgG response was 1402 (500) mIU/mL (range: 1105–4759 mIU/mL; $n = 44$). The median TT-IgG response was 198 (422) mIU/mL (range: 7–2540 mIU/mL; $n = 46$). The median HBV-IgG response was very low at 3.7 (0.5) mIU/mL (range: 3.0 – 4.6 mIU/mL; $n = 29$). The median area of induration for the PPD-DTH skin-test response was 0.709 (0.831) cm^2 (range: 0–2.54 cm^2 with 4 “0” values; $n = 47$). Associations of vaccine responses with microbiota abundance assessed by using the 16S rRNA gene sequence data are summarized in Supplemental Figs 10 and 11.

SUPPLEMENTAL REFERENCES

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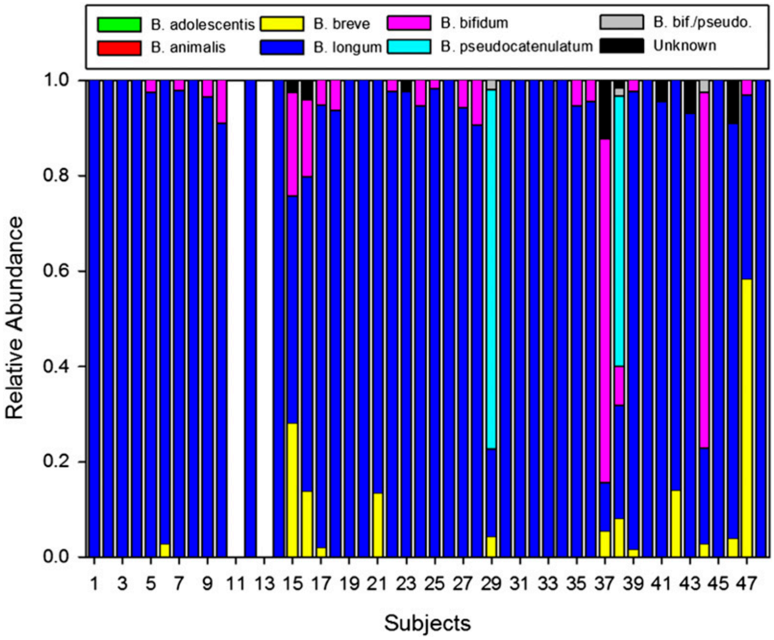
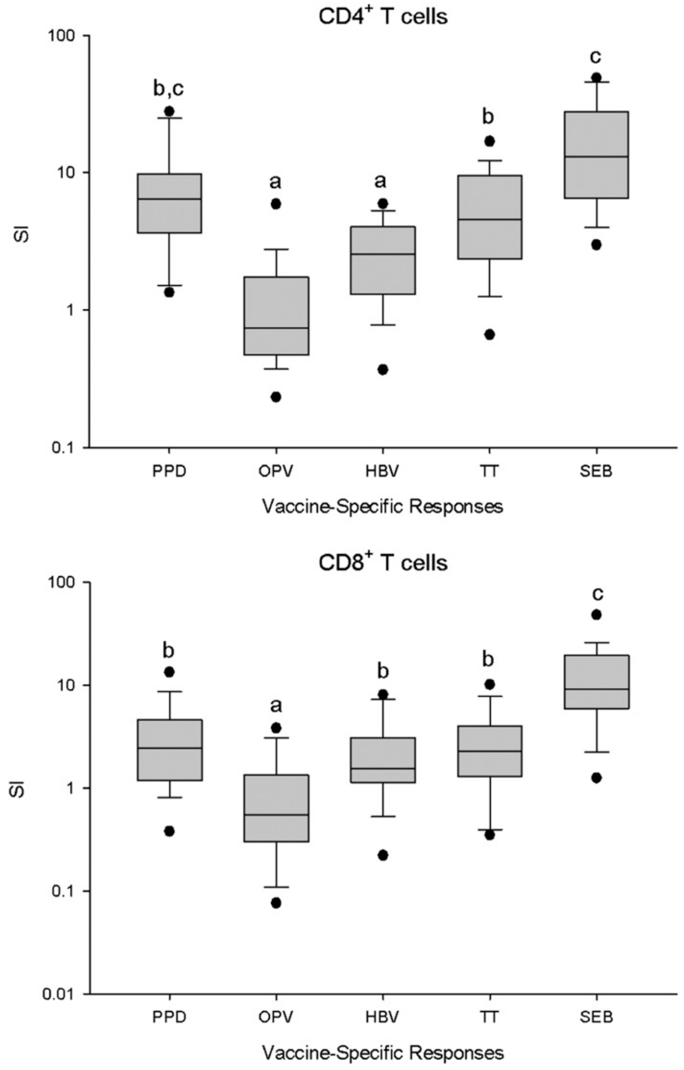


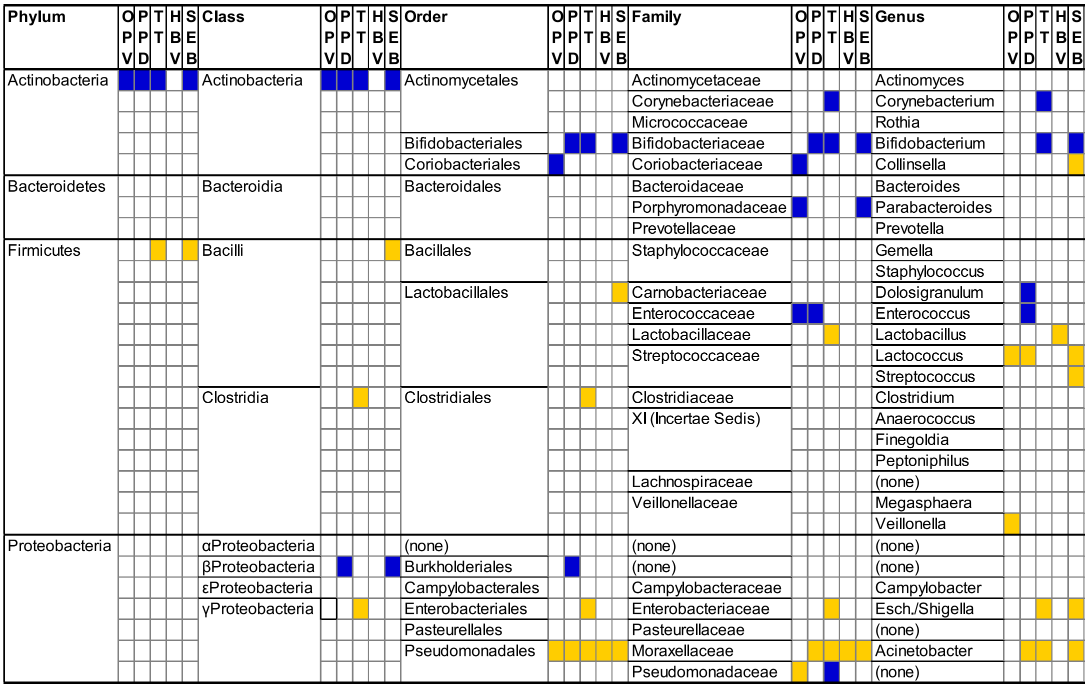
SUPPLEMENTAL FIGURE 8

Relative abundance of different *Bifidobacterium* species at 15 weeks of age in 46 infant stool samples assessed by T-RFLP (*Hae*) analysis. Subject numbers are the same as in Fig 1. No data were available for subjects 11 and 13. No samples were positive for *Bifidobacterium animalis* or *Bifidobacterium adolescentis*.



SUPPLEMENTAL FIGURE 9

SI of peripheral blood CD4$^+$ and CD8$^+$ T cells to vaccine antigens in infants at 15 weeks of age. The SI is shown in box plots (indicating the 5th, 10th, 25th, 50th, 75th, 90th, and 95th percentiles) for the BCG tuberculosis vaccine using PPD antigen to induce proliferation, the OPV vaccine, the HBV vaccine, the TT vaccine, and the positive control for polyclonal T-cell proliferation, SEB. Group responses without the same superscript letter superscript are significantly different ($P < .05$) from one another by using Kruskal-Wallis 1-way ANOVA of ranks and Dunn's method for all pairwise multiple comparisons. One subject (number 47) received antibiotics at 2 weeks of age.



Phylum	OPV	PPD	TT	HBV	SEB	Class	OPV	PPD	TT	HBV	SEB	Order	OPV	PPD	TT	HBV	SEB	Family	OPV	PPD	TT	HBV	SEB	Genus	OPV	PPD	TT	HBV	SEB
Actinobacteria	🟦	🟦	🟦		🟦	Actinobacteria	🟦	🟦	🟦		🟦	Actinomycetales						Actinomycetaceae						Actinomyces					
																		Corynebacteriaceae			🟦			Corynebacterium			🟦		
																		Micrococcaceae						Rothia					
												Bifidobacteriales		🟦	🟦		🟦	Bifidobacteriaceae		🟦	🟦		🟦	Bifidobacterium			🟦		🟦
												Coriobacteriales	🟦					Coriobacteriaceae	🟦					Collinsella					🟨
Bacteroidetes						Bacteroidia						Bacteroidales						Bacteroidaceae						Bacteroides					
																		Porphyromonadaceae	🟦				🟦	Parabacteroides					
																		Prevotellaceae						Prevotella					
Firmicutes			🟨		🟨	Bacilli					🟨	Bacillales						Staphylococcaceae						Gemella					
																								Staphylococcus					
												Lactobacillales					🟨	Carnobacteriaceae						Dolosigranulum		🟦			
																		Enterococcaceae	🟦	🟦				Enterococcus		🟦			
																		Lactobacillaceae			🟨			Lactobacillus				🟨	
																		Streptococcaceae						Lactococcus	🟨	🟨			🟨
																								Streptococcus					🟨
						Clostridia			🟨			Clostridiales			🟨			Clostridiaceae						Clostridium					
																		XI (Incertae Sedis)						Anaerococcus					
																								Finegoldia					
																								Peptoniphilus					
																		Lachnospiraceae						(none)					
																		Veillonellaceae						Megasphaera					
																								Veillonella	🟨				
Proteobacteria						αProteobacteria						(none)						(none)						(none)					
						βProteobacteria		🟦			🟦	Burkholderiales		🟦				(none)						(none)					
						εProteobacteria						Campylobacterales						Campylobacteraceae						Campylobacter					
						γProteobacteria			🟨			Enterobacteriales			🟨			Enterobacteriaceae			🟨			Esch./Shigella			🟨		🟨
												Pasteurellales						Pasteurellaceae						(none)					
												Pseudomonadales	🟨	🟨	🟨	🟨	🟨	Moraxellaceae		🟨	🟨	🟨	🟨	Acinetobacter		🟨	🟨		🟨
																		Pseudomonadaceae	🟨		🟦			(none)					

SUPPLEMENTAL FIGURE 10

Heat map showing positive (dark blue rectangles) and negative (light orange rectangles) associations of microbiota relative abundance (at the phylum, class, order, family, and genus levels) with T-cell proliferation responses (SI) to the indicated vaccines (OPV, PPD to assess response to the BCG vaccine against tuberculosis, TT, HBV, and the polyclonal T-cell stimulant SEB). Significant ($P < .05$) associations were characterized as positive or negative by using Spearman correlation analysis of continuous data (T-cell SI and relative abundance of microbiota) and the Wilcoxon test to compare relative abundance of microbiota in “high” and “low” vaccine responders (those above or below the median T-cell SI response of interest) as described in Methods. Both CD4 and CD8 responses were analyzed for OPV, PPD, and SEB, whereas only CD4 responses were considered for TT and HBV. Median microbiota relative abundance for vaccine high and low responders for CD4 and CD8 are shown in Supplemental Figs 11 and 12. Esch., *Escherichia*.

Taxa	Group	OPV Vaccine			Tuberculosis Vaccine			TT Vaccine			HBV			Positive Control (SEB)		
		Ratio	Median	IQR	Ratio	Median	IQR	Ratio	Median	IQR	Ratio	Median	IQR	Ratio	Median	IQR
Phylum																
Actinobacteria (A)	above	1.18	8.6E-01	1.7E-01	1.19	8.7E-01	1.7E-01	1.25	8.6E-01	1.1E-01	1.07	8.3E-01	3.6E-01	1.18	8.6E-01	1.7E-01
	below		7.3E-01	4.8E-01		7.3E-01	3.4E-01		6.8E-01	3.8E-01		7.8E-01	4.1E-01		7.3E-01	4.5E-01
Bacteroidetes (B)	above	2.65	5.5E-04	6.4E-03	0.16	1.8E-04	4.3E-03	0.11	2.0E-04	8.7E-04	0.26	2.3E-04	3.3E-03	0.63	2.9E-04	8.4E-03
	below		2.1E-04	2.3E-03		1.1E-03	9.2E-03		1.8E-03	9.7E-03		8.9E-04	9.6E-03		4.6E-04	3.9E-03
Firmicutes (F)	above	0.67	8.5E-02	7.4E-02	0.57	8.0E-02	5.8E-02	0.58	8.3E-02	5.2E-02	0.96	9.3E-02	9.3E-02	0.55	7.6E-02	5.7E-02
	below		1.3E-01	1.8E-01		1.4E-01	1.6E-01		1.4E-01	2.6E-01		9.7E-02	1.6E-01		1.4E-01	1.4E-01
Proteobacteria (P)	above	0.47	2.8E-02	1.3E-01	0.37	2.1E-02	1.6E-01	0.30	2.1E-02	9.2E-02	0.55	3.2E-02	1.7E-01	0.37	2.1E-02	1.4E-01
	below		5.8E-02	1.4E-01		5.8E-02	1.2E-01		6.8E-02	1.5E-01		5.8E-02	1.4E-01		5.8E-02	1.3E-01
Class																
A-Actinobacteria	above	1.18	8.6E-01	1.7E-01	1.19	8.7E-01	1.7E-01	1.25	8.6E-01	1.1E-01	1.07	8.3E-01	3.6E-01	1.18	8.6E-01	1.7E-01
	below		7.3E-01	4.8E-01		7.3E-01	3.4E-01		6.8E-01	3.8E-01		7.8E-01	4.1E-01		7.3E-01	4.5E-01
B-Bacteroidia	above	2.65	5.5E-04	6.4E-03	0.15	1.7E-04	4.3E-03	0.10	1.8E-04	8.7E-04	0.26	2.3E-04	3.3E-03	0.62	2.9E-04	8.4E-03
	below		2.1E-04	2.3E-03		1.1E-03	9.2E-03		1.7E-03	9.6E-03		8.9E-04	9.6E-03		4.6E-04	3.9E-03
F-Bacilli	above	0.79	7.0E-02	5.9E-02	0.70	7.6E-02	5.3E-02	0.68	7.7E-02	4.2E-02	0.98	8.0E-02	9.0E-02	0.64	6.9E-02	5.8E-02
	below		8.9E-02	1.4E-01		1.1E-01	1.4E-01		1.1E-01	2.5E-01		8.1E-02	1.3E-01		1.1E-01	1.5E-01
F-Clostridia	above	1.01	3.5E-03	1.1E-02	0.29	1.9E-03	4.8E-03	0.25	1.5E-03	7.7E-03	0.40	2.2E-03	5.4E-03	0.55	2.4E-03	1.2E-02
	below		3.5E-03	1.8E-02		6.6E-03	2.2E-02		6.1E-03	2.1E-02		5.5E-03	2.3E-02		4.4E-03	2.2E-02
P-Alphaproteobacteria	above	-	0.0E+00	1.5E-05	-	0.0E+00	1.4E-05	-	0.0E+00	1.5E-05	-	0.0E+00	1.4E-05	-	0.0E+00	1.4E-05
	below		0.0E+00	1.6E-05		0.0E+00	2.1E-05		0.0E+00	2.1E-05		0.0E+00	2.1E-05		0.0E+00	2.1E-05
P-Betaproteobacteria	above	-	0.0E+00	2.3E-05	-	0.0E+00	4.0E-05	-	0.0E+00	1.4E-05	-	0.0E+00	2.1E-05	-	7.1E-06	2.3E-05
	below		0.0E+00	1.5E-05		0.0E+00	0.0E+00		0.0E+00	1.8E-05		0.0E+00	0.0E+00		0.0E+00	0.0E+00
P-Epsilonproteobacteria	above	-	0.0E+00	4.1E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.9E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.8E-05
	below		0.0E+00	2.6E-05		0.0E+00	3.9E-05		0.0E+00	3.5E-05		0.0E+00	7.6E-05		0.0E+00	3.1E-05
P-Gammaproteobacteria	above	0.47	2.8E-02	1.0E-01	0.27	1.6E-02	1.1E-01	0.24	1.6E-02	6.2E-02	0.47	2.8E-02	1.7E-01	0.37	2.1E-02	6.6E-02
	below		5.8E-02	1.4E-01		5.8E-02	1.2E-01		6.7E-02	1.5E-01		5.8E-02	1.2E-01		5.8E-02	1.4E-01
Order																
A-Actinomycetales	above	0.47	1.5E-03	3.7E-03	1.02	1.8E-03	3.4E-03	1.80	2.7E-03	3.4E-03	0.62	1.6E-03	3.4E-03	1.60	2.7E-03	3.0E-03
	below		3.3E-03	3.5E-03		1.8E-03	3.8E-03		1.5E-03	3.7E-03		2.6E-03	4.1E-03		1.7E-03	3.9E-03
A-Bifidobacteriales	above	1.17	8.4E-01	1.7E-01	1.18	8.5E-01	1.6E-01	1.25	8.5E-01	1.4E-01	1.08	8.2E-01	3.4E-01	1.18	8.5E-01	1.8E-01
	below		7.2E-01	4.7E-01		7.2E-01	4.2E-01		6.8E-01	4.3E-01		7.6E-01	4.1E-01		7.2E-01	4.4E-01
A-Coriobacteriales	above	-	1.8E-04	1.8E-02	3.23	5.4E-05	3.7E-04	0.81	3.2E-05	1.8E-04	11.02	9.3E-05	7.3E-03	0.14	8.4E-06	3.7E-04
	below		0.0E+00	6.2E-05		1.7E-05	5.2E-03		4.0E-05	4.6E-03		8.4E-06	3.0E-03		6.2E-05	5.2E-03
B-Bacteroidales	above	2.65	5.5E-04	6.4E-03	0.15	1.7E-04	4.3E-03	0.10	1.8E-04	8.7E-04	0.26	2.3E-04	3.3E-03	0.62	2.9E-04	8.4E-03
	below		2.1E-04	2.3E-03		1.1E-03	9.2E-03		1.7E-03	9.6E-03		8.9E-04	9.6E-03		4.6E-04	3.9E-03
F-Bacillales	above	1.15	5.4E-04	1.1E-03	1.07	5.2E-04	1.0E-03	1.61	6.4E-04	8.3E-04	1.31	5.8E-04	1.1E-03	0.86	4.2E-04	6.4E-04
	below		4.7E-04	6.6E-04		4.9E-04	6.9E-04		4.0E-04	1.2E-03		4.4E-04	6.4E-04		4.9E-04	1.2E-03

SUPPLEMENTAL FIGURE 11

Relative abundance of stool bacteria in infants above and below median vaccine responses (CD4 T-cell SI). Positive and negative associations are highlighted in blue and orange, respectively; statistical analysis is described in the legend to Supplemental Figure 10. Esch., *Escherichia*; IQR, interquartile range.

F-Lactobacillales	above	0.77	6.6E-02	5.6E-02	0.70	7.4E-02	5.0E-02	0.73	7.5E-02	4.1E-02	0.99	7.8E-02	8.6E-02	0.63	6.6E-02	5.6E-02
	below		8.6E-02	1.4E-01		1.0E-01	1.4E-01		1.0E-01	2.5E-01		7.9E-02	1.3E-01		1.0E-01	1.6E-01
F-Clostridiales	above	1.01	3.5E-03	1.1E-02	0.29	1.9E-03	4.8E-03	0.25	1.5E-03	7.7E-03	0.40	2.2E-03	5.4E-03	0.55	2.4E-03	1.2E-02
	below		3.5E-03	1.7E-02		6.6E-03	2.2E-02		6.1E-03	2.1E-02		5.5E-03	2.3E-02		4.4E-03	2.2E-02
P-Burkholderiales	above	-	0.0E+00	2.3E-05	-	0.0E+00	4.0E-05	-	0.0E+00	1.4E-05	-	0.0E+00	1.9E-05	-	0.0E+00	2.3E-05
	below		0.0E+00	0.0E+00		0.0E+00	0.0E+00		0.0E+00	8.4E-06		0.0E+00	0.0E+00		0.0E+00	0.0E+00
P-Campylobacterales	above	-	0.0E+00	4.1E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.9E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.8E-05
	below		0.0E+00	2.6E-05		0.0E+00	3.9E-05		0.0E+00	3.5E-05		0.0E+00	7.6E-05		0.0E+00	3.1E-05
P-Enterobacteriales	above	0.47	2.6E-02	9.5E-02	0.27	1.5E-02	1.0E-01	0.24	1.5E-02	5.9E-02	0.47	2.6E-02	1.6E-01	0.36	2.0E-02	6.2E-02
	below		5.6E-02	1.3E-01		5.6E-02	1.1E-01		6.2E-02	1.4E-01		5.6E-02	1.1E-01		5.6E-02	1.4E-01
P-Pasteurellales	above	-	0.0E+00	0.0E+00	-	0.0E+00	2.7E-05	-	0.0E+00	3.6E-05	-	0.0E+00	0.0E+00	-	0.0E+00	3.6E-05
	below		0.0E+00	2.2E-05		0.0E+00	0.0E+00		0.0E+00	0.0E+00		0.0E+00	6.2E-05		0.0E+00	0.0E+00
P-Pseudomonadales	above	0.43	4.4E-05	5.8E-05	0.59	4.8E-05	7.2E-05	0.40	4.9E-05	4.2E-05	0.46	4.5E-05	4.8E-05	0.45	4.6E-05	3.4E-05
	below		1.0E-04	2.1E-04		8.1E-05	2.2E-04		1.2E-04	4.0E-04		9.7E-05	2.7E-04		1.0E-04	2.2E-04
Family																
A-Actinomycetaceae	above	-	0.0E+00	6.0E-05	-	0.0E+00	6.0E-05	0.00	0.0E+00	6.7E-05	-	0.0E+00	4.8E-05	-	0.0E+00	1.1E-04
	below		0.0E+00	5.4E-05		0.0E+00	5.4E-05		7.0E-06	6.1E-05		0.0E+00	9.2E-05		0.0E+00	4.2E-05
A-Corynebacteriaceae	above	1.75	9.6E-05	1.4E-04	1.96	1.1E-04	1.4E-04	2.07	9.6E-05	1.3E-04	1.65	8.2E-05	1.2E-04	1.42	9.6E-05	1.4E-04
	below		5.5E-05	1.1E-04		5.5E-05	1.1E-04		4.6E-05	1.1E-04		5.0E-05	1.1E-04		6.7E-05	1.1E-04
A-Micrococcaceae	above	0.55	1.0E-03	1.8E-03	1.01	1.0E-03	2.5E-03	1.34	1.4E-03	2.3E-03	0.82	1.0E-03	2.4E-03	1.44	1.4E-03	2.0E-03
	below		1.8E-03	2.2E-03		1.0E-03	2.2E-03		1.0E-03	2.4E-03		1.3E-03	2.3E-03		9.5E-04	2.4E-03
A-Bifidobacteriadeae	above	1.17	8.4E-01	1.7E-01	1.18	8.5E-01	1.6E-01	1.25	8.5E-01	1.4E-01	1.08	8.2E-01	3.4E-01	1.18	8.5E-01	1.8E-01
	below		7.2E-01	4.7E-01		7.2E-01	4.2E-01		6.8E-01	4.3E-01		7.6E-01	4.1E-01		7.2E-01	4.4E-01
A-Coriobacteriaceae	above	-	1.8E-04	1.8E-02	3.22	5.4E-05	3.7E-04	0.81	3.2E-05	1.8E-04	10.99	9.3E-05	7.3E-03	0.14	8.5E-06	3.7E-04
	below		0.0E+00	6.2E-05		1.7E-05	5.2E-03		4.0E-05	4.6E-03		8.5E-06	3.0E-03		6.2E-05	5.2E-03
B-Bacteroidaceae	above	0.73	6.0E-05	2.8E-03	0.27	3.0E-05	6.2E-04	0.73	5.7E-05	7.3E-04	0.21	3.8E-05	5.3E-04	0.34	2.8E-05	2.8E-03
	below		8.1E-05	8.3E-04		1.1E-04	1.5E-03		7.8E-05	2.2E-03		1.8E-04	2.2E-03		8.2E-05	6.3E-04
B-Porphyromonedaceae	above	0.00	0.0E+00	1.9E-04	0.00	0.0E+00	6.3E-05	-	8.3E-06	6.5E-05	0.00	0.0E+00	4.9E-05	-	1.0E-05	1.9E-04
	below		1.4E-05	3.8E-05		1.4E-05	5.6E-05		0.0E+00	4.7E-05		1.5E-05	7.8E-05		0.0E+00	3.8E-05
B-Prevotellaceae	above	-	0.0E+00	4.4E-05	-	0.0E+00	0.0E+00	-	0.0E+00	0.0E+00	-	0.0E+00	2.4E-05	-	0.0E+00	3.8E-05
	below		0.0E+00	1.3E-05		0.0E+00	3.6E-05		0.0E+00	8.3E-05		0.0E+00	2.5E-05		0.0E+00	0.0E+00
F-Staphylococcaceae	above	1.23	4.4E-04	6.7E-04	1.04	4.2E-04	5.9E-04	1.70	5.4E-04	5.3E-04	1.37	4.6E-04	5.7E-04	0.71	3.3E-04	5.0E-04
	below		3.6E-04	5.4E-04		4.0E-04	6.9E-04		3.1E-04	1.0E-03		3.4E-04	6.6E-04		4.7E-04	9.7E-04
F-Camobacteriaceae	above	3.01	7.1E-05	1.2E-04	3.25	7.6E-05	1.3E-04	3.45	7.9E-05	1.5E-04	4.17	9.0E-05	1.5E-04	3.01	7.1E-05	1.3E-04
	below		2.3E-05	7.7E-05		2.3E-05	7.7E-05		2.3E-05	7.2E-05		2.2E-05	7.1E-05		2.3E-05	7.7E-05
F-Enterococcaceae	above	1.58	4.4E-04	2.6E-03	1.90	4.4E-04	2.2E-03	0.87	2.9E-04	2.3E-03	0.97	3.0E-04	2.6E-03	6.21	1.0E-03	2.6E-03
	below		2.8E-04	1.4E-03		2.3E-04	2.0E-03		3.3E-04	1.7E-03		3.1E-04	1.7E-03		1.6E-04	7.4E-04
F-Lactobacillaceae	above	0.88	1.4E-04	2.1E-03	0.28	6.3E-05	8.0E-04	0.06	6.3E-05	4.5E-04	0.05	6.3E-05	1.5E-04	0.12	5.3E-05	6.1E-04
	below		1.6E-04	4.7E-03		2.2E-04	5.2E-03		1.0E-03	6.7E-03		1.4E-03	5.1E-03		4.3E-04	5.1E-03
F-Streptococcaceae	above	0.78	3.9E-02	4.2E-02	0.89	4.1E-02	4.7E-02	0.95	4.4E-02	3.3E-02	1.00	4.4E-02	4.8E-02	0.80	4.0E-02	4.6E-02
	below		5.0E-02	9.2E-02		4.6E-02	9.0E-02		4.6E-02	1.3E-01		4.4E-02	7.6E-02		5.0E-02	6.9E-02

SUPPLEMENTAL FIGURE 11
Continued.

F-Clostridiaceae	above	0.36	1.8E-05	3.8E-04	0.22	1.6E-05	3.8E-04	0.20	2.6E-05	2.9E-04	1.47	5.1E-05	5.8E-04	0.14	1.0E-05	2.9E-04
	below		4.9E-05	4.7E-04		7.0E-05	4.7E-04		1.3E-04	1.3E-03		3.5E-05	3.4E-04		7.0E-05	4.7E-04
F-XI (Incertae Sedis)	above	5.37	7.8E-05	1.3E-04	0.48	3.0E-05	1.0E-04	0.20	1.8E-05	7.6E-05	1.25	3.8E-05	9.8E-05	1.00	3.8E-05	1.7E-04
	below		1.5E-05	1.8E-04		6.3E-05	2.0E-04		9.0E-05	2.1E-04		3.0E-05	2.1E-04		3.8E-05	1.0E-04
Lachnospiraceae	above	-	0.0E+00	5.7E-05	-	0.0E+00	1.8E-05	-	6.4E-06	2.1E-05	-	0.0E+00	2.4E-05	-	0.0E+00	6.2E-05
	below		0.0E+00	2.1E-05		0.0E+00	1.3E-04		0.0E+00	7.8E-05		0.0E+00	2.1E-05		0.0E+00	2.1E-05
F-Veillonellaceae	above	0.13	2.2E-04	1.1E-03	1.43	8.4E-04	1.8E-03	0.25	3.7E-04	1.6E-03	0.16	2.6E-04	1.5E-03	1.44	8.5E-04	4.2E-03
	below		1.7E-03	6.0E-03		5.9E-04	6.3E-03		1.5E-03	6.3E-03		1.6E-03	8.2E-03		5.9E-04	1.9E-03
P-Campylobacteraceae	above	-	0.0E+00	4.1E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.9E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.8E-05
	below		0.0E+00	2.6E-05		0.0E+00	3.9E-05		0.0E+00	3.5E-05		0.0E+00	7.6E-05		0.0E+00	3.1E-05
P-Enterobacteriaceae	above	0.47	2.6E-02	9.5E-02	0.27	1.5E-02	1.0E-01	0.24	1.5E-02	5.9E-02	0.47	2.6E-02	1.6E-01	0.36	2.0E-02	6.2E-02
	below		5.6E-02	1.3E-01		5.6E-02	1.1E-01		6.2E-02	1.4E-01		5.6E-02	1.1E-01		5.6E-02	1.4E-01
P-Pasteurellaceae	above	-	0.0E+00	0.0E+00	-	0.0E+00	2.7E-05	-	0.0E+00	3.6E-05	-	0.0E+00	0.0E+00	-	0.0E+00	3.6E-05
	below		0.0E+00	2.2E-05		0.0E+00	0.0E+00		0.0E+00	0.0E+00		0.0E+00	6.2E-05		0.0E+00	0.0E+00
P-Moraxellaceae	above	0.45	3.2E-05	4.8E-05	0.41	3.0E-05	4.4E-05	0.24	2.9E-05	3.1E-05	0.44	3.4E-05	4.1E-05	0.36	3.0E-05	3.1E-05
	below		7.2E-05	2.3E-04		7.2E-05	2.3E-04		1.2E-04	4.0E-04		7.8E-05	3.0E-04		8.3E-05	2.2E-04
P-Pseudomonadaceae	above	0.00	0.0E+00	1.5E-05	-	1.4E-05	2.2E-05	-	1.5E-05	3.0E-05	0.00	0.0E+00	1.5E-05	-	1.4E-05	2.1E-05
	below		1.4E-05	3.1E-05		0.0E+00	2.0E-05		0.0E+00	7.0E-06		7.0E-06	3.1E-05		0.0E+00	2.1E-05
Genus																
A-Actinomyces	above	-	0.0E+00	4.5E-05	-	0.0E+00	3.4E-05	-	0.0E+00	3.0E-05	-	0.0E+00	3.4E-05	-	0.0E+00	1.0E-04
	below		0.0E+00	3.7E-05		0.0E+00	3.7E-05		0.0E+00	5.3E-05		0.0E+00	8.2E-05		0.0E+00	3.0E-05
A-Corynebacterium	above	1.75	9.6E-05	1.5E-04	1.95	1.1E-04	1.4E-04	2.07	9.6E-05	1.4E-04	1.65	8.2E-05	1.2E-04	1.42	9.6E-05	1.4E-04
	below		5.5E-05	1.1E-04		5.5E-05	1.1E-04		4.6E-05	1.1E-04		5.0E-05	1.1E-04		6.7E-05	1.1E-04
A-Rothia	above	0.53	9.3E-04	1.7E-03	0.98	1.0E-03	2.3E-03	1.27	1.3E-03	2.2E-03	0.78	9.4E-04	2.2E-03	1.40	1.3E-03	1.9E-03
	below		1.7E-03	2.2E-03		1.0E-03	2.2E-03		1.0E-03	2.4E-03		1.2E-03	2.3E-03		9.2E-04	2.4E-03
A-Bifidobacterium	above	1.14	7.1E-01	1.2E-01	1.16	7.2E-01	1.3E-01	1.22	7.2E-01	9.5E-02	1.07	7.0E-01	2.9E-01	1.14	7.1E-01	1.2E-01
	below		6.2E-01	3.9E-01		6.2E-01	3.5E-01		5.9E-01	3.5E-01		6.5E-01	3.3E-01		6.2E-01	3.9E-01
A-Collinsella	above		3.0E-05	2.5E-03	1.24	2.1E-05	7.6E-05	0.19	7.7E-06	3.5E-05	3.31	2.8E-05	6.0E-04	0.00	0.0E+00	2.8E-05
	below		0.0E+00	3.8E-05		1.7E-05	2.5E-03		4.0E-05	3.0E-03		8.4E-06	2.2E-03		3.8E-05	3.4E-03
B-Bacteroides	above	0.73	6.0E-05	2.8E-03	0.27	3.0E-05	6.2E-04	0.73	5.7E-05	7.3E-04	0.21	3.8E-05	5.3E-04	0.34	2.8E-05	2.8E-03
	below		8.1E-05	8.3E-04		1.1E-04	1.5E-03		7.8E-05	2.2E-03		1.8E-04	2.2E-03		8.2E-05	6.3E-04
B-Parabacteroides	above	-	0.0E+00	1.8E-04	-	0.0E+00	6.3E-05	-	0.0E+00	6.5E-05	-	0.0E+00	4.9E-05	-	0.0E+00	1.8E-04
	below		0.0E+00	3.8E-05		0.0E+00	4.4E-05		0.0E+00	3.2E-05		0.0E+00	4.1E-05		0.0E+00	1.9E-05
B-Prevotella	above	-	0.0E+00	4.4E-05	-	0.0E+00	0.0E+00	-	0.0E+00	0.0E+00	-	0.0E+00	9.4E-06	-	0.0E+00	2.8E-05
	below		0.0E+00	1.3E-05		0.0E+00	3.6E-05		0.0E+00	3.8E-05		0.0E+00	2.5E-05		0.0E+00	0.0E+00
F-Gemella	above	0.28	6.6E-06	6.0E-05	0.66	1.5E-05	6.9E-05	0.29	6.6E-06	6.3E-05	0.95	2.0E-05	8.4E-05	0.63	1.5E-05	8.3E-05
	below		2.3E-05	6.2E-05		2.2E-05	7.5E-05		2.3E-05	1.0E-04		2.1E-05	6.9E-05		2.3E-05	7.5E-05
F-Staphylococcus	above	0.61	1.5E-04	4.4E-04	1.57	2.0E-04	4.8E-04	1.89	2.4E-04	4.6E-04	1.07	2.0E-04	5.8E-04	0.48	1.5E-04	2.4E-04
	below		2.5E-04	5.4E-04		1.3E-04	5.4E-04		1.2E-04	9.9E-04		1.9E-04	5.1E-04		3.1E-04	6.5E-04
F-Dolosigranulum	above	-	1.7E-05	5.5E-05	-	3.2E-05	7.0E-05	-	2.5E-05	7.0E-05	1.82	1.5E-05	6.2E-05	-	2.0E-05	6.2E-05
	below		0.0E+00	2.9E-05		0.0E+00	2.0E-05		0.0E+00	2.1E-05		8.2E-06	2.4E-05		0.0E+00	2.6E-05

SUPPLEMENTAL FIGURE 11

Continued.

F-Enterococcus	above	0.84	4.3E-05	1.5E-04	3.10	6.5E-05	1.8E-04	0.34	2.9E-05	1.3E-04	7.40	6.1E-05	3.7E-04	4.24	7.0E-05	4.0E-04
	below		5.1E-05	6.2E-04		2.1E-05	6.2E-04		8.5E-05	6.6E-04		8.2E-06	5.6E-04		1.6E-05	5.1E-04
F-Lactobacillus	above	0.35	3.3E-05	3.8E-04	0.53	3.0E-05	3.8E-04	0.17	1.8E-05	1.3E-04	0.01	7.3E-06	7.4E-05	0.06	7.3E-06	1.2E-04
	below		9.3E-05	1.2E-03		5.6E-05	1.1E-03		1.0E-04	1.5E-03		6.4E-04	1.9E-03		1.2E-04	1.2E-03
F-Lactococcus	above	0.66	1.4E-04	8.6E-05	0.75	1.6E-04	9.2E-05	0.78	1.7E-04	7.4E-05	0.90	1.7E-04	9.1E-05	0.74	1.6E-04	9.4E-05
	below		2.2E-04	2.1E-04		2.1E-04	1.8E-04		2.2E-04	2.2E-04		1.9E-04	2.1E-04		2.1E-04	1.5E-04
F-Streptococcus	above	0.82	3.6E-02	4.0E-02	0.98	3.7E-02	4.4E-02	0.89	3.8E-02	3.9E-02	1.08	4.1E-02	4.6E-02	0.53	2.5E-02	3.8E-02
	below		4.4E-02	6.1E-02		3.8E-02	6.0E-02		4.2E-02	1.2E-01		3.8E-02	4.8E-02		4.7E-02	5.4E-02
F-Clostridium	above	0.00	0.0E+00	1.4E-04	-	0.0E+00	1.8E-04	-	7.7E-06	2.0E-04	-	7.5E-06	2.0E-04	0.00	0.0E+00	8.5E-05
	below		1.5E-05	5.5E-05		0.0E+00	5.5E-05		0.0E+00	4.8E-05		0.0E+00	4.8E-05		1.5E-05	1.7E-04
F-Anaerococcus	above	-	3.0E-05	8.2E-05	0.39	7.1E-06	4.6E-05	0.00	0.0E+00	4.4E-05	-	1.4E-05	4.6E-05	-	1.6E-05	8.2E-05
	below		0.0E+00	4.4E-05		1.8E-05	7.0E-05		1.8E-05	7.9E-05		0.0E+00	7.9E-05		0.0E+00	6.0E-05
F-Finegoldia	above	-	1.5E-05	5.2E-05	-	0.0E+00	1.5E-05	-	0.0E+00	1.5E-05	-	0.0E+00	1.9E-05	-	7.3E-06	3.9E-05
	below		0.0E+00	1.5E-05		0.0E+00	2.2E-05		0.0E+00	3.6E-05		0.0E+00	2.5E-05		0.0E+00	2.1E-05
F-Peptoniphilus	above	-	2.2E-05	6.0E-05	-	1.0E-05	4.0E-05	0.00	0.0E+00	3.0E-05	-	0.0E+00	4.7E-05	-	2.0E-05	6.5E-05
	below		0.0E+00	7.7E-05		0.0E+00	8.1E-05		2.1E-05	8.7E-05		0.0E+00	8.2E-05		0.0E+00	7.2E-05
F-Megasphera	above	-	0.0E+00	2.9E-05	-	0.0E+00	2.5E-05	-	0.0E+00	6.6E-06	-	0.0E+00	1.7E-05	-	0.0E+00	4.6E-04
	below		0.0E+00	0.0E+00		0.0E+00	2.1E-05		0.0E+00	1.5E-03		0.0E+00	1.5E-03		0.0E+00	2.1E-05
F-Veillonella	above	0.21	5.5E-05	1.6E-04	0.44	5.9E-05	3.8E-04	0.39	5.2E-05	6.5E-04	0.29	5.5E-05	4.0E-04	0.44	5.9E-05	3.8E-04
	below		2.6E-04	8.9E-04		1.3E-04	8.9E-04		1.3E-04	5.7E-04		1.9E-04	1.0E-03		1.4E-04	7.4E-04
P-Campylobacter	above	-	0.0E+00	4.1E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.9E-05	-	0.0E+00	2.4E-05	-	0.0E+00	2.8E-05
	below		0.0E+00	2.6E-05		0.0E+00	3.9E-05		0.0E+00	3.5E-05		0.0E+00	7.6E-05		0.0E+00	3.1E-05
P-Esch./Shigella	above	0.62	1.3E-02	3.9E-02	0.29	7.3E-03	3.8E-02	0.18	6.3E-03	2.5E-02	0.41	1.1E-02	4.1E-02	0.45	9.5E-03	3.8E-02
	below		2.1E-02	4.0E-02		2.5E-02	3.4E-02		3.5E-02	4.4E-02		2.7E-02	4.5E-02		2.1E-02	5.2E-02
P-Acinetobacter	above	0.73	3.2E-05	3.8E-05	0.49	3.0E-05	3.2E-05	0.26	2.9E-05	3.1E-05	0.56	3.4E-05	3.0E-05	0.48	3.0E-05	3.1E-05
	below		4.4E-05	2.1E-04		6.1E-05	2.3E-04		1.1E-04	4.0E-04		6.2E-05	2.8E-04		6.2E-05	2.4E-04

SUPPLEMENTAL FIGURE 11
Continued.

	Group	OPV Vaccine			Tuberculosis Vaccine			Positive Control (SEB)		
		Ratio	Median	IQR	Ratio	Median	IQR	Ratio	Median	IQR
Phylum										
Actinobacteria (A)	above	1.08	8.50E-01	1.88E-01	1.06	8.29E-01	1.77E-01	1.09	8.38E-01	2.77E-01
	below		7.84E-01	4.97E-01		7.84E-01	4.15E-01		7.67E-01	4.12E-01
Bacteroidetes (B)	above	1.49	3.93E-04	6.30E-03	4.15	5.46E-04	1.72E-02	0.47	2.93E-04	4.95E-03
	below		2.63E-04	2.64E-03		1.32E-04	2.37E-03		6.28E-04	5.95E-03
Firmicutes (F)	above	0.94	8.86E-02	1.04E-01	0.97	8.94E-02	1.07E-01	0.97	8.94E-02	9.15E-02
	below		9.38E-02	1.36E-01		9.21E-02	1.53E-01		9.21E-02	1.32E-01
Proteobacteria (P)	above	0.44	2.61E-02	9.57E-02	0.81	4.01E-02	1.46E-01	0.36	2.08E-02	1.41E-01
	below		5.93E-02	1.40E-01		4.92E-02	1.36E-01		5.80E-02	1.24E-01
Class										
A-Actinobacteria	above	1.08	8.50E-01	1.88E-01	1.06	8.29E-01	1.77E-01	1.09	8.38E-01	2.77E-01
	below		7.84E-01	4.97E-01		7.84E-01	4.15E-01		7.67E-01	4.12E-01
B-Bacteroidia	above	1.58	3.93E-04	6.32E-03	4.74	5.46E-04	1.72E-02	0.45	2.86E-04	4.95E-03
	below		2.49E-04	2.64E-03		1.15E-04	2.29E-03		6.28E-04	5.95E-03
F-Bacilli	above	1.03	7.96E-02	1.04E-01	1.04	8.08E-02	1.11E-01	1.12	8.33E-02	8.76E-02
	below		7.75E-02	1.42E-01		7.75E-02	1.13E-01		7.44E-02	1.45E-01
F-Clostridia	above	0.57	2.40E-03	1.72E-02	0.53	3.18E-03	1.20E-02	1.48	4.23E-03	1.82E-02
	below		4.23E-03	1.15E-02		6.04E-03	2.24E-02		2.85E-03	6.80E-03
P-Alphaproteobacteria	above	0.00	0.00E+00	0.00E+00	-	0.00E+00	1.82E-05	-	0.00E+00	1.56E-05
	below		1.27E-05	2.03E-05		0.00E+00	1.27E-05		0.00E+00	1.57E-05
P-Betaproteobacteria	above	-	0.00E+00	3.98E-05	-	7.10E-06	5.85E-05	-	0.00E+00	2.29E-05
	below		0.00E+00	1.42E-05		0.00E+00	0.00E+00		0.00E+00	1.42E-05
P-Epsilonproteobacteria	above	-	0.00E+00	3.51E-05	-	0.00E+00	3.66E-05	-	7.34E-06	4.08E-05
	below		0.00E+00	1.47E-05		0.00E+00	2.57E-05		0.00E+00	1.27E-05
P-Gammaproteobacteria	above	0.44	2.60E-02	9.54E-02	0.50	2.44E-02	1.01E-01	0.27	1.59E-02	6.42E-02
	below		5.93E-02	1.42E-01		4.92E-02	1.35E-01		5.78E-02	1.24E-01
Order										
A-Actinomycetales	above	0.43	1.59E-03	2.66E-03	1.76	2.67E-03	3.06E-03	1.69	2.67E-03	3.99E-03
	below		3.68E-03	4.50E-03		1.51E-03	4.81E-03		1.58E-03	3.23E-03
A-Bifidobacteriales	above	1.12	8.40E-01	1.69E-01	1.07	8.20E-01	1.51E-01	1.09	8.32E-01	2.71E-01
	below		7.52E-01	4.92E-01		7.66E-01	5.11E-01		7.66E-01	4.02E-01
A-Coriobacteriales	above	5.77	1.04E-04	2.27E-02	3.23	5.45E-05	2.49E-03	0.55	2.36E-05	3.69E-04
	below		1.81E-05	1.35E-04		1.69E-05	2.18E-03		4.26E-05	3.91E-03
B-Bacteroidales	above	1.58	3.93E-04	6.32E-03	4.74	5.46E-04	1.72E-02	0.45	2.86E-04	4.95E-03
	below		2.49E-04	2.64E-03		1.15E-04	2.29E-03		6.28E-04	5.95E-03
F-Bacillales	above	0.50	3.55E-04	7.30E-04	0.58	4.08E-04	7.76E-04	1.15	5.40E-04	7.76E-04
	below		7.08E-04	8.34E-04		7.08E-04	8.87E-04		4.68E-04	1.00E-03

SUPPLEMENTAL FIGURE 12

Relative abundance of stool bacteria in infants above and below median vaccine responses (CD8 T-cell SI). Positive and negative associations are highlighted in blue and orange, respectively; statistical analysis is described in the legend to Supplemental Figure 10. Esch., *Escherichia*; IQR, interquartile range.

F-Lactobacillales	above	1.04	7.80E-02	9.31E-02	1.06	7.91E-02	1.01E-01	1.13	8.17E-02	7.72E-02
	below		7.48E-02	1.41E-01		7.48E-02	1.12E-01		7.24E-02	1.43E-01
F-Clostridiales	above	0.57	2.40E-03	1.72E-02	0.53	3.18E-03	1.20E-02	1.48	4.23E-03	1.82E-02
	below		4.23E-03	1.15E-02		6.04E-03	2.24E-02		2.85E-03	6.75E-03
P-Burkholderiales	above	-	0.00E+00	3.98E-05	89[a]	0.00E+00	5.85E-05	-	0.00E+00	2.29E-05
	below		0.00E+00	1.42E-05		0.00E+00	0.00E+00		0.00E+00	0.00E+00
P-Campylobacterales	above	-	0.00E+00	3.51E-05	-	0.00E+00	3.66E-05	-	7.34E-06	4.08E-05
	below		0.00E+00	1.47E-05		0.00E+00	2.57E-05		0.00E+00	1.27E-05
P-Enterobacteriales	above	0.44	2.50E-02	8.94E-02	0.50	2.35E-02	9.68E-02	0.27	1.52E-02	6.15E-02
	below		5.64E-02	1.36E-01		4.73E-02	1.27E-01		5.64E-02	1.19E-01
P-Pasteurellales	above	-	0.00E+00	0.00E+00	-	0.00E+00	2.15E-05	-	0.00E+00	3.15E-05
	below		0.00E+00	3.15E-05		0.00E+00	0.00E+00		0.00E+00	0.00E+00
P-Pseudomonadales	above	0.65	4.68E-05	1.01E-04	0.71	5.16E-05	7.88E-05	0.54	4.90E-05	4.49E-05
	below		7.23E-05	2.11E-04		7.23E-05	2.22E-04		9.02E-05	3.33E-04
Family										
A-Actinomycetaceae	above	-	0.00E+00	3.98E-05	-	6.95E-06	9.98E-05	-	0.00E+00	6.78E-05
	below		0.00E+00	8.13E-05		0.00E+00	5.42E-05		0.00E+00	3.74E-05
A-Corynebacteriaceae	above	0.92	7.14E-05	9.62E-05	1.20	8.02E-05	1.02E-04	1.42	8.47E-05	1.18E-04
	below		7.75E-05	1.27E-04		6.71E-05	1.44E-04		5.98E-05	1.17E-04
A-Micrococcaceae	above	0.38	1.01E-03	1.09E-03	1.39	1.37E-03	2.06E-03	1.39	1.37E-03	2.10E-03
	below		2.63E-03	3.39E-03		9.88E-04	3.02E-03		9.88E-04	2.41E-03
A-Bifidobacteriaceae	above	1.12	8.40E-01	1.69E-01	1.07	8.20E-01	1.51E-01	1.09	8.32E-01	2.71E-01
	below		7.52E-01	4.92E-01		7.66E-01	5.11E-01		7.66E-01	4.02E-01
A-Coriobacteriaceae	above	5.76	1.04E-04	2.27E-02	3.22	5.45E-05	2.49E-03	0.55	2.36E-05	3.69E-04
	below		1.81E-05	1.35E-04		1.69E-05	2.18E-03		4.26E-05	3.91E-03
B-Bacteroidaceae	above	0.84	6.83E-05	9.69E-04	4.48	1.29E-04	3.92E-03	0.96	7.21E-05	9.89E-04
	below		8.14E-05	1.17E-03		2.88E-05	8.27E-04		7.48E-05	1.52E-03
B-Porphyromonedaceae	above	-	2.87E-05	2.20E-04	-	1.74E-05	7.20E-05	-	2.87E-05	2.70E-04
	below		0.00E+00	2.05E-05		0.00E+00	3.80E-05		0.00E+00	2.05E-05
B-Prevotellaceae	above	-	0.00E+00	4.41E-05	-	0.00E+00	1.82E-05	-	0.00E+00	7.25E-06
	below		0.00E+00	1.27E-05		0.00E+00	1.45E-05		0.00E+00	3.64E-05
F-Staphylococcaceae	above	0.32	2.02E-04	4.13E-04	0.70	3.33E-04	5.30E-04	1.55	4.98E-04	5.74E-04
	below		6.39E-04	5.91E-04		4.79E-04	6.90E-04		3.21E-04	5.45E-04
F-Camobacteriaceae	above	0.57	3.82E-05	7.43E-05	2.08	6.03E-05	1.60E-04	1.14	6.20E-05	9.73E-05
	below		6.68E-05	1.57E-04		2.90E-05	8.13E-05		5.42E-05	9.35E-05
F-Enterococcaceae	above	7.40	6.62E-04	2.32E-03	12.11	1.45E-03	4.83E-03	2.32	5.37E-04	2.29E-03
	below		8.94E-05	1.44E-03		1.20E-04	4.90E-04		2.31E-04	7.27E-04
F-Lactobacillaceae	above	1.66	1.69E-04	7.89E-04	0.22	9.32E-05	8.00E-04	0.89	1.46E-04	2.08E-03
	below		1.02E-04	4.75E-03		4.28E-04	4.33E-03		1.64E-04	4.34E-03
F-Streptococcaceae	above	0.86	4.08E-02	4.68E-02	0.86	4.03E-02	4.90E-02	1.09	4.43E-02	3.51E-02
	below		4.77E-02	9.22E-02		4.69E-02	1.04E-01		4.08E-02	9.28E-02

SUPPLEMENTAL FIGURE 12
Continued.

F-Clostridiaceae	above	0.15	7.50E-06	8.07E-04	0.32	1.55E-05	5.78E-04	0.14	1.02E-05	5.47E-04
	below		4.88E-05	4.08E-04		4.88E-05	3.45E-04		7.03E-05	4.08E-04
F-XI (Incertae Sedis)	above	5.30	7.69E-05	1.94E-04	1.70	5.36E-05	1.67E-04	1.70	5.36E-05	2.30E-04
	below		1.45E-05	8.91E-05		3.15E-05	1.38E-04		3.15E-05	1.05E-04
F-Lachnospiraceae	above	-	7.50E-06	6.13E-04	-	0.00E+00	5.67E-05	-	0.00E+00	5.92E-04
	below		0.00E+00	1.47E-05		0.00E+00	2.05E-05		0.00E+00	1.57E-05
F-Veillonellaceae	above	0.16	2.61E-04	1.55E-03	1.43	8.44E-04	1.82E-03	1.43	8.46E-04	6.08E-03
	below		1.63E-03	6.27E-03		5.91E-04	4.56E-03		5.91E-04	1.82E-03
P-Campylobacteraceae	above	-	0.00E+00	3.52E-05	-	0.00E+00	3.66E-05	-	7.35E-06	4.08E-05
	below		0.00E+00	1.47E-05		0.00E+00	2.57E-05		0.00E+00	1.27E-05
P-Enterobacteriaceae	above	0.44	2.50E-02	8.94E-02	0.50	2.35E-02	9.68E-02	0.27	1.52E-02	6.15E-02
	below		5.64E-02	1.36E-01		4.73E-02	1.27E-01		5.64E-02	1.19E-01
P-Pasteurellaceae	above	-	0.00E+00	0.00E+00	-	0.00E+00	2.15E-05	-	0.00E+00	3.15E-05
	below		0.00E+00	3.15E-05		0.00E+00	0.00E+00		0.00E+00	0.00E+00
P-Moraxellaceae	above	0.91	4.09E-05	1.02E-04	0.91	4.07E-05	7.26E-05	0.47	3.19E-05	5.07E-05
	below		4.47E-05	2.07E-04		4.49E-05	2.28E-04		6.77E-05	3.48E-04
P-Pseudomonadaceae	above	0.00	0.00E+00	1.40E-05	-	1.36E-05	1.78E-05	-	1.39E-05	2.15E-05
	below		1.46E-05	2.90E-05		0.00E+00	2.26E-05		0.00E+00	1.49E-05
Genus										
A-Actinomyces	above	-	0.00E+00	1.50E-05	-	0.00E+00	7.42E-05	-	0.00E+00	4.86E-05
	below		0.00E+00	6.77E-05		0.00E+00	3.61E-05		0.00E+00	3.74E-05
A-Corynebacterium	above	0.92	7.14E-05	1.01E-04	1.20	8.02E-05	1.06E-04	1.41	8.46E-05	1.30E-04
	below		7.75E-05	1.27E-04		6.71E-05	1.44E-04		5.98E-05	1.17E-04
A-Rothia	above	0.39	9.63E-04	1.05E-03	1.40	1.29E-03	1.96E-03	1.51	1.29E-03	1.98E-03
	below		2.48E-03	2.98E-03		9.21E-04	2.99E-03		8.53E-04	2.38E-03
A-Bifidobacterium	above	1.08	7.08E-01	1.35E-01	1.06	6.97E-01	1.15E-01	1.08	7.03E-01	2.11E-01
	below		6.55E-01	4.17E-01		6.55E-01	4.04E-01		6.50E-01	3.27E-01
A-Collinsella	above	1.52	2.36E-05	3.29E-03	-	2.36E-05	1.80E-03	0.25	7.75E-06	4.56E-05
	below		1.55E-05	3.80E-05		0.00E+00	1.32E-04		3.14E-05	2.55E-03
B-Bacteroides	above	0.84	6.83E-05	9.69E-04	4.48	1.29E-04	3.92E-03	0.96	7.20E-05	9.89E-04
	below		8.14E-05	1.17E-03		2.88E-05	8.27E-04		7.48E-05	1.52E-03
B-Parabacteroides	above	-	8.23E-06	8.71E-05	-	0.00E+00	5.03E-05	-	8.23E-06	1.81E-04
	below		0.00E+00	0.00E+00		0.00E+00	3.80E-05		0.00E+00	0.00E+00
B-Prevotella	above	-	0.00E+00	2.90E-05	-	0.00E+00	9.35E-06	-	0.00E+00	7.25E-06
	below		0.00E+00	1.27E-05		0.00E+00	1.45E-05		0.00E+00	1.87E-05
F-Gemella	above	0.80	1.80E-05	8.38E-05	1.13	2.23E-05	9.77E-05	0.42	1.71E-05	3.59E-05
	below		2.23E-05	6.29E-05		1.97E-05	6.29E-05		4.10E-05	1.31E-04
F-Staphylococcus	above	0.33	1.21E-04	2.03E-04	0.40	1.25E-04	2.72E-04	1.88	2.35E-04	5.49E-04
	below		3.66E-04	5.33E-04		3.12E-04	5.38E-04		1.25E-04	4.35E-04
F-Dolosigranulum	above	-	1.81E-05	3.25E-05	0.61	9.09E-06	4.86E-05	-	2.16E-05	5.47E-05
	below		0.00E+00	5.87E-05		1.50E-05	2.90E-05		0.00E+00	2.57E-05

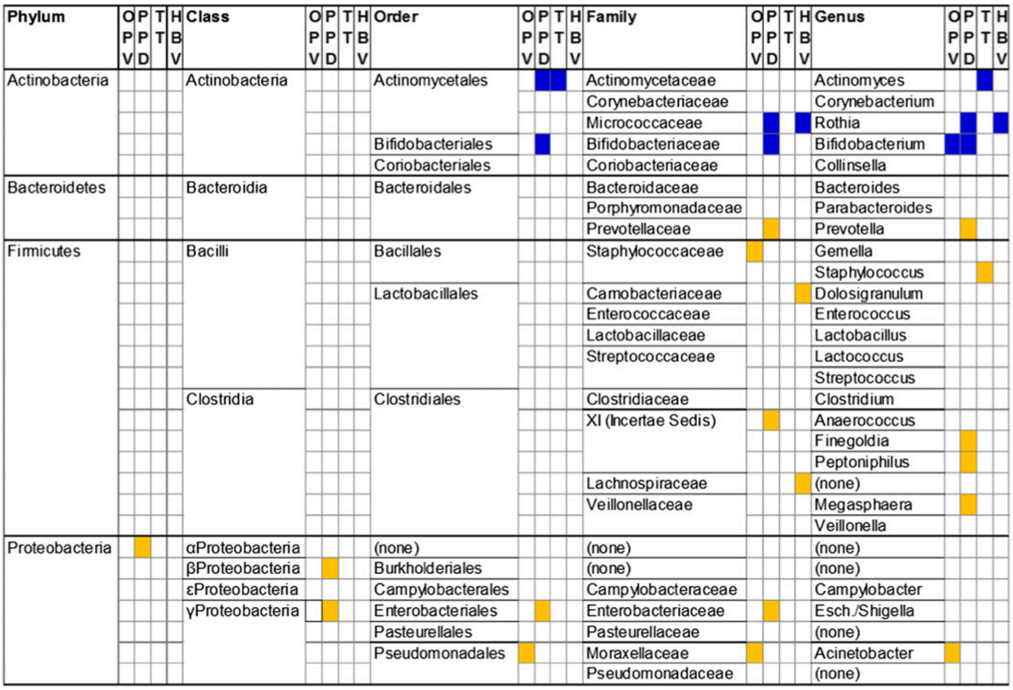
SUPPLEMENTAL FIGURE 12
Continued.

F-Enterococcus	above	-	6.55E-05	1.82E-04	8.33	1.37E-04	8.21E-04	2.19	6.55E-05	2.08E-04
	below		0.00E+00	5.98E-04		1.65E-05	7.34E-05		2.99E-05	6.23E-04
F-Lactobacillus	above	2.48	5.05E-05	3.76E-04	0.29	3.29E-05	3.54E-04	1.27	5.69E-05	8.55E-04
	below		2.03E-05	1.04E-03		1.15E-04	1.04E-03		4.49E-05	9.77E-04
F-Lactococcus	above	0.67	1.35E-04	1.03E-04	0.81	1.53E-04	9.69E-05	1.02	1.83E-04	1.04E-04
	below		2.01E-04	2.07E-04		1.90E-04	2.08E-04		1.79E-04	2.20E-04
F-Streptococcus	above	0.84	3.75E-02	4.45E-02	0.86	3.72E-02	4.66E-02	1.01	3.81E-02	4.12E-02
	below		4.44E-02	4.53E-02		4.33E-02	3.99E-02		3.78E-02	7.75E-02
F-Clostridium	above	-	0.00E+00	2.04E-04	-	0.00E+00	2.38E-04	-	0.00E+00	2.38E-04
	below		0.00E+00	4.18E-05		0.00E+00	3.26E-05		0.00E+00	4.18E-05
F-Anaerococcus	above	-	4.00E-05	1.04E-04	-	1.81E-05	5.91E-05	-	4.31E-05	1.35E-04
	below		0.00E+00	4.39E-05		0.00E+00	5.98E-05		0.00E+00	3.78E-05
F-Finegoldia	above	-	0.00E+00	4.07E-05	-	0.00E+00	1.96E-05	-	7.25E-06	4.01E-05
	below		0.00E+00	1.82E-05		0.00E+00	4.51E-05		0.00E+00	2.05E-05
F-Peptoniphilus	above	-	2.03E-05	7.47E-05	-	1.05E-05	7.79E-05	-	9.84E-06	6.50E-05
	below		0.00E+00	3.15E-05		0.00E+00	4.49E-05		0.00E+00	7.23E-05
F-Megasphera	above	-	0.00E+00	1.72E-05	-	0.00E+00	1.72E-05	-	0.00E+00	4.89E-04
	below		0.00E+00	9.12E-04		0.00E+00	9.12E-04		0.00E+00	0.00E+00
F-Veillonella	above	0.29	7.66E-05	2.41E-04	2.93	2.26E-04	8.18E-04	0.58	7.75E-05	3.79E-04
	below		2.61E-04	9.16E-04		7.71E-05	2.44E-04		1.34E-04	7.79E-04
P-Campylobacter	above	-	0.00E+00	3.51E-05	-	0.00E+00	3.66E-05	-	7.34E-06	4.08E-05
	below		0.00E+00	1.47E-05		0.00E+00	2.57E-05		0.00E+00	1.27E-05
P-Esch./Shigella	above	0.61	1.29E-02	4.01E-02	0.52	1.09E-02	3.44E-02	0.35	7.30E-03	3.75E-02
	below		2.11E-02	3.88E-02		2.11E-02	4.88E-02		2.11E-02	4.48E-02
P-Acinetobacter	above	0.93	4.09E-05	1.02E-04	0.91	4.07E-05	7.26E-05	0.65	2.92E-05	3.89E-05
	below		4.39E-05	1.16E-04		4.47E-05	1.97E-04		4.51E-05	3.48E-04

[a] Ratio calculated with means as median values were both zero.

SUPPLEMENTAL FIGURE 12

Continued.



Phylum	OPV	PPD	TT	HBV	Class	OPV	PPD	TT	HBV	Order	OPV	PPD	TT	HBV	Family	OPV	PPD	TT	HBV	Genus	OPV	PPD	TT	HBV
Actinobacteria					Actinobacteria					Actinomycetales		🟦	🟦		Actinomycetaceae					Actinomyces			🟦	
															Corynebacteriaceae					Corynebacterium				
															Micrococcaceae		🟦		🟦	Rothia		🟦		🟦
										Bifidobacteriales		🟦			Bifidobacteriaceae		🟦			Bifidobacterium	🟦	🟦		
										Coriobacteriales					Coriobacteriaceae					Collinsella				
Bacteroidetes					Bacteroidia					Bacteroidales					Bacteroidaceae					Bacteroides				
															Porphyromonadaceae					Parabacteroides				
															Prevotellaceae		🟧			Prevotella		🟧		
Firmicutes					Bacilli					Bacillales					Staphylococcaceae	🟧				Gemella				
																				Staphylococcus			🟧	
										Lactobacillales					Carnobacteriaceae				🟧	Dolosigranulum				
															Enterococcaceae					Enterococcus				
															Lactobacillaceae					Lactobacillus				
															Streptococcaceae					Lactococcus				
																				Streptococcus				
					Clostridia					Clostridiales					Clostridiaceae					Clostridium				
															XI (Incertae Sedis)		🟧			Anaerococcus				
																				Finegoldia		🟧		
																				Peptoniphilus		🟧		
															Lachnospiraceae				🟧	(none)				
															Veillonellaceae					Megasphaera		🟧		
																				Veillonella				
Proteobacteria		🟧			αProteobacteria					(none)					(none)					(none)				
					βProteobacteria		🟧			Burkholderiales					(none)					(none)				
					εProteobacteria					Campylobacterales					Campylobacteraceae					Campylobacter				
					γProteobacteria		🟧			Enterobacteriales		🟧			Enterobacteriaceae		🟧			Esch./Shigella				
										Pasteurellales					Pasteurellaceae					(none)				
										Pseudomonadales	🟧				Moraxellaceae	🟧				Acinetobacter	🟧			
															Pseudomonadaceae					(none)				

SUPPLEMENTAL FIGURE 13

Heat map showing positive (dark blue rectangles) and negative (light orange rectangles) associations of microbiota relative abundance (at the phylum, class, order, family, and genus levels) with vaccine-specific IgG responses to the indicated vaccines (OPV, TT, and HBV vaccine) and with the DTH skin-test response to PPD to assess response to the BCG vaccine against tuberculosis. Significant ($P < .05$) associations were characterized as positive or negative by using Spearman correlation analysis of continuous data (IgG concentrations and area of induration for the skin test, and relative abundance of microbiota) and the Wilcoxon test to compare relative abundance of microbiota in "high" and "low" vaccine responders (those above or below the median response of interest) as described in Methods. Median microbiota relative abundance for vaccine high and low responders are shown in Supplemental Fig 14. Esch., *Escherichia*.

	Group	OPV IgG			Tuberculosis Skin Test			TT IgG			HBV IgG		
		Ratio	Median	IQR	Ratio	Median	IQR	Ratio	Median	IQR	Ratio	Median	IQR
Phylum													
Actinobacteria (A)	above	1.03	8.03E-01	2.35E-01	1.16	8.46E-01	2.45E-01	1.01	8.30E-01	2.70E-01	0.80	6.60E-01	3.80E-01
	below		7.81E-01	4.02E-01		7.29E-01	4.91E-01		8.20E-01	4.14E-01		8.27E-01	1.90E-01
Bacteroidetes (B)	above	1.95	3.47E-04	9.25E-03	0.22	8.14E-05	6.83E-03	1.57	3.23E-04	2.64E-03	0.15	1.72E-04	1.19E-03
	below		1.78E-04	2.37E-03		3.64E-04	3.08E-03		2.06E-04	5.92E-03		1.12E-03	2.44E-02
Firmicutes (F)	above	0.81	8.31E-02	8.00E-02	1.13	9.38E-02	1.07E-01	1.08	9.21E-02	8.84E-02	0.82	8.76E-02	2.61E-01
	below		1.02E-01	3.01E-01		8.31E-02	1.49E-01		8.50E-02	1.39E-01		1.07E-01	9.33E-02
Proteobacteria (P)	above	1.18	4.88E-02	1.58E-01	0.44	3.00E-02	6.20E-02	0.61	3.35E-02	1.36E-01	1.29	3.86E-02	1.62E-01
	below		4.13E-02	1.36E-01		6.81E-02	2.07E-01		5.50E-02	1.47E-01		3.00E-02	1.77E-01
Class													
A-Actinobacteria	above	1.03	8.03E-01	2.35E-01	1.16	8.46E-01	2.45E-01	1.01	8.30E-01	2.70E-01	0.80	6.60E-01	3.80E-01
	below		7.81E-01	4.02E-01		7.29E-01	4.91E-01		8.20E-01	4.14E-01		8.27E-01	1.90E-01
B-Bacteroidia	above	2.03	3.47E-04	9.25E-03	0.23	8.14E-05	6.83E-03	1.57	3.23E-04	2.64E-03	0.15	1.65E-04	1.19E-03
	below		1.71E-04	2.29E-03		3.56E-04	3.06E-03		2.06E-04	5.92E-03		1.12E-03	2.44E-02
F-Bacilli	above	0.91	7.60E-02	7.19E-02	1.14	8.63E-02	1.11E-01	1.06	8.21E-02	8.46E-02	1.25	8.29E-02	2.68E-01
	below		8.33E-02	2.69E-01		7.58E-02	1.24E-01		7.71E-02	1.31E-01		6.60E-02	1.07E-01
F-Clostridia	above	0.88	2.17E-03	5.82E-03	0.40	1.24E-03	1.16E-02	0.57	1.95E-03	1.86E-02	0.24	1.05E-03	3.33E-03
	below		2.46E-03	2.25E-02		3.13E-03	1.43E-02		3.41E-03	5.98E-03		4.38E-03	1.59E-02
P-Alphaproteobacteria	above	-	0.00E+00	2.03E-05	-	0.00E+00	2.05E-05	-	0.00E+00	2.05E-05	0.00	0.00E+00	1.46E-05
	below		0.00E+00	1.42E-05		0.00E+00	1.61E-05		0.00E+00	1.46E-05		1.47E-05	2.22E-05
P-Betaproteobacteria	above	-	0.00E+00	1.87E-05	0.32[a]	0.00E+00	0.00E+00	-	0.00E+00	1.85E-05	-	0.00E+00	1.85E-05
	below		0.00E+00	2.34E-05		0.00E+00	3.93E-05		0.00E+00	2.34E-05		0.00E+00	1.42E-05
P-Epsilonproteobacteria	above	-	0.00E+00	9.77E-05	-	0.00E+00	3.94E-05	-	0.00E+00	4.40E-05	-	6.34E-06	1.60E-02
	below		0.00E+00	1.62E-05		0.00E+00	2.83E-05		0.00E+00	1.93E-05		0.00E+00	1.47E-05
P-Gammaproteobacteria	above	0.86	3.55E-02	1.43E-01	0.45	2.84E-02	6.21E-02	1.18	3.34E-02	6.76E-02	0.53	1.58E-02	1.43E-01
	below		4.13E-02	1.35E-01		6.31E-02	2.05E-01		2.84E-02	1.48E-01		3.00E-02	1.77E-01
Order													
A-Actinomycetales	above	1.91	3.20E-03	3.89E-03	2.68	3.93E-03	4.00E-03	2.89	3.68E-03	3.82E-03	2.36	3.29E-03	4.62E-03
	below		1.68E-03	4.55E-03		1.47E-03	2.72E-03		1.27E-03	2.86E-03		1.40E-03	3.30E-03
A-Bifidobacteriales	above	1.04	8.00E-01	2.47E-01	1.16	8.40E-01	2.60E-01	1.07	8.23E-01	2.70E-01	0.85	6.48E-01	3.72E-01
	below		7.72E-01	4.70E-01		7.26E-01	4.76E-01		7.66E-01	4.16E-01		7.64E-01	1.89E-01
A-Coriobacteriales	above	2.21	6.21E-05	3.91E-03	0.38	2.07E-05	5.33E-04	0.27	2.07E-05	9.10E-04	1.90	8.10E-05	9.17E-03
	below		2.81E-05	1.06E-03		5.45E-05	1.77E-02		7.71E-05	5.21E-03		4.26E-05	5.33E-04
B-Bacteroidales	above	2.03	3.47E-04	9.25E-03	0.23	8.14E-05	6.83E-03	1.57	3.23E-04	2.64E-03	0.15	1.65E-04	1.19E-03
	below		1.71E-04	2.29E-03		3.56E-04	3.06E-03		2.06E-04	5.92E-03		1.12E-03	2.44E-02
F-Bacillales	above	0.34	3.28E-04	3.97E-04	1.06	4.68E-04	9.97E-04	0.72	4.02E-04	7.39E-04	0.75	3.65E-04	9.42E-04
	below		9.55E-04	2.00E-03		4.42E-04	7.67E-04		5.61E-04	1.25E-03		4.85E-04	2.05E-03

SUPPLEMENTAL FIGURE 14

Relative abundance of bacteria in stool of high (above median) and low (below median) vaccine responders. Positive and negative associations are highlighted in blue and orange, respectively; statistical analysis is described in the legend to Supplemental Figure 13. Esch., *Escherichia*; IQR, interquartile range.

F-Lactobacillales	above	0.90	7.31E-02	7.11E-02	1.14	8.46E-02	1.05E-01	1.08	8.07E-02	8.32E-02	1.37	8.15E-02	2.64E-01
	below		8.17E-02	2.66E-01		7.39E-02	1.19E-01		7.48E-02	1.27E-01		5.95E-02	9.21E-02
F-Clostridiales	above	0.88	2.17E-03	5.82E-03	0.40	1.24E-03	1.16E-02	0.57	1.95E-03	1.85E-02	0.24	1.05E-03	3.33E-03
	below		2.46E-03	2.25E-02		3.13E-03	1.43E-02		3.41E-03	5.98E-03		4.38E-03	1.58E-02
P-Burkholderiales	above	-	0.00E+00	1.85E-05	-	0.00E+00	0.00E+00	-	0.00E+00	1.85E-05	-	0.00E+00	1.85E-05
	below		0.00E+00	2.34E-05		0.00E+00	3.93E-05		0.00E+00	2.34E-05		0.00E+00	1.42E-05
P-Campylobacterales	above	-	0.00E+00	9.77E-05	-	0.00E+00	3.94E-05	-	0.00E+00	4.40E-05	-	6.34E-06	1.60E-02
	below		0.00E+00	1.62E-05		0.00E+00	2.83E-05		0.00E+00	1.93E-05		0.00E+00	1.47E-05
P-Enterobacteriales	above	0.84	3.33E-02	1.37E-01	0.44	2.67E-02	5.83E-02	1.21	3.22E-02	6.46E-02	0.53	1.54E-02	1.37E-01
	below		3.98E-02	1.27E-01		6.03E-02	1.91E-01		2.67E-02	1.41E-01		2.89E-02	1.67E-01
P-Pasteurellales	above	-	0.00E+00	2.23E-05	-	0.00E+00	2.07E-05	-	0.00E+00	2.23E-05	-	0.00E+00	4.87E-05
	below		0.00E+00	0.00E+00		0.00E+00	1.57E-05		0.00E+00	0.00E+00		0.00E+00	0.00E+00
P-Pseudomonadales	above	0.80	5.05E-05	7.72E-05	0.77	4.65E-05	2.33E-04	1.27	6.29E-05	2.30E-04	1.46	6.54E-05	2.30E-04
	below		6.29E-05	2.13E-04		6.07E-05	8.13E-05		4.94E-05	1.28E-04		4.47E-05	6.18E-05
Family													
A-Actinomycetaceae	above	-	0.00E+00	8.13E-05	-	0.00E+00	1.56E-04	-	0.00E+00	2.20E-04	0.00	0.00E+00	1.39E-05
	below		0.00E+00	6.77E-05		0.00E+00	5.36E-05		0.00E+00	3.61E-05		2.99E-05	1.47E-04
A-Corynebacteriaceae	above	0.60	5.72E-05	1.10E-04	0.97	7.09E-05	1.19E-04	0.78	6.71E-05	1.12E-04	1.22	8.20E-05	8.46E-05
	below		9.55E-05	1.26E-04		7.31E-05	1.03E-04		8.64E-05	1.10E-04		6.71E-05	1.28E-04
A-Micrococcaceae	above	1.51	1.59E-03	2.49E-03	2.83	2.63E-03	2.73E-03	2.47	2.13E-03	2.61E-03	2.57	2.22E-03	3.26E-03
	below		1.06E-03	2.38E-03		9.30E-04	1.24E-03		8.63E-04	1.58E-03		8.63E-04	1.98E-03
A-Bifidobacteriaceae	above	1.04	8.00E-01	2.47E-01	1.16	8.40E-01	2.60E-01	1.07	8.23E-01	2.70E-01	0.85	6.48E-01	3.72E-01
	below		7.72E-01	4.70E-01		7.26E-01	4.76E-01		7.66E-01	4.16E-01		7.64E-01	1.89E-01
A-Coriobacteriaceae	above	2.21	6.21E-05	3.91E-03	0.38	2.07E-05	5.33E-04	0.27	2.07E-05	9.10E-04	1.90	8.10E-05	9.17E-03
	below		2.81E-05	1.06E-03		5.45E-05	1.77E-02		7.71E-05	5.21E-03		4.26E-05	5.33E-04
B-Bacteroidaceae	above	0.54	2.87E-05	6.28E-04	0.23	2.23E-05	6.08E-04	0.27	2.23E-05	1.17E-03	1.25	5.62E-05	5.86E-04
	below		5.33E-05	8.27E-04		9.70E-05	9.87E-04		8.14E-05	6.08E-04		4.48E-05	8.27E-04
B-Porphyromonedaceae	above	-	0.00E+00	5.61E-05	0.00	0.00E+00	1.18E-04	0.00	0.00E+00	9.77E-05	-	0.00E+00	2.05E-05
	below		0.00E+00	8.78E-05		8.25E-06	7.20E-05		1.65E-05	5.61E-05		0.00E+00	2.76E-04
B-Prevotellaceae	above	-	0.00E+00	3.64E-05	0.34[a]	0.00E+00	0.00E+00	-	0.00E+00	3.61E-05	-	0.00E+00	3.61E-05
	below		0.00E+00	1.27E-05		0.00E+00	6.10E-05		0.00E+00	1.27E-05		0.00E+00	1.45E-05
F-Staphylococcaceae	above	0.28	1.91E-04	3.29E-04	1.01	3.58E-04	5.89E-04	0.63	2.83E-04	5.55E-04	0.68	2.76E-04	5.80E-04
	below		6.82E-04	1.40E-03		3.55E-04	6.00E-04		4.49E-04	9.19E-04		4.05E-04	1.45E-03
F-Camobacteriaceae	above	0.89	3.71E-05	1.54E-04	0.26	1.85E-05	7.62E-05	0.39	2.09E-05	1.64E-04	0.08	9.25E-06	7.61E-05
	below		4.16E-05	8.64E-05		7.10E-05	1.40E-04		5.42E-05	9.35E-05		1.13E-04	1.61E-04
F-Enterococcaceae	above	0.95	2.56E-04	2.52E-03	0.34	1.35E-04	2.06E-03	1.20	3.13E-04	1.43E-03	0.06	8.64E-05	4.77E-04
	below		2.69E-04	7.27E-04		3.92E-04	2.05E-03		2.60E-04	2.76E-03		1.45E-03	5.35E-03
F-Lactobacillaceae	above	0.31	5.12E-05	7.36E-04	8.95	7.36E-04	5.06E-03	0.73	1.20E-04	5.05E-03	1.86	3.14E-04	1.88E-03
	below		1.65E-04	4.32E-03		8.23E-05	3.01E-04		1.64E-04	7.36E-04		1.69E-04	7.81E-03
F-Streptococcaceae	above	1.09	4.85E-02	5.10E-02	1.07	4.69E-02	6.47E-02	1.17	4.77E-02	5.63E-02	1.41	5.05E-02	9.41E-02
	below		4.47E-02	1.09E-01		4.37E-02	6.95E-02		4.09E-02	9.46E-02		3.57E-02	5.19E-02

SUPPLEMENTAL FIGURE 14

Continued.

F-Clostridiaceae	above	0.00	0.00E+00	1.81E-04	1.05	1.85E-05	2.39E-04	1.23	1.85E-05	4.72E-04	0.05	9.25E-06	7.61E-05
	below		5.96E-05	1.35E-03		1.77E-05	3.77E-04		1.50E-05	1.90E-04		1.90E-04	1.35E-03
F-XI (Incertae Sedis)	above	1.23	3.74E-05	1.81E-04	0.00	0.00E+00	8.91E-05	0.67	2.93E-05	2.00E-04	0.60	4.05E-05	1.95E-04
	below		3.04E-05	1.14E-04		6.55E-05	2.11E-04		4.39E-05	1.14E-04		6.77E-05	1.86E-04
F-Lachnospiraceae	above	-	0.00E+00	2.07E-05	-	0.00E+00	1.50E-05	-	0.00E+00	2.07E-05	0.00	0.00E+00	0.00E+00
	below		0.00E+00	1.50E-05		0.00E+00	1.14E-04		0.00E+00	9.25E-05		1.47E-05	1.09E-03
F-Veillonellaceae	above	0.83	7.88E-04	1.86E-03	0.41	4.59E-04	1.96E-03	1.77	8.15E-04	1.68E-03	0.84	6.37E-04	1.98E-03
	below		9.45E-04	2.08E-03		1.11E-03	3.76E-03		4.61E-04	1.95E-03		7.62E-04	2.04E-03
P-Campylobacteraceae	above	-	0.00E+00	9.77E-05	-	0.00E+00	3.94E-05	-	0.00E+00	4.40E-05	-	6.35E-06	1.60E-02
	below		0.00E+00	1.62E-05		0.00E+00	2.83E-05		0.00E+00	1.93E-05		0.00E+00	1.47E-05
P-Enterobacteriaceae	above	0.84	3.33E-02	1.37E-01	0.44	2.67E-02	5.83E-02	1.21	3.22E-02	6.46E-02	0.53	1.54E-02	1.37E-01
	below		3.98E-02	1.27E-01		6.03E-02	1.91E-01		2.67E-02	1.41E-01		2.89E-02	1.67E-01
P-Pasteurellaceae	above	-	0.00E+00	2.23E-05	-	0.00E+00	2.07E-05	-	0.00E+00	2.23E-05	-	0.00E+00	4.87E-05
	below		0.00E+00	0.00E+00		0.00E+00	1.58E-05		0.00E+00	0.00E+00		0.00E+00	0.00E+00
P-Moraxellaceae	above	0.81	3.60E-05	7.12E-05	0.78	3.45E-05	2.50E-04	0.79	3.45E-05	2.05E-04	1.60	4.63E-05	2.09E-04
	below		4.46E-05	2.29E-04		4.44E-05	1.01E-04		4.39E-05	1.38E-04		2.90E-05	5.30E-05
P-Pseudomonadaceae	above	-	1.36E-05	2.07E-05	-	1.39E-05	2.07E-05	-	1.47E-05	2.23E-05	0.49	6.95E-06	2.23E-05
	below		0.00E+00	1.49E-05		0.00E+00	2.15E-05		0.00E+00	1.46E-05		1.42E-05	2.07E-05
Genus													
A-Actinomyces	above	-	0.00E+00	6.10E-05	-	0.00E+00	1.47E-04	14.1[a]	0.00E+00	2.20E-04	-	0.00E+00	0.00E+00
	below		0.00E+00	6.77E-05		0.00E+00	3.68E-05		0.00E+00	0.00E+00		0.00E+00	1.11E-04
A-Corynebacterium	above	0.60	5.72E-05	1.10E-04	0.97	7.09E-05	1.19E-04	0.78	6.71E-05	1.12E-04	1.22	8.19E-05	8.47E-05
	below		9.55E-05	1.26E-04		7.31E-05	1.10E-04		8.64E-05	1.17E-04		6.71E-05	1.41E-04
A-Rothia	above	1.51	1.56E-03	2.35E-03	2.71	2.48E-03	2.55E-03	2.54	2.13E-03	2.54E-03	2.56	2.14E-03	2.98E-03
	below		1.03E-03	2.38E-03		9.14E-04	1.19E-03		8.38E-04	1.49E-03		8.38E-04	1.94E-03
A-Bifidobacterium	above	1.04	6.80E-01	1.57E-01	1.13	7.08E-01	1.85E-01	1.04	6.87E-01	2.45E-01	0.87	5.74E-01	3.07E-01
	below		6.53E-01	3.96E-01		6.25E-01	3.93E-01		6.63E-01	3.35E-01		6.63E-01	1.24E-01
A-Collinsella	above	-	1.88E-05	2.48E-03	0.00	0.00E+00	3.80E-05	0.00	0.00E+00	1.32E-04	-	2.12E-05	3.41E-03
	below		0.00E+00	1.32E-04		2.54E-05	2.51E-03		1.69E-05	2.55E-03		0.00E+00	9.02E-05
B-Bacteroides	above	0.54	2.87E-05	6.28E-04	0.23	2.23E-05	6.08E-04	0.27	2.23E-05	1.17E-03	1.25	5.62E-05	5.86E-04
	below		5.33E-05	8.27E-04		9.70E-05	9.87E-04		8.14E-05	6.08E-04		4.48E-05	8.27E-04
B-Parabacteroides	above	-	0.00E+00	5.61E-05	-	0.00E+00	4.44E-05	-	0.00E+00	9.77E-05	-	0.00E+00	0.00E+00
	below		0.00E+00	4.44E-05		0.00E+00	7.20E-05		0.00E+00	4.44E-05		0.00E+00	4.44E-05
B-Prevotella	above	-	0.00E+00	1.87E-05	0.34[a]	0.00E+00	0.00E+00	-	0.00E+00	3.61E-05	-	0.00E+00	3.61E-05
	below		0.00E+00	1.27E-05		0.00E+00	4.25E-05		0.00E+00	1.27E-05		0.00E+00	1.45E-05
F-Gemella	above	2.49	4.27E-05	8.95E-05	1.30	2.23E-05	5.56E-05	2.53	4.10E-05	1.03E-04	0.77	1.71E-05	4.65E-05
	below		1.71E-05	6.29E-05		1.71E-05	1.07E-04		1.62E-05	7.48E-05		2.22E-05	7.48E-05
F-Staphylococcus	above	0.29	1.21E-04	2.02E-04	0.84	1.25E-04	5.12E-04	0.44	1.23E-04	3.07E-04	1.65	2.09E-04	5.48E-04
	below		4.16E-04	1.10E-03		1.50E-04	5.72E-04		2.81E-04	6.45E-04		1.27E-04	9.59E-04
F-Dolosigranulum	above	0.00	0.00E+00	1.85E-05	0.00	0.00E+00	5.08E-05	0.00	0.00E+00	5.87E-05	0.00	0.00E+00	4.65E-05
	below		2.40E-05	6.68E-05		1.57E-05	3.26E-05		1.50E-05	4.65E-05		1.82E-05	5.87E-05

SUPPLEMENTAL FIGURE 14
Continued.

F-Enterococcus	above	0.97	3.94E-05	6.85E-04	0.00	0.00E+00	2.36E-04	1.70	4.89E-05	5.06E-04	0.00	0.00E+00	6.49E-05
	below		4.07E-05	1.55E-04		5.01E-05	5.52E-04		2.88E-05	6.23E-04		6.61E-05	9.27E-04
F-Lactobacillus	above	0.15	1.02E-05	2.22E-04	4.90	1.02E-04	1.24E-03	0.45	2.03E-05	7.44E-04	-	7.20E-05	9.77E-04
	below		6.88E-05	1.04E-03		2.07E-05	1.16E-04		4.47E-05	1.44E-04		0.00E+00	1.04E-03
F-Lactococcus	above	0.93	1.78E-04	7.61E-05	1.06	1.87E-04	7.75E-05	0.96	1.87E-04	4.23E-05	1.00	1.95E-04	5.27E-05
	below		1.92E-04	2.13E-04		1.77E-04	1.18E-04		1.95E-04	2.25E-04		1.96E-04	2.10E-04
F-Streptococcus	above	1.22	4.64E-02	4.90E-02	1.15	4.33E-02	6.25E-02	1.20	4.45E-02	5.24E-02	3.27	4.76E-02	7.87E-02
	below		3.79E-02	9.13E-02		3.77E-02	4.24E-02		3.71E-02	4.90E-02		1.46E-02	4.28E-02
F-Clostridium	above	-	0.00E+00	1.85E-05	-	0.00E+00	3.26E-05	-	0.00E+00	5.45E-05	-	0.00E+00	2.54E-05
	below		0.00E+00	2.39E-04		0.00E+00	1.42E-04		0.00E+00	1.15E-04		0.00E+00	3.08E-04
F-Anaerococcus	above	0.00	0.00E+00	5.98E-05	0.00	0.00E+00	4.40E-05	0.00	0.00E+00	8.91E-05	0.00	0.00E+00	6.96E-05
	below		7.10E-06	8.91E-05		3.02E-05	1.04E-04		1.81E-05	5.98E-05		4.22E-05	1.05E-04
F-Finegoldia	above	-	0.00E+00	1.82E-05	0.00	0.00E+00	0.00E+00	-	0.00E+00	1.82E-05	-	0.00E+00	2.05E-05
	below		0.00E+00	1.62E-05		7.25E-06	5.87E-05		0.00E+00	2.11E-05		0.00E+00	2.11E-05
F-Peptoniphilus	above	-	0.00E+00	4.49E-05	0.00	0.00E+00	1.97E-05	-	0.00E+00	7.71E-05	0.00	0.00E+00	8.35E-05
	below		0.00E+00	7.23E-05		2.35E-05	7.92E-05		0.00E+00	4.87E-05		2.26E-05	1.05E-04
F-Megasphera	above	-	0.00E+00	0.00E+00	0.83[a]	0.00E+00	0.00E+00	-	0.00E+00	9.12E-04	-	0.00E+00	0.00E+00
	below		0.00E+00	3.61E-05		0.00E+00	9.35E-04		0.00E+00	0.00E+00		0.00E+00	1.32E-05
F-Veillonella	above	6.16	2.22E-04	8.36E-04	0.58	7.88E-05	6.81E-04	0.25	6.22E-05	4.96E-04	0.37	5.01E-05	8.99E-04
	below		3.60E-05	2.46E-04		1.35E-04	5.33E-04		2.45E-04	9.23E-04		1.35E-04	4.71E-04
P-Campylobacter	above	-	0.00E+00	9.77E-05	-	0.00E+00	3.94E-05	-	0.00E+00	4.40E-05	-	6.34E-06	1.60E-02
	below		0.00E+00	1.62E-05		0.00E+00	2.83E-05		0.00E+00	1.93E-05		0.00E+00	1.47E-05
P-Esch./Shigella	above	0.98	1.51E-02	3.78E-02	0.74	1.47E-02	3.54E-02	1.43	1.61E-02	3.78E-02	0.25	4.08E-03	3.69E-02
	below		1.54E-02	5.10E-02		1.97E-02	6.45E-02		1.13E-02	4.42E-02		1.61E-02	4.75E-02
P-Acinetobacter	above	0.67	2.95E-05	7.12E-05	1.00	3.45E-05	2.09E-04	0.84	3.15E-05	1.14E-04	1.62	3.42E-05	2.09E-04
	below		4.42E-05	1.34E-04		3.44E-05	5.65E-05		3.74E-05	7.29E-05		2.11E-05	3.02E-05

[a] Ratio calculated with means as median values were both zero.

SUPPLEMENTAL FIGURE 14

Continued.

SUPPLEMENTAL TABLE 3 Schedule of Study Procedures

Procedure	Age of Infant					
	Birth [a]	6 Weeks	10 Weeks	11 Weeks	14 Weeks	15 Weeks
Anthropometry	Weight, length	Weight, length	Weight, length			Weight, length
Ultrasound		TI		TI		TI
Vaccination	BCG, OPV	HBV, Hib, DPT, OPV	HBV, Hib, DPT, OPV		HBV, Hib, DPT, OPV	
Blood cell counts		CBC, FACS for T cells				CBC, FACS for T cells
Vaccine-specific memory T cells						PPD, OPV, HBV, TT (SEB)
BCG vaccine response						DTH skin test to PPD
Antibody in lymphocyte supernatant assay						TT IgG
16S rRNA gene sequence, PCR for *Bifidobacterium*		Stool microbiota		Stool microbiota		Stool microbiota

CBC, complete blood count; FACS, fluorescence-activated cell sorter; Hib, *Haemophilus influenzae* type b.

[a] Vaccines administered within 48 hours of birth.

SUPPLEMENTAL TABLE 4 Primers and Probes Used for *Bifidobacterium*-Specific PCR Assays

Primer/Probe	Taxonomy	Sequence (5′ to 3′)	Temperature (C°)	Reference
Uni334F	Bacteria	ACTCCTACGGGAGGCAGCAGT	65.5	Hartman et al[55]
Uni514R	Bacteria	ATTACCGCGGCTGCTGGC	65.5	Hartman et al[55]
Bif F	Bifidobacteria	GCGTGCTTAACACATGCAAGTC	60	Penders et al[56]
Bif R	Bifidobacteria	CACCCGTTTCCAGGAGCTATT	60	Penders et al[56]
Bif P	Bifidobacteria	[6-FAM]TCACGCATTACTCACCCGTTCGCC[TAMRA]	60	Penders et al[56]
FWD_BL_BI	*B longum* group	[HEX]-AAAACGTCCATCCATCACA	54	Present study
REV_BL	*B longum* group	ACGACCAGGTTCCACTTGAT	54	Present study
REV_BI	*B longum* group	CGCCTCAGTTCTTTAATGT	54	Present study
NBIF389	Bifidobacteria	[HEX]-GCCTTCGGGTTGTAAAC	52	Lewis et al[24]
NBIF1018REV	Bifidobacteria	GACCATGCACCACCTGTG	52	Lewis et al.[24]

SUPPLEMENTAL TABLE 5 Number and Percentage of Stool Samples Positive for the Indicated Bacterial Phyla by 16S rDNA Sequence Analysis in 48 Subjects

Age	*Actinobacteria*	*Proteobacteria*	*Firmicutes*	*Bacteroidetes*	*Tenericutes*	*Fusobacteria*	*Verrucomicrobia*
6 weeks							
n	48	47	48	23	6	3	4
%	100	97.9	100	47.9	12.5	6.2	8.3
11 weeks							
n	48	47	48	30	10	4	2
%	100	97.9	100	62.5	20.8	8.3	4.2
15 weeks							
n	48	48	48	34	8	3	2
%	100	100	100	70.8	16.7	6.2	4.2

SUPPLEMENTAL TABLE 6 Relative Abundance of Bacterial Phyla Determined by 16S rDNA Sequence Analysis in 48 Subjects

	6 Weeks			11 Weeks			15 Weeks			ANOVA	Pairwise ($P < .05$)		
	Median	25%	75%	Median	25%	75%	Median	25%	75%	P	6 vs 11 wk	6 vs 15 wk	11 vs 15 wk
Actinobacteria	0.923	0.774	0.963	0.874	0.723	0.947	0.861	0.638	0.944	.305			
Proteobacteria	0.006	0.001	0.064	0.026	0.005	0.112	0.027	0.003	0.125	.025	Yes		
Firmicutes	0.043	0.017	0.117	0.069	0.024	0.153	0.057	0.030	0.126	.560			
Bacteroidetes	0	0	1.8×10^{-4}	6.0×10^{-5}	0	1.7×10^{-3}	1.2×10^{-4}	0	4.1×10^{-3}	.002		Yes	

SUPPLEMENTAL TABLE 7 Diversity by Week as Indicated by Richness (OTU) and SDI

	6 Weeks ($n = 48$)		11 Weeks ($n = 48$)		15 Weeks ($n = 48$)		ANOVA	Pairwise ($P < .05$)		
	Mean	SD	Mean	SD	Mean	SD	P	6 vs 11 wk	6 vs 15 wk	11 vs 15 wk
Phylum										
OTU	4.146	1.091	4.271	0.984	4.396	0.917	0.239			
SDI	0.385	0.287	0.464	0.275	0.506	0.293	0.018		Yes	
Class										
OTU	5.333	1.589	5.625	1.496	5.854	1.288	0.056			
SDI	0.395	0.303	0.493	0.308	0.541	0.333	0.008		Yes	
Order										
OTU	8.229	2.106	8.771	2.176	9.354	1.768	0.002		Yes	
SDI	0.456	0.322	0.54	0.334	0.586	0.347	0.030		Yes	

OTU, operational taxonomic unit; SDI, Shannon Diversity Index.

SUPPLEMENTAL TABLE 8 Mean Relative Abundance of Stool Microbiota Identified in >25% of Samples as Determined by DNA Sequence Analysis of the V4 Region of the 16S rRNA Gene at 15 Weeks of Age

Phylum	Relative Abundance	Class	Relative Abundance	Order	Relative Abundance	Family	Relative Abundance	Genus	Relative Abundance
Actinobacteria	0.71353	*Actinobacteria*	0.71353	*Actinomycetales*	0.00366	*Actinomycetaceae*	0.00014	*Actinomyces*	0.00008
						Corynebacteriaceae	0.00009	*Corynebacterium*	0.00009
						Micrococcaceae	0.00232	*Rothia*	0.00224
				Bifidobacteriales	0.70127	*Bifidobacteriaceae*	0.70127	*Bifidobacterium*	0.59627
				Coriobacteriales	0.00786	*Coriobacteriaceae*	0.00786	*Collinsella*	0.00547
Bacteroidetes	0.01250	*Bacteroidia*	0.01248	*Bacteroidales*	0.01248	*Bacteroidaceae*	0.01037	*Bacteroides*	0.01037
						Porphyromonadaceae	0.00123	*Parabacteroides*	0.00022
						Prevotellaceae	0.00079	*Prevotella*	0.00079
Firmicutes	0.14731	*Bacilli*	0.13146	*Bacillales*	0.00086	*Staphylococcaceae*	0.00064	*Gemella*	0.00010
								Staphylococcus	0.00047
				Lactobacillales	0.12775	*Carnobacteriaceae*	0.00007	*Dolosigranulum*	0.00003
						Enterococcaceae	0.00277	*Enterococcus*	0.00032
						Lactobacillaceae	0.01223	*Lactobacillus*	0.01044
						Streptococcaceae	0.07264	*Lactococcus*	0.00241
								Streptococcus	0.06312
		Clostridia	0.01014	*Clostridiales*	0.01013	*Clostridiaceae*	0.00372	*Clostridium*	0.00159
						XI (Incertae Sedis)	0.00013	*Anaerococcus*	0.00006
								Finegoldia	0.00003
								Peptoniphilus	0.00004
						Lachnospiraceae	0.00070	(none)	
						Veillonellaceae	0.00390	*Megasphaera*	0.00267
								Veillonella	0.00063
Proteobacteria	0.12227	α*Proteobacteria*	0.00002	None		None		None	
		β*Proteobacteria*	0.00011	*Burkholderiales*	0.00010	None		None	
		ε*Proteobacteria*	0.00653	*Campylobacterales*	0.00653	*Campylobacteraceae*	0.00649	*Campylobacter*	0.00649
		γ*Proteobacteria*	0.11542	*Enterobacteriales*	0.11162	*Enterobacteriaceae*	0.11162	*Escherichia/Shigella*	0.03643
				Pasteurellales	0.00008	*Pasteurellaceae*	0.00008	(none)	
				Pseudomonadales	0.00021	*Moraxellaceae*	0.00020	*Acinetobacter*	0.00018
						Pseudomonadaceae	0.00001	None	
Other/unassigned	0.00439		0.01033		0.01745		0.06073		0.25945

Each column sums to 1.0.

SUPPLEMENTAL TABLE 9 Stool Microbiota Levels (Relative Abundance) by BF Status at 15 Weeks of Age

Microbiota	Exclusive BF or BF with Supplemental Water or Juice ($n = 33$)			Other BF, Including Supplemental Milk or Formula ($n = 15$)			P
	Median	25th Percentile	75th Percentile	Median	25th Percentile	75th Percentile	
Bacteroidaceae	2.64×10^{-5}	0	14.6×10^{-5}	62.8×10^{-5}	8.14×10^{-5}	1010×10^{-5}	.0059
Bacteroides	2.64×10^{-5}	0	14.6×10^{-5}	62.8×10^{-5}	8.14×10^{-5}	1010×10^{-5}	.0059
Enterococcus	2.88×10^{-5}	0	19.9×10^{-5}	23.6×10^{-5}	0	76.6×10^{-5}	.046
B longum [a]	0.979	0.947	1.000	0.888	0.477	0.979	.011

All taxa identified by 16S rRNA gene sequence analysis or *Bifidobacterium*-specific PCR and T-RFLP were compared by using these BF categories, and all significant associations ($P < .05$ by Wilcoxon rank-sum test) are shown here. The same analysis was performed to compare exclusive ($n = 22$) with nonexclusive BF ($n = 26$) at 15 weeks and only 1 taxon (*Pseudomonadaceae*) showed a significant ($P = .037$) association (exclusive BF: 1.44×10^{-5}, $0/31.5 \times 10^{-5}$; nonexclusive BF: 0, $0/1.47 \times 10^{-5}$). BF, breastfeeding.

[a] Relative abundance within the genus *Bifidobacterium*.

SUPPLEMENTAL TABLE 10 Association of Stool Microbiota With Nutritional Status (Length-For-Age z Score) Assessed by Spearman Correlation Analysis

Taxon	n	R	P
16S rRNA gene sequence (relative abundance)			
Actinobacteria (phylum)	48	0.348	.015
Actinobacteria (class)	48	0.348	.015
Bifidobacteriales	48	0.332	.021
Bifidobacteriaceae	48	0.332	.021
Bifidobacterium	48	0.342	.017
Gammaproteobacteria	48	−0.318	.028
Enterobacteriales	48	−0.305	.035
Pseudomonadales	48	−0.287	.048
Enterobacteriaceae	48	−0.305	.035
Escherichia/Shigella	48	−0.308	.033
Bifidobacterium-specific PCR and T-RFLP (per g of stool)			
Bifidobacterium	48	0.317	.028
B longum	46	0.355	.016
B longum subspecies *infantis*	46	0.343	.020

Taxa at all phylogenetic levels were compared with nutritional status (weight-for-length, length-for-age, and weight-for-age) by using the Spearman-Wilcoxon method as described in Methods using nutritional status as continuous (z score) or categorical (above and below median z score) variables. Significant correlations were found only with length-for age (shown here). Additional positive associations of microbiota with nutritional status were seen with categorical analysis for weight-for-length with *B longum* and *B longum* subspecies *infantis* and a negative association of weight-for-age with *Clostridium*.

SUPPLEMENTAL TABLE 11 Multiple Linear Regression Analysis to Determine Contributions of *Bifidobacterium* Abundance and Length-for-Age *z* Scores to Predict Thymus Size

Variable	Coefficient	SE	*P*
Model $R^2 = 0.2179$ ($P = .013$)			
Intercept	−0.08825	0.14187	.54
Bifidobacterium (relative abundance)	0.14757	0.14334	.31
Length-for-age *z* score	0.36378	0.14307	.015
Interaction	0.28661	0.17065	.10
Model $R^2 = 0.2505$ ($P = .0057$)			
Intercept	−0.05155	0.13803	.71
Bifidobacterium (per g of stool)	0.29036	0.14747	.055
Length-for-age *z* score	0.28641	0.13946	.046
Interaction	0.14743	0.1714	.39
Model $R^2 = 0.3254$ ($P = .001$)			
Intercept	−0.16047	0.13706	.25
B longum (per g of stool)	0.32238	0.13958	.026
Length-for-age *z* score	0.27918	0.13965	.052
Interaction	0.4242	0.1741	.019
Model $R^2 = 0.2951$ ($P = .0023$)			
Intercept	−0.13536	0.1386	.33
B longum subspecies *infantis* (per g of stool)	0.28432	0.14067	.0498
Length-for-age *z* score	0.28209	0.14183	.053
Interaction	0.36648	0.17039	.037

All variables transformed to normalized ranks.