

SUPPLEMENTARY INFORMATION

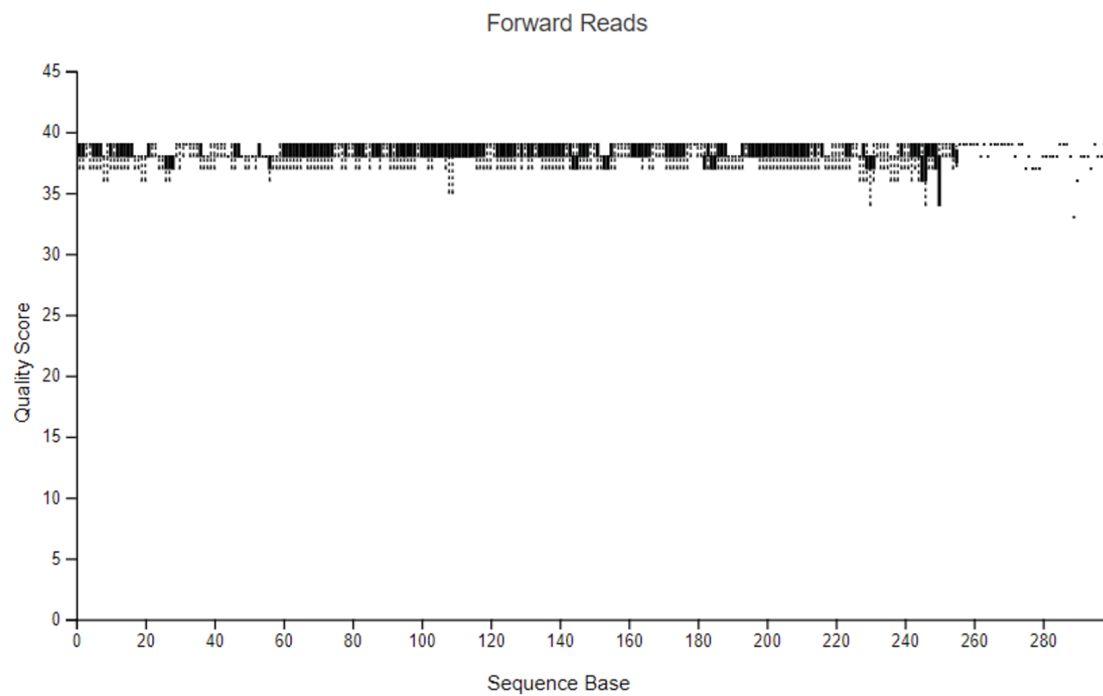


Figure S1. Demultiplexed sequence reads generated using Forward reads only. The anemia FASTQ manifest file was passed through the demultiplex pipeline and visualized on QIIME2 View. The truncation length was chosen based on the quality of the reads, which are consistent throughout. A Phred score of 35 was selected as an arbitrary quality threshold.

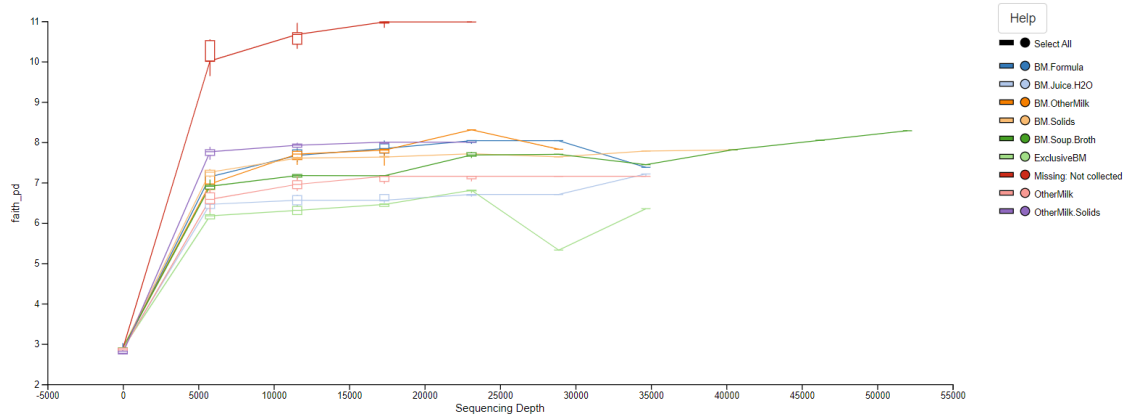


Figure S2. Alpha rarefaction curve filtered for 6-month-old infants. The demultiplexed sequences were denoised and clustered using a pre-trained trained classifier for the F515-R808 primer pair. Sequencing depth of 25090 was chosen based on the saturation point/plateauing of the alpha rarefaction curve.

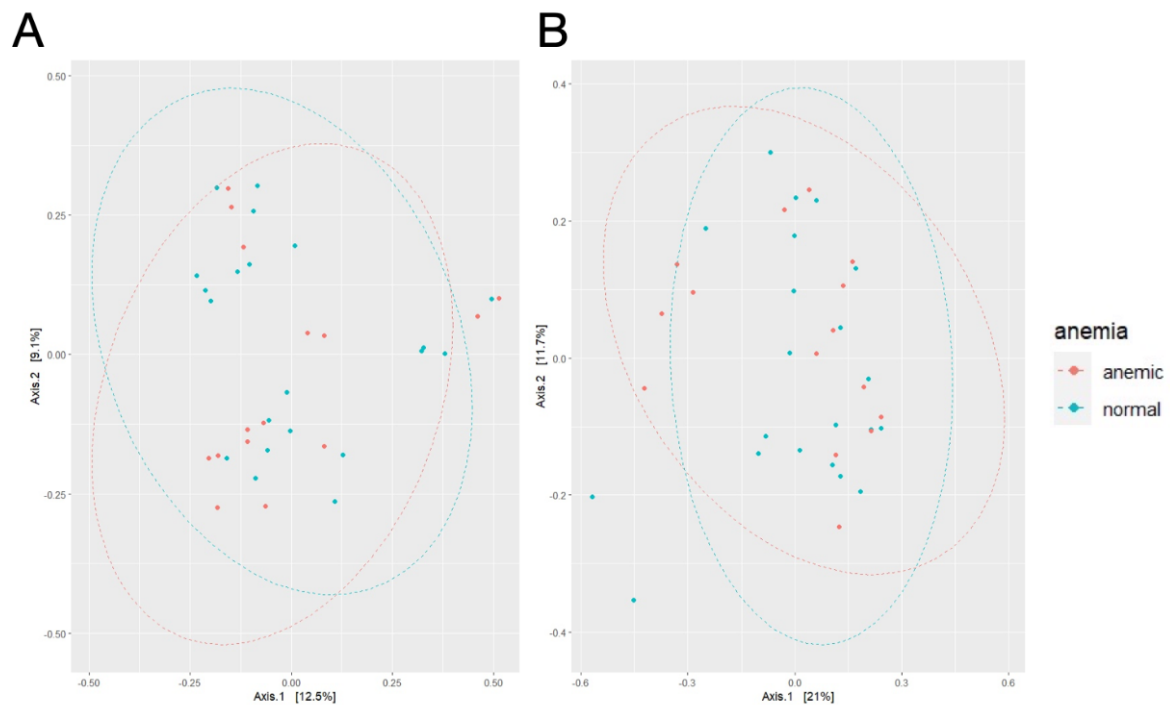


Figure S3. Beta diversity analyses of microbial community between anemic and normal 6-month-old infants. The beta diversity metric was conducted using the (A) unweighted unifrac metric and the (B) Jaccard metric. Blue ellipses show clustering of normal infants and red ellipses show clustering of anemic infants.

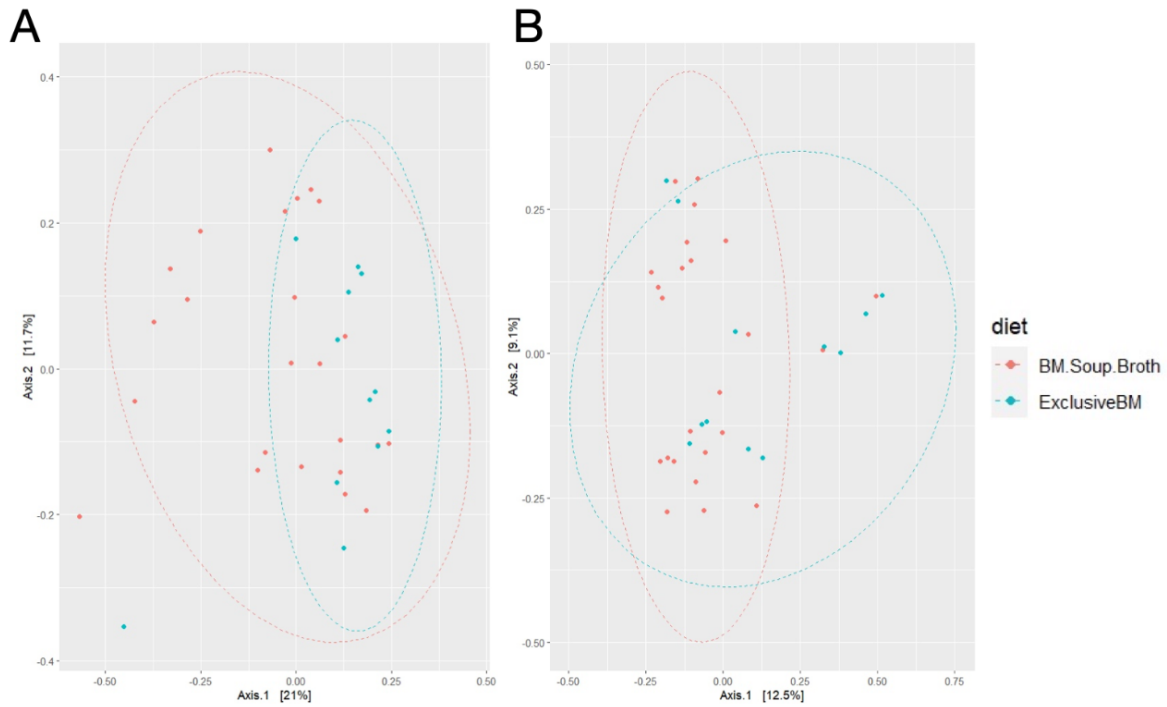


Figure S4. Beta diversity analyses of microbial community across diets in normal 6-month-old infants. The beta diversity metric was conducted using the (A) unweighted unifracs metric and the (B) Jaccard metric. Blue ellipses show clustering of infants fed Breast milk only and red ellipses show clustering of infants fed breast milk with soup and broth.

Table S1. Significantly differentially expressed enzymes in anemic infants fed breast milk only relative to a complete diet. The output of the PICRUST2 pipeline was analyzed in R, and only the significantly up or down-regulated enzymes (Log_2 fold change < 1.5 and $\text{padj} > 0.05$) are shown.

Enzyme	Log_2 fold change	Upregulated Downregulated	Role	Relevance to research question/ Consequence
Thiamine pyrimidinylase	21.0	Upregulated	Pyrimidine catabolism	Increased nitrogen metabolism (49)
Hydroxydechloroatrazine ethyl aminohydrolase	19.6		Hydrolyzes C-N bonds, atrazine degradation (50)	Increased atrazine degradation as energy source in iron-limited environments (51)
Phosphonoacetate hydrolase	19.6		Amino phosphonate metabolism, hydrolyzes C-P bonds (52)	Upregulation of hydrolysis pathways for energy (52)
Cytosol ananyl aminopeptidase	19.6		Release of N-terminal amino acid, particularly alanine (53)	Increased amino acids levels
Scyllo-inositol-2-dehydrogenase(NAD P+)	19.3		NADPH-dependent reduction of scyllo-inosose (SIS) to scyllo-inositol (SI). (54)	Scyllo-inositol may act as siderophore, increase antioxidant activity(55)

4-oxalomesaconate hydratase	18.6	Hydrolyses C-O bonds (56)	Upregulation of hydrolysis pathways for energy
Erythritol kinase	18.5	Phosphorylates erythritol (57)	increased synthesis of amino acids and 2,3-dihydroxybenzoic acid (a siderophore) (57)
Ureidoglycolate amidohydrolase	18.2	Purine catabolism (58)	Increased nitrogen metabolism
Isochorismate lyase	17.5	cleavage of isochorismate to give salicylate and pyruvate (59)	Increased siderophore synthesis (59)
4-hydroxyphenylacetate decarboxylase	17.4	Catalyses formation of p-cresol (60)	Key pathway for bacterial pathogenesis (61)
2,3-diketo-5-methylthiopentyl -1-phosphate enolase	16.7	Methionine salvage pathway (62)	Methionine is starting point for siderophore synthesis (62)
Acyl-CoA oxidase	15.8	Metabolism of Fatty Acids (63)	Increased fatty acid metabolism (64)

Menaquinol oxidase	-29.9	Downregulated	Heme-copper family of oxygen reductases (65)	Hampered growth of <i>Bacillus subtilis</i> , a beneficial commensal organism
Aminoacrobonyl semialdehyde decarboxylase	-18.2		Tryptophan catabolism (66)	Increased chances of inflammation (67)
Glutamyl endopeptidase	-16.9		extracellular bacterial serine proteases (68)	Disbalance in activity contributes to IBD
Galactose-6-phosphate isomerase	-6.7		Galactose metabolism (69)	Impaired ability to use galactose as carbohydrate source (70)
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine	-6.0		Peptidoglycan biosynthesis (71)	Decreased bacterial growth, energy conservation mechanism
Lactocepin	-5.8		Degrades pro-inflammatory cytokines (72)	Increased chances of gut inflammation/IBD
Glyceraldehyde-3-Phosphate-dehydrogenase	-5.7		Glycolysis (73)	Decreased energy metabolism(73)

Glutamyl aminopeptidase	-5.4	Cleaved glutamic and aspartic amino acids from N-terminus of polypeptides (68)	Increases amino acids concentration
Maltose-6-phosphate phosphatase	-4.8	Starch and sucrose metabolism (50)	Decreased energy metabolism
Cellulose synthase (UDP forming)	-4.2	Produces and transports UDP-glucose to the plasma membrane (77)	Decreased production of cellulose for glucan chains(74)
Glucan-1,6-alpha glucosidase	-4.1	Hydrolysis of alpha-D-glucans and oligosaccharides (75)	Decreased energy metabolism