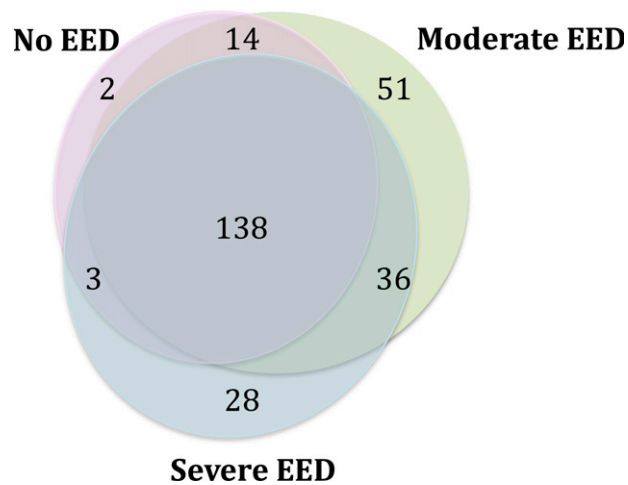


PHYLA	L:M < 0.15 n=8	0.15 ≤ L:M ≤ 0.45 n=49	L:M > 0.45 n=24	ANOVA
<b>Bacteroidetes</b>	63.10 ± 11.64	60.92 ± 14.56	57.47 ± 17.27	0.558
<b>Firmicutes</b>	26.80 ± 8.28	33.49 ± 14.33	36.38 ± 15.00	0.254
<b>Proteobacteria</b>	9.19 ± 5.61	4.22 ± 5.50	4.20 ± 4.59	0.045*
<b>Actinobacteria</b>	0.62 ± 0.73	0.90 ± 1.21	1.49 ± 1.27	0.086
<b>Unclassified_Bacteria</b>	0.10 ± 0.14	0.15 ± 0.21	0.24 ± 0.51	0.438
<b>Tenericutes</b>	0.08 ± 0.20	0.04 ± 0.10	0.06 ± 0.16	0.659
<b>Elusimicrobia</b>	0.06 ± 0.16	0.07 ± 0.35	0.02 ± 0.07	0.774
<b>Fusobacteria</b>	0.04 ± 0.05	0.01 ± 0.01	0.11 ± 0.47	0.297
<b>Cyanobacteria/Chloroplast</b>	0.01 ± 0.01	0.05 ± 0.13	0.04 ± 0.06	0.612
<b>Spirochaetes</b>	0.01 ± 0.01	0.15 ± 0.61	0.00 ± 0.00	0.402

SUPPLEMENTAL FIGURE 1. 16S RNA bacterial sequences represented in fecal samples from 81 Malawian children. Pie charts of average values of relative abundance (percentage of sequences) of the most abundant bacterial phyla found in the fecal microbiota of children with no environmental enteric dysfunction (EED) (lactulose:mannitol [L:M] < 0.15), moderate EED (0.15 ≤ L:M ≤ 0.45), and severe EED.



SUPPLEMENTAL FIGURE 2. Venn diagram represents the 272 different genera present in each lactulose:mannitol (L:M) category of the children studied: no environmental enteric dysfunction (EED) (L:M < 0.15), moderate EED (0.15 ≤ L:M ≤ 0.45), and severe EED (L:M > 0.45).

SUPPLEMENTAL TABLE 1  
Associations of bacterial genera with EED classification

Genera	No EED <sup>1</sup>	Moderate EED <sup>1</sup>	Severe EED <sup>1</sup>	ANOVA test 3 categories no EED, moderate and severe EED	Spearman's correlation coefficient (P value)	Fold-Change (no EED vs. severe EED)	LefSe linear discriminant analyses LDA Score (log 10) >2
<i>Acidaminobacter</i>	0.0004 ± 0.0011	0.0000 ± 0.0000	0.0000 ± 0.0000	0.0089	0.1350	1.0026	
<i>Actinobacillus</i>	0.1247 ± 0.3334	0.0065 ± 0.0142	0.0273 ± 0.1182	0.0387	0.0135	1.96348	>2.5
<i>Allisonella</i>	0.0409 ± 0.0443	0.0612 ± 0.0671	0.0930 ± 0.0688	0.0761	0.0332	-1.43513	
<i>Anaerococcus</i>	0.0007 ± 0.0014	0.0001 ± 0.0004	0.0004 ± 0.0010	0.0370	0.0370	1.00259	3
<i>Anaeroglobus</i>	0.0030 ± 0.0085	0.0008 ± 0.0026	0.0055 ± 0.0132	0.0616	0.0021	-1.01751	>2
<i>Anaeroplasma</i>	0.0727 ± 0.2046	0.0013 ± 0.0069	0.0000 ± 0.0000	0.0097	0.1300	1.65575	
<i>Arthrobacter</i>	0.0004 ± 0.0011	0.0001 ± 0.0004	0.0000 ± 0.0000	0.1395	0.0435	1.0026	
<i>Bacillus</i>	0.0000 ± 0.0000	0.0000 ± 0.0000	0.0006 ± 0.0020	0.0624	0.0291	-1.00434	
<i>Betaproteobacteria_Unclassified</i>	0.0004 ± 0.0011	0.0060 ± 0.0307	0.0000 ± 0.0000	0.5619	0.0071	1.0026	>3
<i>Blautia</i>	0.5490 ± 0.7562	0.6304 ± 0.4992	0.3261 ± 0.3274	0.0479	0.0082	4.6881	
<i>Cetobacterium</i>	0.0180 ± 0.0420	0.0013 ± 0.0056	0.0016 ± 0.0057	0.0071	0.4970	1.12006	
<i>Citrobacter</i>	0.0041 ± 0.0071	0.0002 ± 0.0010	0.0012 ± 0.0034	0.0025	0.3760	1.0201	>2.5
<i>Clostridiaceae_1_Unclassified</i>	0.0251 ± 0.0289	0.0146 ± 0.0359	0.0073 ± 0.0155	0.3371	0.0417	1.13162	
<i>Clostridium_sensu_stricto</i>	0.5722 ± 0.7017	0.3599 ± 0.7218	0.2080 ± 0.4417	0.3628	0.0097	12.4845	>3
<i>Clostridium_XI</i>	0.4700 ± 0.7036	0.2458 ± 0.3686	0.0287 ± 0.0474	0.0064	0.0001	21.2974	>3
<i>Clostridium_XIX</i>	0.0090 ± 0.0220	0.0048 ± 0.0119	0.1041 ± 0.4596	0.2736	0.0106	-1.93294	
<i>Clostridium_XVIII</i>	0.1408 ± 0.1772	0.0966 ± 0.1916	0.0337 ± 0.0577	0.1747	0.0035	2.10117	>2.5
<i>Coprobacillus</i>	0.0296 ± 0.0587	0.0233 ± 0.0444	0.0050 ± 0.0114	0.1328	0.0186	1.1858	
<i>Coprococcus</i>	0.3028 ± 0.5230	0.3395 ± 0.4550	0.3192 ± 0.7738	0.9802	0.0478	-1.12029	
<i>Corynebacterium</i>	0.0000 ± 0.0000	0.0007 ± 0.0017	0.0028 ± 0.0061	0.0499	0.0094	-1.01925	>2.5
<i>Enterobacter</i>	0.4055 ± 0.8506	0.0648 ± 0.1331	0.0574 ± 0.0946	0.0063	0.2290	11.1616	
<i>Enterobacteriaceae_Unclassified</i>	0.6881 ± 1.6563	0.0471 ± 0.0941	0.1356 ± 0.3618	0.0102	0.4720	46.0591	
<i>Erysipelotrichaceae_incertae_sedis</i>	0.5029 ± 0.7094	0.3325 ± 0.5341	0.1775 ± 0.3285	0.2371	0.0284	9.54208	
<i>Erysipelotrichaceae_Unclassified</i>	0.2300 ± 0.4292	0.1440 ± 0.2791	0.0338 ± 0.0711	0.1071	0.0027	3.8956	
<i>Escherichia/Shigella</i>	0.4268 ± 0.6794	0.1007 ± 0.1894	0.1775 ± 0.2932	0.0184	0.6310	5.63191	
<i>Faecalibacterium</i>	6.4128 ± 4.8694	7.5115 ± 6.7945	4.1582 ± 3.9255	0.0821	0.0214	6.12E+06	>4
<i>Fusobacteriales_Unclassified</i>	0.0022 ± 0.0042	0.0005 ± 0.0014	0.0000 ± 0.0000	0.0061	0.0121	1.0157	
<i>Fusobacterium</i>	0.0116 ± 0.0304	0.0021 ± 0.0043	0.0029 ± 0.0053	0.0531	0.9370	1.06242	
<i>Gemmiger</i>	0.0146 ± 0.0187	0.0080 ± 0.0159	0.0066 ± 0.0134	0.4467	0.0286	1.05701	
<i>Haemophilus</i>	0.7502 ± 1.1655	0.1285 ± 0.1530	0.1336 ± 0.2278	0.0003	0.0345	71.7567	
<i>Klebsiella</i>	0.6440 ± 1.8117	0.0333 ± 0.2151	0.0002 ± 0.0012	0.0164	0.0320	86.6513	>3
<i>Kocuria</i>	0.0011 ± 0.0022	0.0001 ± 0.0006	0.0000 ± 0.0000	0.0036	0.2160	1.00782	
<i>Lachnobacterium</i>	0.0026 ± 0.0054	0.0021 ± 0.0052	0.0015 ± 0.0052	0.8310	0.0275	1.00777	
<i>Lachnospiraceae_Unclassified</i>	1.2701 ± 1.0673	1.4919 ± 1.2200	1.2138 ± 1.8659	0.7167	0.0238	1.47682	
<i>Lactobacillaceae_Unclassified</i>	0.0000 ± 0.0000	0.0048 ± 0.0123	0.0088 ± 0.0142	0.1864	0.0098	-1.06254	>2
<i>Lactobacillales_Unclassified</i>	0.0045 ± 0.0068	0.0266 ± 0.0602	0.0380 ± 0.0575	0.3469	0.0350	-1.26105	
<i>Lactococcus</i>	0.0105 ± 0.0197	0.0106 ± 0.0511	0.0003 ± 0.0008	0.5780	0.0130	1.07353	
<i>Leuconostoc</i>	0.0682 ± 0.1880	0.0022 ± 0.0091	0.0000 ± 0.0000	0.0092	0.0066	1.60402	>2.5
<i>Megasphaera</i>	2.7955 ± 7.2795	3.1740 ± 6.0261	12.0244 ± 12.7508	0.0003	0.0077	-6.05E+27	>4.5
<i>Mitsuokella</i>	0.0832 ± 0.1830	0.4976 ± 0.9385	1.3349 ± 1.6813	0.0067	0.0053	-5859.95	>3.5
<i>Moraxella</i>	0.0007 ± 0.0014	0.0000 ± 0.0000	0.0008 ± 0.0022	0.0390	0.3640	-1.00002	>3
<i>Neisseria</i>	0.0067 ± 0.0108	0.0024 ± 0.0046	0.0115 ± 0.0237	0.0325	0.1430	-1.0335	
<i>Olsenella</i>	0.2292 ± 0.5724	0.1233 ± 0.2824	0.4793 ± 0.6936	0.0125	0.0139	-5.66382	>3
<i>Oribacterium</i>	0.0041 ± 0.0032	0.0033 ± 0.0061	0.0039 ± 0.0153	0.9566	0.0086	1.0016	>2
<i>Pasteurella</i>	0.0116 ± 0.0192	0.0025 ± 0.0050	0.0054 ± 0.0105	0.0274	0.2640	1.0442	
<i>Pasteurellaceae_Unclassified</i>	0.0461 ± 0.0837	0.0071 ± 0.0115	0.0145 ± 0.0312	0.0072	0.8590	1.2446	
<i>Phocoenobacter</i>	0.0022 ± 0.0052	0.0002 ± 0.0007	0.0004 ± 0.0014	0.0153	0.1330	1.01305	
<i>Pragia</i>	0.0007 ± 0.0021	0.0001 ± 0.0004	0.0000 ± 0.0000	0.0331	0.2580	1.00521	
<i>Raoultella</i>	0.0288 ± 0.0815	0.0002 ± 0.0013	0.0000 ± 0.0000	0.0093	0.3400	1.22119	
<i>Roseburia</i>	0.7379 ± 0.6209	1.2583 ± 1.7382	0.5931 ± 0.9121	0.1689	0.0213	2.72723	

(continued)

SUPPLEMENTAL TABLE 1  
Continued

Genera	No EED <sup>1</sup>	Moderate EED <sup>1</sup>	Severe EED <sup>1</sup>	ANOVA test3 categories moderate and severe EED	Spearman's correlation coefficient (P value)	Fold-Change (no EED vs. severe EED)	LefSe linear discriminate analyses LDA Score(log 10) >2
<i>Salmonella</i>	0.0367 ± 0.0524	0.0058 ± 0.0130	0.0419 ± 0.1064	0.0455	0.3600	-1.03698	
<i>Schwartzia</i>	0.0004 ± 0.0011	0.0000 ± 0.0000	0.0000 ± 0.0000	0.0089	0.1040	1.0026	
<i>Streptococcus</i>	2.4028 ± 2.8099	2.0381 ± 4.5856	2.1341 ± 6.5959	0.9823	0.0360	6.43869	
<i>Subdoligranulum</i>	0.2673 ± 0.2737	0.2359 ± 0.2880	0.0813 ± 0.1184	0.0348	0.0013	3.63018	3
<i>Succinivibrio</i>	5.3763 ± 5.4325	2.2617 ± 4.2070	0.7123 ± 2.0520	0.0140	0.0034	1.10E+14	>4
<i>Sutterella</i>	0.0513 ± 0.1013	0.1540 ± 0.2653	0.4689 ± 0.5102	0.0008	0.0002	-18.0796	>3
<i>Syntrophococcus</i>	0.0671 ± 0.0551	0.0650 ± 0.1163	0.0277 ± 0.0796	0.3241	0.0004	1.3138	>2
<i>Turicibacter</i>	0.0198 ± 0.0381	0.0147 ± 0.0330	0.0005 ± 0.0014	0.0908	0.0036	1.1435	>2
<i>Veillonellaceae_ Unclassified</i>	0.0251 ± 0.0398	0.0237 ± 0.0298	0.0547 ± 0.0512	0.0060	0.0043	-1.22749	>2
<i>Yokenella</i>	0.0015 ± 0.0032	0.0001 ± 0.0006	0.0001 ± 0.0006	0.0061	0.2080	1.00956	

<sup>1</sup>Genera abundance (% of total bacterial) data are expressed as: means ± standard deviations (SD).