Supplementary Information

Figure S1 The Shannon and Simpson indices were used to estimate diversity (i.e., a combined assessment of the number of 97% similar bacterial taxa and their abundance) of infancy fecal microbiota between infants with and without food allergy (Data shown as mean with SEM).

Figure S2 Rarefaction curves were used to estimate richness (in this case the number of taxa at a 97% similarity level) of infancy fecal microbiota between infants with and without food allergy. The vertical axis shows the number of OTUs that would be expected to be found after sampling the number of tags or sequences shown on the horizontal axis (A). Rank abundance curve of bacterial OTUs derived from two groups (B).

Figure S3 Rarefaction analysis of pyrosequencing tags in infancy fecal microbiota from infants with food allergy (n=34) and healthy controls (n=45).

Figure S4 Differentiation in bacterial communities from all infants (interindividual variations). Community differentiation was measured by using the unweighted UniFrac algorithm; the scale bar indicated the distance between clusters in UniFrac units. Red bars showed the infants with IgE-mediated food allergy, while green bars showed the infants with non-IgE-mediated food allergy.

Figure S5 3D PCoA plots of individual fecal microbiota in infants with IgE-mediated food allergy infants (n=17), non-IgE-mediated food allergy infants (n=17) and healthy controls (n=45) obtained by Mothur program and Sigmaplot. Each symbol represents a sample. Infancy fecal microbiota from infants with food allergy and healthy controls, IgE-mediated and non-IgE-mediated almost group together.

Figure S6 A Venn diagram illustrating overlap of OTUs in fecal microbiota between infants with and without food allergy.

Figure S7 Percent relative abundance for the genus *Clostridium sensu stricto* is depicted across all food allergy samples, demonstrating an IgE-mediated food allergy enrichment in most individuals.

Table S1 List of the 79 10-bp barcodes used to tag each PCR product analyzed as part of the study.

Table S2 Comparison of phylotypes coverage and diversity estimation of the 16S rRNA gene libraries for individuals at 97% similarity from the pyrosequencing analysis.

Table S3 Differences in bacterial abundances between infants with and without food allergy in the phylum level.

Table S4 Differences in bacterial abundances between infants with and without food allergy in the genus level.

Figure S1

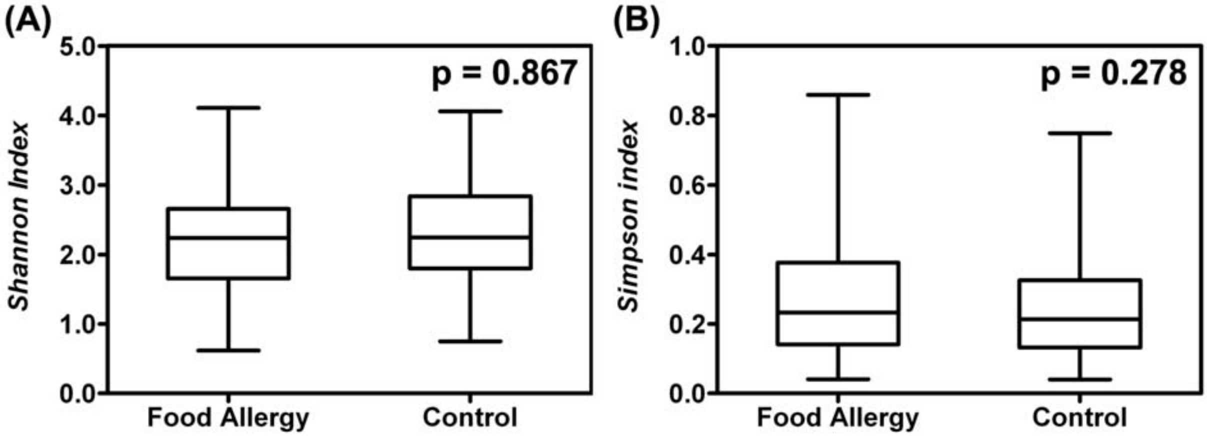

(A)
Shannon Index
5.0
4.0
3.0
2.0
1.0
0.0
p = 0.867
Food Allergy
Control
(B)
Simpson index
1.0
0.8
0.6
0.4
0.2
0.0
p = 0.278
Food Allergy
Control

Figure S2

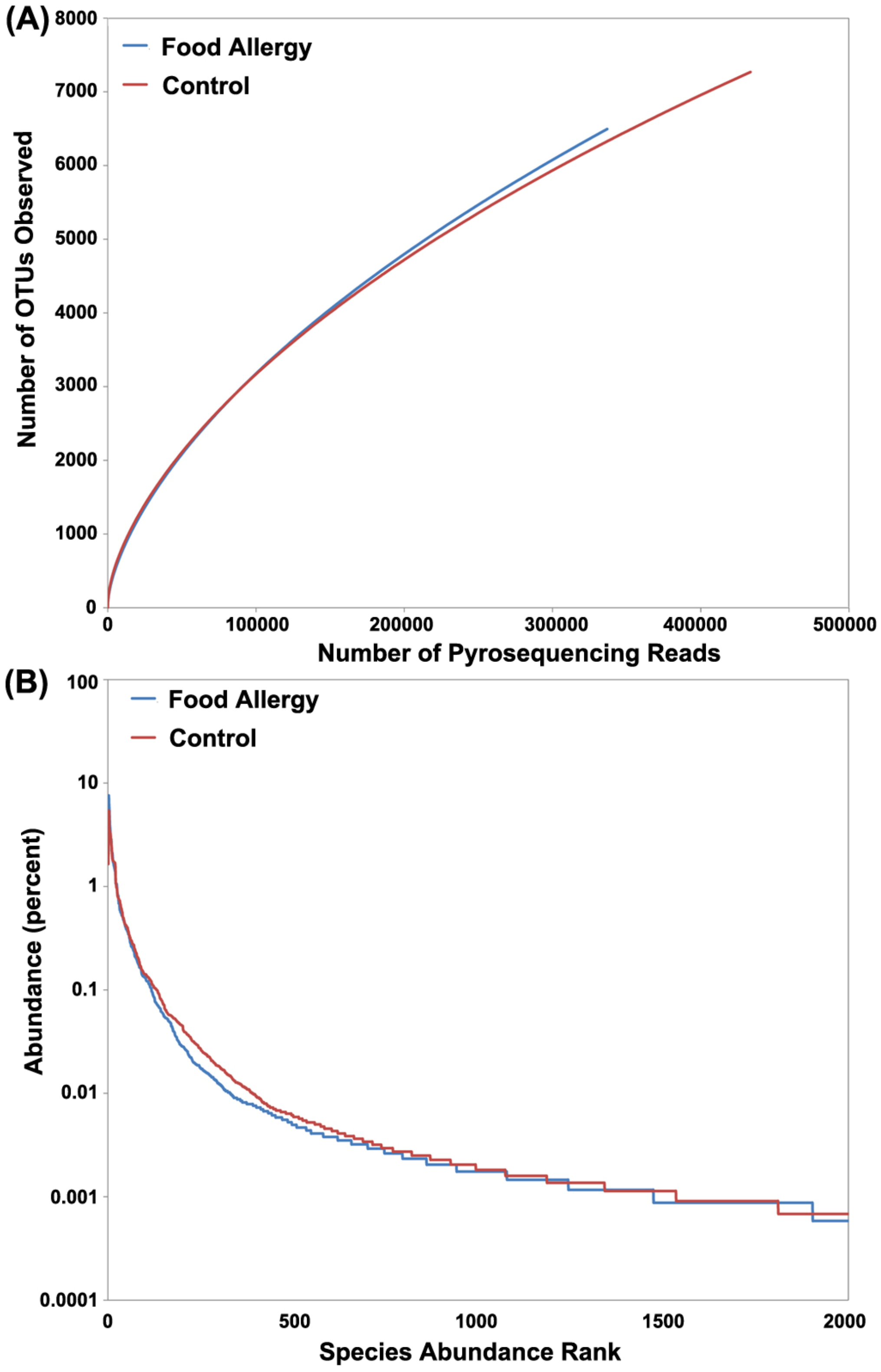
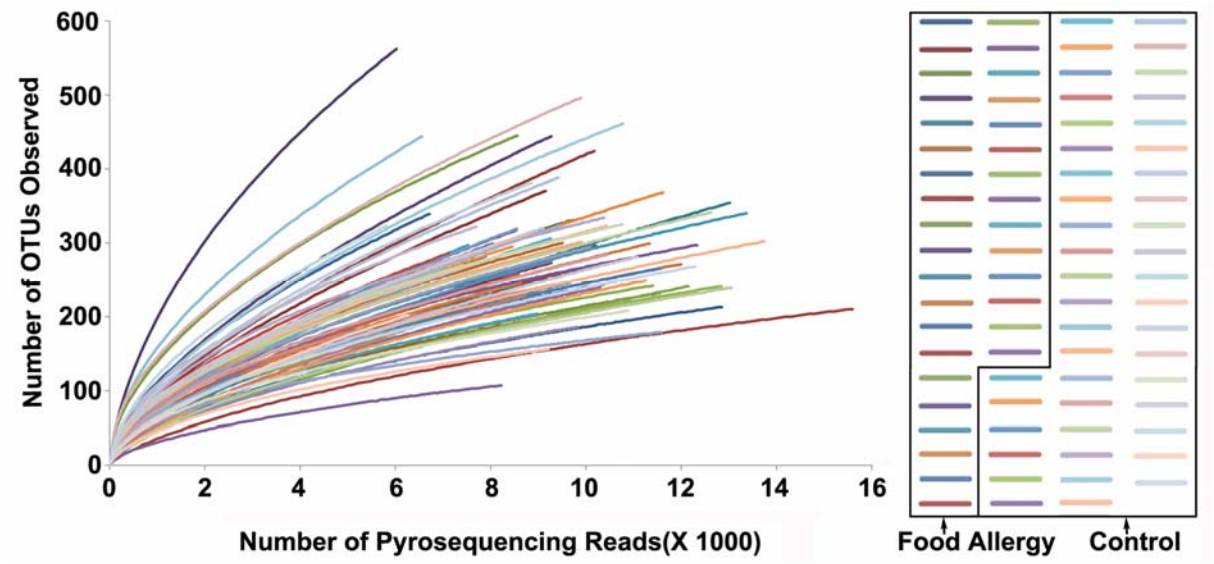

(A)
Food Allergy
Control
Number of OTUs Observed
0
1000
2000
3000
4000
5000
6000
7000
8000
0
100000
200000
300000
400000
500000
Number of Pyrosequencing Reads
(B)
Food Allergy
Control
Abundance (percent)
100
10
1
0.1
0.01
0.001
0.0001
0
500
1000
1500
2000
Species Abundance Rank

Figure S3



Number of OTUs Observed
0
100
200
300
400
500
600
0
2
4
6
8
10
12
14
16
Number of Pyrosequencing Reads(X 1000)
Food Allergy
Control

Figure S4

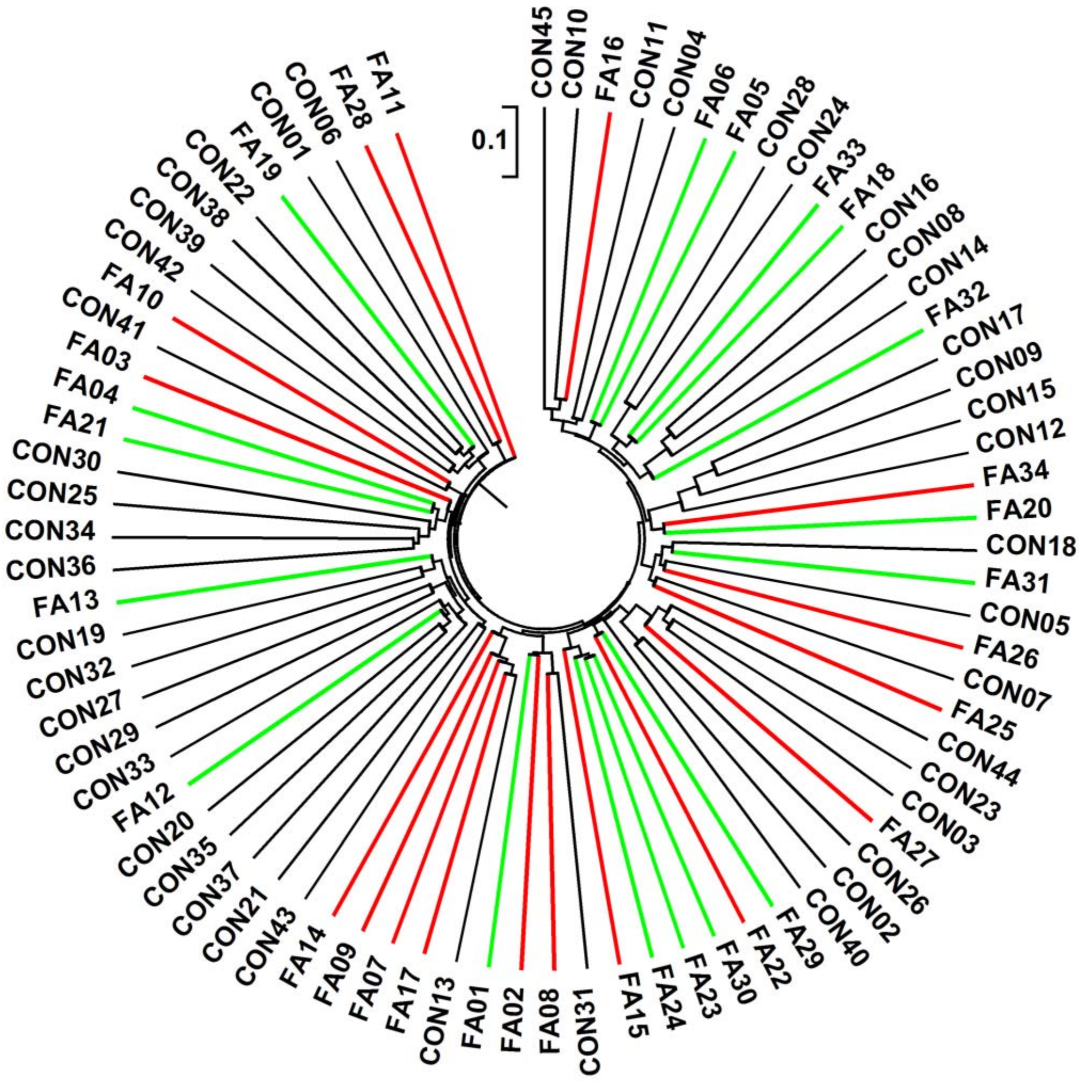
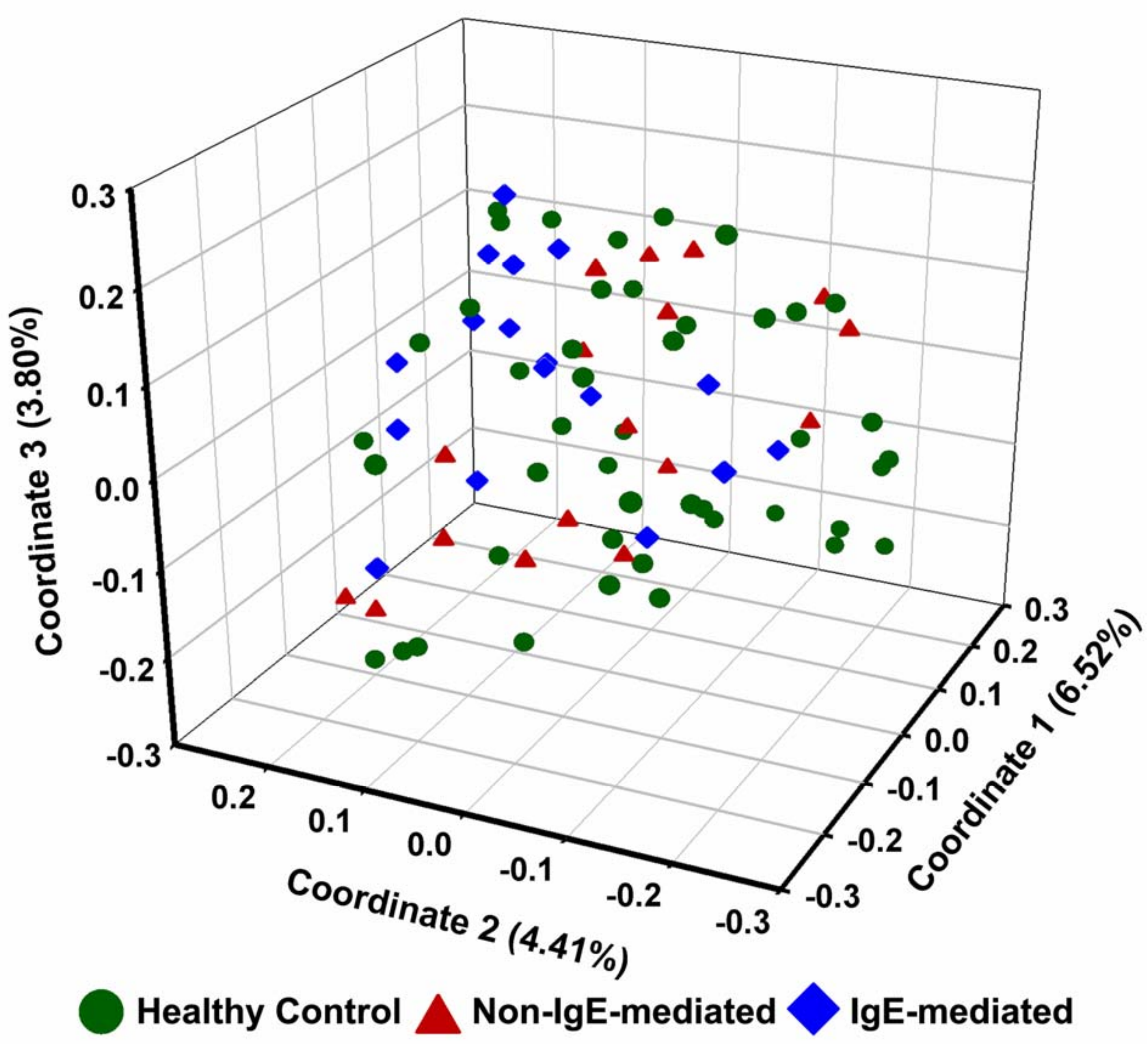

0.1
CON45
CON10
FA16
CON11
CON04
FA06
FA05
CON28
CON24
FA33
FA18
CON16
CON08
CON14
FA32
CON17
CON09
CON15
CON12
FA34
FA20
CON18
FA31
CON05
FA26
CON07
FA25
CON44
CON23
CON03
FA27
CON26
CON02
CON40
FA29
FA22
FA30
FA23
FA24
FA15
CON31
FA08
FA02
FA01
CON13
FA17
FA07
FA09
FA14
CON43
CON21
CON37
CON35
CON20
FA12
CON33
CON29
CON27
CON32
CON19
FA13
CON36
CON34
CON25
CON30
FA21
FA04
FA03
CON41
FA10
CON42
CON39
CON38
CON22
FA19
CON01
CON06
FA28
FA11

Figure S5



Coordinate 3 (3.80%)
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Coordinate 2 (4.41%)
0.2
0.1
0.0
-0.1
-0.2
-0.3
Coordinate 1 (6.52%)
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
● Healthy Control
▲ Non-IgE-mediated
◆ IgE-mediated

Figure S6

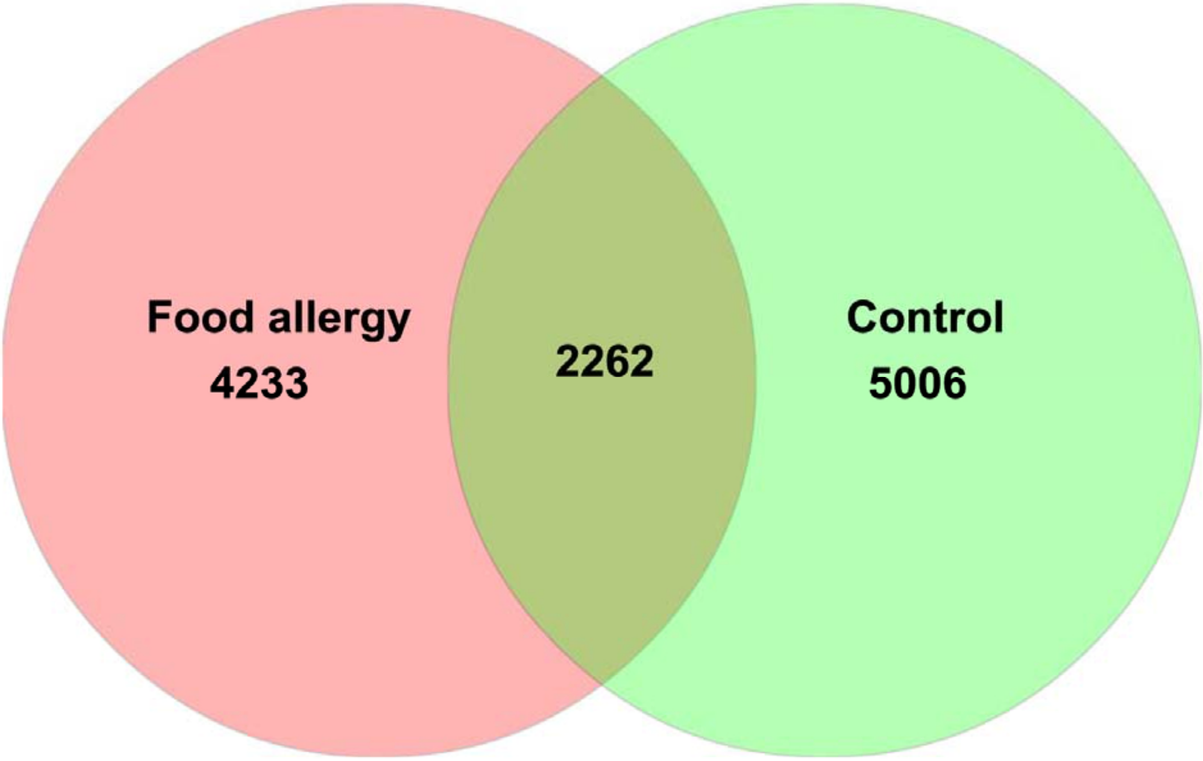


Figure S7

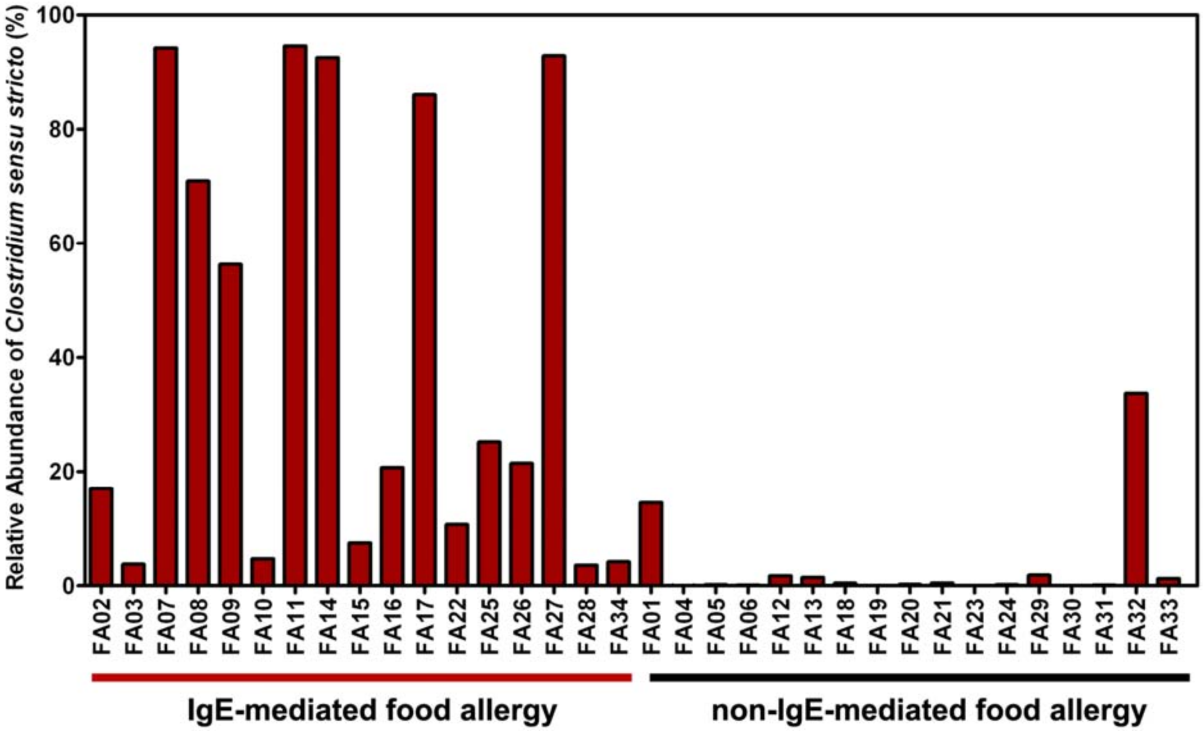

Relative Abundance of *Clostridium sensu stricto* (%)
100
80
60
40
20
0
FA02
FA03
FA07
FA08
FA09
FA10
FA11
FA14
FA15
FA16
FA17
FA22
FA25
FA26
FA27
FA28
FA34
FA01
FA04
FA05
FA06
FA12
FA13
FA18
FA19
FA20
FA21
FA23
FA24
FA29
FA30
FA31
FA32
FA33
IgE-mediated food allergy
non-IgE-mediated food allergy

Table S1 List of the 79 10-bp barcodes used to tag each PCR product analyzed as part of the study

Sample ID	Barcode	Sample ID	Barcode
FA01	CTCTACAGCG	CON07	ATCTGAGACG
FA02	CTGTCGTGCG	CON08	ATGCTACGTC
FA03	CTGTGACGTG	CON09	ATGTGACTAC
FA04	GACGCTGTCG	CON10	CACGAGACAG
FA05	GACGTATGAC	CON11	CACGCGAGTC
FA06	GACTAGCTAG	CON12	ACTCGCGTCG
FA07	GAGACGTCGC	CON13	CACGCTACGA
FA08	GAGAGAGACG	CON14	AGACTCGACG
FA09	GCGTAGACTA	CON15	CACGTGTATA
FA10	GCTCTCTACG	CON16	CACTACGATG
FA11	GTACACTGTA	CON17	CACTATACTC
FA12	GTACGCGACA	CON18	CAGCGTACTG
FA13	GTACTATAGA	CON19	CAGTCTCTAG
FA14	GTACTGAGTC	CON20	CATAGTCGCG
FA15	GTAGCTAGCG	CON21	CGAGACACTA
FA16	GTAGTCACTG	CON22	CGAGAGTGTG
FA17	GTAGTGTCAC	CON23	CGAGTCATCG
FA18	GTATACATAG	CON24	CGATCGTATA
FA19	GTCATCGTCG	CON25	CGCAGTACGC
FA20	GTCGACACGC	CON26	CGCGATCGTA
FA21	GTCGAGTGAG	CON27	CGCGCTATAC
FA22	GTCTACTATC	CON28	AGTACGAGAG
FA23	GTGTCTAGAC	CON29	CGTACAGATA
FA24	GTGTGTATCG	CON30	CGTAGCTCTC
FA25	ACACGACGAC	CON31	CGTATAGTGC
FA26	ACACGTAGTA	CON32	CGTCAGCGAC
FA27	ACACTACTCG	CON33	CGTCGCAGTG
FA28	ACGACACGTA	CON34	CGTCTCACGA
FA29	ACGAGTAGAC	CON35	CGTGACTCAG
FA30	ACGCGTCTAG	CON36	CTACACGCTC
FA31	ACGTACACAC	CON37	CTACGATATG
FA32	ACGTACTGTG	CON38	CTAGACAGAC
FA33	ACGTAGATCG	CON39	CTAGTACTCA
FA34	ACTACGTCTC	CON40	CTATATGTCG
CON01	ATAGAGCTAG	CON41	CTATCGACAC
CON02	ATATAGAGTA	CON42	CTATGTAGAG
CON03	ATCGCTCACG	CON43	CTCACGTACA
CON04	ATCGTCAGTC	CON44	CTCGAGTCTC
CON05	ACTATACGAG	CON45	CTCGTCGAGA
CON06	ATCTCTCGTA		

Table S2 Comparison of phylotypes coverage and diversity estimation of the 16S rRNA gene libraries for individuals at 97% similarity from the pyrosequencing analysis

Sample	Reads	OTUs	Good's	ACE	Chao 1	Shannon	Simpson
FA01	7894	282	97.75%	1249	708	2.4839	0.1882
FA02	9271	273	98.23%	1115	564	2.1561	0.2956
FA03	9734	331	98.04%	1186	701	2.7608	0.1332
FA04	6023	562	94.95%	1452	1193	4.1087	0.0479
FA05	9172	252	98.22%	1098	640	2.4762	0.1392
FA06	9546	204	98.84%	593	415	2.4291	0.1876
FA07	12851	213	99.12%	557	405	0.7498	0.7998
FA08	9153	370	97.40%	1957	1075	2.3229	0.3215
FA09	9029	254	98.14%	1295	692	2.1876	0.1900
FA10	9272	444	96.95%	2070	1258	2.9092	0.1468
FA11	13021	354	98.23%	1408	828	0.6154	0.8596
FA12	9504	300	98.32%	982	565	2.8613	0.1202
FA13	6716	339	97.04%	1238	777	3.3446	0.0844
FA14	10172	424	97.25%	2493	1205	2.4862	0.2272
FA15	11550	232	98.92%	740	467	1.6382	0.4904
FA16	8513	232	98.44%	824	598	1.5972	0.4395
FA17	10612	247	98.82%	553	468	1.6612	0.4522
FA18	11996	271	98.80%	722	495	1.9684	0.3481
FA19	10214	296	98.43%	745	573	1.8843	0.3614
FA20	15596	210	99.28%	557	364	0.9454	0.6054
FA21	8559	445	97.29%	1146	864	3.9579	0.0409
FA22	8530	317	97.66%	1358	841	2.7586	0.1415
FA23	9653	246	98.54%	781	586	1.6405	0.4214
FA24	11335	299	98.48%	998	619	1.9241	0.3146
FA25	8046	299	97.55%	2171	989	3.0146	0.0938
FA26	9993	267	98.46%	810	554	2.4498	0.1515
FA27	12152	241	98.68%	1193	730	0.8035	0.7808
FA28	4031	113	98.61%	268	204	1.6401	0.3409
FA29	13369	340	98.59%	1121	749	2.6232	0.1809
FA30	8630	246	98.34%	777	545	2.0980	0.2381
FA31	8222	183	98.71%	638	382	2.4120	0.1399
FA32	10830	277	98.41%	879	697	2.2933	0.1752
FA33	11403	242	98.91%	610	480	1.9481	0.3215
FA34	12334	297	98.79%	698	612	2.0151	0.3361
CON01	7530	297	97.41%	1594	747	2.6497	0.1386
CON02	11615	368	98.02%	1622	865	2.8040	0.1157
CON03	11537	265	98.74%	712	547	1.7204	0.3325
CON04	7129	286	97.63%	1208	650	2.9835	0.1191
CON05	12840	241	98.95%	448	462	2.1425	0.1852
CON06	8227	107	99.30%	300	194	0.7495	0.7490
CON07	8976	204	98.71%	677	451	1.3170	0.5715

CON08	8454	295	97.92%	1053	630	1.8024	0.3287
CON09	9270	275	98.23%	750	572	1.9956	0.2519
CON10	8584	257	98.16%	1094	657	2.2970	0.1974
CON11	6934	265	97.74%	1053	625	2.7636	0.1322
CON12	10300	240	98.64%	702	439	2.2481	0.1616
CON13	9264	306	97.94%	1126	718	2.1350	0.2386
CON14	11258	249	98.66%	860	539	1.9881	0.2215
CON15	8549	319	97.56%	1248	837	2.5908	0.1439
CON16	8712	228	98.30%	1154	539	2.0375	0.2325
CON17	6978	265	97.52%	1051	703	2.0383	0.2864
CON18	9823	186	98.95%	519	355	1.5704	0.4401
CON19	8726	220	98.71%	547	438	2.2071	0.2334
CON20	9912	301	98.38%	835	601	2.8027	0.1323
CON21	11578	179	99.33%	374	296	1.5564	0.4987
CON22	9648	247	98.75%	623	449	2.2457	0.2929
CON23	13056	239	98.98%	702	476	1.0206	0.6678
CON24	10076	294	98.42%	861	536	2.8797	0.1041
CON25	6558	444	96.19%	1495	1079	4.0590	0.0400
CON26	13741	302	98.76%	908	730	1.7628	0.3232
CON27	9464	323	97.87%	1696	903	3.2146	0.0835
CON28	10456	284	98.45%	938	767	2.6186	0.1498
CON29	12631	341	98.50%	1276	779	2.8830	0.1533
CON30	10380	334	98.44%	763	618	2.6092	0.1857
CON31	10778	461	97.49%	1622	1007	2.6566	0.2352
CON32	10431	323	98.26%	1080	720	2.2482	0.2882
CON33	9416	388	97.49%	1478	954	2.8757	0.1568
CON34	9892	496	97.22%	1887	1050	3.9979	0.0534
CON35	10762	325	98.47%	814	633	2.9035	0.1218
CON36	7697	322	97.77%	976	656	3.1291	0.1263
CON37	9100	320	97.79%	1757	878	3.1819	0.0815
CON38	9211	156	99.16%	351	283	1.2213	0.5708
CON39	8858	381	97.53%	1255	772	2.6568	0.1652
CON40	8866	314	97.89%	1486	760	3.1390	0.0989
CON41	10888	208	99.03%	547	440	1.6200	0.4921
CON42	11085	281	98.40%	1376	661	1.4205	0.5577
CON43	5808	323	96.87%	1068	756	2.7679	0.2132
CON44	6268	202	97.91%	917	506	2.0833	0.2324
CON45	12288	268	98.81%	821	539	1.7970	0.3734

Abbreviations: FA, food allergy; CON, healthy control.

Table S3 Differences in bacterial abundances between infants with and without food allergy in the phylum level

Phylum	**Healthy Control**		**Food Allergy**		**Metastats P value**	**Metastats Q value**[2]
	Mean	**SE**[1]	**Mean**	**SE**		
Firmicutes	65.1942%	0.0723%	70.9426%	0.0782%	0.0000E+00	0.0000E+00
Bacteroidetes	18.5105%	0.0590%	16.0376%	0.0632%	3.5967E-177	3.6137E-176
Proteobacteria	13.6629%	0.0522%	11.7269%	0.0554%	2.7742E-140	2.0905E-139
Actinobacteria	1.2238%	0.0167%	1.1258%	0.0182%	8.0713E-05	3.4755E-04

[1] SE: standard error.

[2] A comparison of fecal microbiota between infants with and without food allergy was performed using Metastats. Q value indicates that the false discovery rate and that a lower value is generally preferred to avoid a false positive result.

Table S4 Differences in bacterial abundances between infants with and without food allergy in the genus level

Phylum	**Genus**	**Healthy Control**		**Food Allergy**		**Metastats P value**	**Metastats Q value**
		Mean	**SE**	**Mean**	**SE**		
Firmicutes	Clostridium sensu stricto	10.6847%	0.0469%	24.4033%	0.0740%	0.0000E+00	0.0000E+00
Bacteroidetes	Bacteroides	16.8892%	0.0569%	14.0645%	0.0599%	4.2370E-251	1.0356E-249
Firmicutes	Streptococcus	12.3256%	0.0499%	8.5618%	0.0482%	0.0000E+00	0.0000E+00
Firmicutes	Enterococcus	2.3616%	0.0231%	8.2707%	0.0475%	0.0000E+00	0.0000E+00
Firmicutes	Veillonella	13.5559%	0.0520%	7.5845%	0.0456%	0.0000E+00	0.0000E+00
Proteobacteria	Escherichia/Shigella	6.1238%	0.0364%	7.3779%	0.0450%	4.2412E-106	7.5065E-105
Proteobacteria	Klebsiella	3.6074%	0.0283%	3.1108%	0.0299%	7.1452E-33	8.1497E-32
Firmicutes	Lactobacillus	1.4427%	0.0181%	3.0401%	0.0296%	0.0000E+00	0.0000E+00
Firmicutes	Staphylococcus	0.4472%	0.0101%	2.2658%	0.0256%	0.0000E+00	0.0000E+00
Firmicutes	Faecalibacterium	1.5428%	0.0187%	1.8434%	0.0232%	2.1470E-24	2.1192E-23
Firmicutes	Clostridium XIVa	0.8797%	0.0142%	1.7906%	0.0228%	5.9084E-273	1.5163E-271
Firmicutes	Blautia	2.3702%	0.0231%	1.7137%	0.0224%	4.9362E-89	7.9174E-88
Firmicutes	Anaerostipes	0.0039%	0.0010%	1.5448%	0.0212%	0.0000E+00	0.0000E+00
Bacteroidetes	Prevotella	0.8899%	0.0143%	1.3923%	0.0202%	9.1911E-97	1.5218E-95
Firmicutes	Clostridium XVIII	0.5277%	0.0110%	1.2935%	0.0195%	1.8086E-284	4.8858E-283
Firmicutes	Flavonifractor	0.7967%	0.0135%	1.0029%	0.0172%	1.1204E-21	1.0649E-20
Firmicutes	Clostridium XI	1.2912%	0.0171%	0.6052%	0.0134%	1.4158E-199	3.0278E-198
Firmicutes	Lachnospiracea_incertae_sedis	1.5624%	0.0188%	0.5521%	0.0128%	0.0000E+00	0.0000E+00
Firmicutes	Megamonas	1.3119%	0.0173%	0.0217%	0.0025%	0.0000E+00	0.0000E+00
Firmicutes	Megasphaera	1.2344%	0.0168%	0.0157%	0.0022%	0.0000E+00	0.0000E+00