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Supplementary Materials for

Biodiversity intervention enhances immune regulation and health-associated commensal microbiota among daycare children

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Table S1. Characteristics of study participants.

Kruskal-Wallis tests showed that there are no differences in days spent in daycare centers or summer cottage, sick days, outdoor recreation (Home yard, neighborhood or nature), animal contact, nutrition (berries and vegetables) and number of siblings between children in intervention, standard and nature-oriented daycares.

Days spend in daycares, summer cottage, and siblings and sick days during the intervention period are presented as mean ± standard deviation (sd).

Outdoor recreation and animal contact during the intervention period are presented at nominal scale (median ± confidence level 95% = cl):

1 = not at all, 2 = rarely, 3 = weekly, 4 = almost daily and 5 = daily.

Nutrition is presented at nominal scale (median ± confidence level 95% = cl):

1 = not at all, 2 = occasionally, 3 = frequently.

	Intervention		**Standard**		**Nature-oriented**		**Kruskal-Wallis test**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Chi-squared**	**P value**
Daycare days	15.800	3.398	14.333	2.664	14.864	3.468	2.169	0.338
Sick days	0.567	0.898	1.233	2.499	0.591	0.908	0.086	0.958
Days in summer cottage	0.967	1.866	0.600	0.910	1.364	1.814	2.176	0.337
Siblings	1.133	0.937	0.867	0.834	1.455	0.963	3.768	0.152
	Median	**cl**	**Median**	**cl**	**Median**	**cl**	**Chi-squared**	**P value**
Outdoor recreation home yard	4	0.431	4	0.700	5	0.265	4.166	0.125
Outdoor recreation surrounding neighbourhood	4	0.300	4	0.478	3	0.333	4.822	0.090
Outdoor recreation nature	3	0.305	2	0.412	2.5	0.380	1.543	0.462
Animal contact	2	0.261	2	0.532	2	0.237	2.605	0.272
Nutrition berries	2	0.194	2	0.310	2	0.202	0.160	0.923
Nutrition vegetables	2	0.300	2	0.390	2	0.271	1.533	0.465

Table S2. Bacterial community composition (PERMANOVA) comparisons in soil (A-C), on skin (D) and in the gut (E and F) between daycare groups. Differences in surface soil bacterial communities (**A**) between intervention and standard daycare centers after the intervention and (**B**) before-after comparisons at class level. (**C**) Comparison of beta-diversity of surface soil bacterial communities between intervention and standard (PERMDISP) daycare soils at genus level after the intervention period. Community composition of bacteria (**D**) on skin at OTU level differed between children in nature-oriented and children in standard daycares at baseline. (**E**) Gut Ruminococcaceae community differed between nature-oriented and standard at baseline, and after intervention period also between children in intervention and standard daycares. (**F**) *Faecalibacterium* community composition in the gut differed between children in nature-oriented and standard daycares after the intervention period. The leftmost panel indicates groups and time points compared. Both relative abundance (left) and presence absence data (right) were compared. PERMANOVA statistics are reported as F statistics, R2 = Coefficient of determination, probability P value and Benjamini-Hochberg adjusted P value and PERMDISP results as F statistics, mean ± sd, P value and Benjamini-Hochberg adjusted P value.

	ABUNDANCE DATA				**PRESENCE/ABSENCE DATA**			
A) Soil: Intervention vs Standard	**F value**	**R2**	**P value**	**P adjust***	**F value**	**R2**	**P value**	**P adjust***
OTU level	2.053	0.079	**0.024**	**0.048**	2.226	0.085	**0.017**	0.102
Genus level	2.368	0.090	**0.023**	**0.048**	1.729	0.067	0.083	0.166
Family level	2.500	0.094	**0.021**	**0.048**	1.486	0.058	0.163	0.244
Order level	2.126	0.081	**0.049**	**0.074**	1.321	0.052	0.244	0.244
Class level	1.840	0.071	0.072	0.086	1.476	0.058	0.227	0.244
Phylum level	1.945	0.075	0.101	0.101	2.827	0.105	0.059	0.166
Phylum Proteobacteria	2.179	0.083	**0.018**	**0.030**	2.083	0.080	**0.022**	**0.037**
Phylum Bacteroidetes	2.014	0.077	**0.011**	**0.030**	2.393	0.091	**0.017**	**0.037**
Phylum Actinobacteria	2.240	0.085	**0.014**	**0.030**	2.720	0.102	**0.015**	**0.037**
Phylum Acidobacteria	2.016	0.077	**0.024**	**0.030**	1.991	0.077	**0.039**	**0.049**
Phylum Verrucomicrobia	1.544	0.060	0.084	0.084	1.615	0.063	0.111	0.111
Class Actinobacteria	2.229	0.085	**0.02**	0.055	2.693	0.101	**0.011**	**0.044**
Class Sphingobacteriia	1.874	0.072	**0.038**	0.084	2.391	0.091	**0.021**	**0.046**
Class Alphaproteobacteria	2.291	0.087	**0.015**	0.055	2.232	0.085	**0.025**	**0.046**
Class Betaproteobacteria	1.945	0.075	0.102	0.121	2.827	0.105	**0.047**	0.054
Class Gammaproteobacteria	1.497	0.059	0.138	0.138	2.159	0.083	**0.025**	**0.046**
Class Flavobacteriia	1.945	0.075	0.101	0.121	2.827	0.105	0.056	0.056
Class Cytophagia	2.512	0.095	**0.007**	0.055	2.515	0.095	**0.012**	**0.044**
Class Acidobacteria Gp4	1.945	0.075	0.082	0.121	2.827	0.105	**0.047**	0.054
Class Deltaproteobacteria	1.794	0.070	**0.01**	0.055	2.059	0.079	**0.011**	**0.044**
Class Spartobacteria	1.945	0.075	0.089	0.121	2.827	0.105	**0.044**	0.054

Class Gemmatimonadetes	1.945	0.075	0.11	0.121	2.827	0.105	**0.049**	0.054
Order Actinomycetales	2.202	0.084	**0.021**	0.063	2.763	0.103	**0.008**	**0.038**
Order Sphingobacteriales	1.874	0.072	**0.037**	0.067	2.391	0.091	**0.015**	**0.038**
Order Flavobacteriales	0.987	0.040	0.456	0.497	1.704	0.066	0.073	0.110
Order Cytophagales	2.512	0.095	**0.006**	0.063	2.515	0.095	**0.016**	**0.038**
Order Xanthomonadales	1.627	0.063	0.075	0.090	2.303	0.088	**0.030**	0.051
Order Rhizobiales	2.398	0.091	**0.013**	0.063	2.292	0.087	**0.012**	**0.038**
Order Rhodospirillales	2.395	0.091	**0.017**	0.063	2.985	0.111	**0.007**	**0.038**
Order Spartobacteria unclassified	1.829	0.071	**0.039**	0.067	2.356	0.089	**0.024**	**0.048**
	ABUNDANCE DATA				**PRESENCE/ABSENCE DATA**			
B) Soil: Intervention before vs after	**F value**	**R2**	**P value**	**P adjust***	**F value**	**R2**	**P value**	**P adjust***
Class Actinobacteria	2.319	0.072	**0.011**	**0.030**	2.243	0.070	**0.016**	0.059
Class Sphingobacteriia	2.255	0.070	**0.011**	**0.030**	2.037	0.064	**0.043**	0.079
Class Alphaproteobacteria	2.073	0.065	**0.018**	**0.040**	1.872	0.059	**0.035**	0.077
Class Betaproteobacteria	1.603	0.051	0.153	0.153	2.046	0.064	0.133	0.147
Class Gammaproteobacteria	2.250	0.070	**0.008**	**0.030**	2.329	0.072	**0.011**	0.059
Class Flavobacteriia	1.603	0.051	0.148	0.153	2.046	0.064	0.132	0.147
Class Cytophagia	1.706	0.054	**0.042**	0.077	2.128	0.066	**0.025**	0.069
Class Acidobacteria Gp4	1.603	0.051	0.143	0.153	2.046	0.064	0.147	0.147
Class Deltaproteobacteria	2.059	0.064	**0.002**	**0.022**	2.741	0.084	**0.001**	**0.011**
Class Spartobacteria	1.603	0.051	0.137	0.153	2.046	0.064	0.147	0.147
Class Gemmatimonadetes	1.603	0.051	0.149	0.153	2.046	0.064	0.136	0.147

C) PERMDISP	**ABUNDANCE DATA**							**PRESENCE/ABSENCE DATA**						
SOIL		**Standard**		**Intervention**					**Standard**		**Intervention**			
Intervention vs Standard	**F**	**Mean**	**sd**	**Mean**	**sd**	**P value**	**P adjust***	**F**	**Mean**	**sd**	**Mean**	**sd**	**P value**	**P adjust***
Actinomycetales unclassified	23.2	0.6	0.1	0.4	0.1	**0.001**	**0.026**	28.7	0.6	0.1	0.3	0.1	**0.001**	**0.026**
Hymenobacter	12.7	0.5	0.2	0.3	0.1	**0.003**	**0.035**	6.5	0.5	0.2	0.3	0.1	**0.008**	0.069
Noviherbaspirillum	13.6	0.5	0.2	0.2	0.1	**0.004**	**0.035**	0.1	0.1	0.3	0.1	0.2	0.718	0.849
Sphingomonas	7.5	0.5	0.2	0.3	0.1	**0.009**	**0.047**	3.4	0.4	0.2	0.3	0.1	0.076	0.395
Marmoricola	6.7	0.4	0.2	0.2	0.2	**0.009**	**0.047**	0.1	0.1	0.2	0.1	0.2	0.806	0.873
Massilia	6.1	0.4	0.2	0.3	0.1	**0.016**	0.069	0.6	0.2	0.2	0.2	0.1	0.54	0.78
Chitinophagaceae unclassified	1.4	0.5	0.1	0.5	0.2	0.277	0.463	1.4	0.5	0.2	0.4	0.1	0.262	0.56
Nocardioides	1.3	0.5	0.2	0.4	0.2	0.282	0.463	0.5	0.4	0.2	0.3	0.1	0.489	0.748
Arthrobacter	1.8	0.4	0.2	0.3	0.2	0.198	0.463	1.9	0.2	0.1	0.2	0.2	0.186	0.56
Intrasporangiaceae unclassified	1.5	0.4	0.3	0.3	0.2	0.223	0.463	1.3	0.3	0.2	0.2	0.1	0.276	0.56
Halomonas	1.5	0.4	0.3	0.3	0.2	0.214	0.463	1.3	0.3	0.2	0.2	0.1	0.28	0.56
Chryseobacterium	1.2	0.6	0.2	0.6	0.2	0.307	0.463	0.2	0.4	0.2	0.4	0.3	0.682	0.849
Burkholderiales unclassified	1.2	0.4	0.2	0.3	0.2	0.298	0.463	5.1	0.4	0.1	0.3	0.2	0.032	0.208
Xanthomonadaceae unclassified	1.7	0.5	0.2	0.6	0.2	0.201	0.463	0	0.5	0.1	0.5	0.2	0.989	0.989
Microbacteriaceae unclassified	0.9	0.4	0.2	0.3	0.1	0.338	0.463	15.6	0.4	0.1	0.3	0.1	0.004	0.052
Sphingomonadaceae unclassified	1.1	0.6	0.1	0.6	0.2	0.305	0.463	1.4	0.6	0.2	0.5	0.5	0.249	0.56
Betaproteobacteria unclassified	2.5	0.6	0.1	0.6	0.2	0.135	0.463	1.0	0.5	0.2	0.5	0.2	0.353	0.612
Comamonadaceae unclassified	0.7	0.5	0.2	0.4	0.2	0.396	0.515	0.7	0.3	0.2	0.3	0.2	0.404	0.657

Pseudomonas	0.5	0.5	0.2	0.6	0.2	0.488	0.604	0.3	0.3	0.3	0.4	0.4	0.605	0.828
Pedobacter	0.1	0.5	0.1	0.5	0.1	0.7	0.827	1.6	0.4	0.2	0.3	0.1	0.215	0.56
Ferruginibacter	0.1	0.6	0.1	0.6	0.2	0.757	0.856	0.1	0.5	0.2	0.4	0.2	0.801	0.873
Flavobacterium	0.0	0.5	0.2	0.5	0.2	0.851	0.899	0.8	0.5	0.2	0.4	0.2	0.352	0.612
Spartobacteria unclassified	0.0	0.6	0.1	0.6	0.2	0.864	0.899	1.5	0.5	0.1	0.5	0.2	0.262	0.56

D) Skin: OTU level. baseline	**Abundance data**			**Presence/absence data**			
	F value	**R2**	**P value**	**F value**	**R2**	**P value**	**P adjust**
Intervention vs standard	0.986	0.021	0.456	0.946	0.020	0.555	0.555
Intervention vs nature-oriented	1.321	0.025	0.060	1.388	0.026	0.070	0.105
Nature-oriented vs standard	1.241	0.040	0.102	1.474	0.047	**0.025**	0.075

E) Gut: Family Ruminococcaceae	**Abundance data**				**Presence/absence data**			
	F value	**R2**	**P value**	**P adjust***	**F value**	**R2**	**P value**	**P adjust***
Intervention before vs after	0.528	0.010	0.871		0.389	0.007	0.919	
Standard before vs after	0.530	0.021	0.895		0.532	0.021	0.808	
Nature before vs after	0.174	0.005	0.997		0.357	0.010	0.903	
Nature vs Standard before	1.928	0.057	**0.047**	0.101	2.448	0.071	**0.020**	0.079
Interventio vs Standard before	1.473	0.036	0.143		1.052	0.026	0.409	
Nature vs Intervention before	0.511	0.011	0.881		1.757	0.037	0.093	
Nature vs Standard after	2.265	0.070	**0.010**	**0.030**	1.222	0.039	0.301	
Intervention vs Standard after	1.942	0.049	**0.027**	0.081	1.463	0.037	0.163	
Nature vs Intervention after	0.644	0.014	0.793		0.613	0.014	0.777	

F) Gut: Genus Faecalibacterium**	**Abundance data**			**Presence/absence data**		
	F value	**R2**	**P value**	**F value**	**R2**	**P value**
Intervention before vs after	0.158	0.003	0.943	-0.027	-0.001	0.876
Standard before vs after	1.293	0.049	0.261	1.122	0.043	0.474
Nature before vs after	0.310	0.008	0.813	0.543	0.014	0.792
Nature vs Standard before	1.705	0.051	0.185	1.554	0.046	0.272
Interventio vs Standard before	1.705	0.041	0.136	1.362	0.033	0.317
Nature vs Intervention before	0.492	0.011	0.770	-0.692	-0.015	0.968
Nature vs Standard after	3.233	0.097	**0.030**	0.150	0.005	1.000
Intervention vs Standard after	2.288	0.057	0.086	0.240	0.006	0.795
Nature vs Intervention after	0.669	0.015	0.592	0.116	0.003	0.950

*Benjamini-Hochberg correction

***Faecalibacterium* was the sole genus analyzed

Table S3. Comparison of bacterial **(A)** relative abundance at genus level between intervention and standard daycare center surface soils and **(B)** between baseline and day-28 at intervention daycare yards (Wilcoxon signed-rank test). **(C)** Comparison of bacterial richness and diversity between intervention and standard daycare center surface soils at total bacterial and class levels (t-test). Data is shown as mean ± standard deviation = sd.

A) Intervention vs standard, Degrees of Freedom = 23	**Mean standard**	**sd**	**Mean intervention**	**sd**	**Statistic**	**P value**	**P adjust**
Flavobacterium	134.3	102.0	233.0	168.4	108.0	0.147	0.491
Chitinophagaceae unclassified	261.1	123.6	202.1	72.9	51.5	0.140	0.484
Sphingomonas	208.6	47.3	159.8	108.3	50.5	0.126	0.484
Massilia	231.4	96.9	141.9	114.9	45.0	0.069	0.365
Hymenobacter	193.7	76.1	114.9	125.2	45.0	0.069	0.365
Ferruginibacter	185.9	110.5	112.4	82.2	46.0	0.077	0.367
Mucilaginibacter	18.3	28.3	94.6	164.6	106.0	0.178	0.494
Pedobacter	82.4	62.3	90.4	83.2	82.0	0.937	1.000
Spartobacteria unclassified	22.7	18.0	81.9	90.5	118.0	0.048	0.300
Nocardioides	84.6	37.3	76.1	51.6	74.0	0.772	0.963
Gammaproteobacteria unclassified	8.3	6.1	64.7	77.2	137.0	**0.003**	0.052
Arthrobacter	71.3	61.0	63.3	79.4	58.0	0.257	0.578
Betaproteobacteria unclassified	28.6	21.9	61.8	92.7	81.5	0.958	1.000
Burkholderiales unclassified	58.3	23.6	61.0	33.0	77.0	0.895	1.000
Chryseobacterium	122.1	263.5	55.1	76.2	87.5	0.712	0.942
Intrasporangiaceae unclassified	63.9	27.3	50.6	30.2	60.5	0.317	0.678
Xanthomonadaceae unclassified	47.7	69.6	49.8	37.3	103.5	0.225	0.563
Microbacteriaceae unclassified	43.1	19.1	47.4	36.5	78.5	0.958	1.000
Comamonadaceae unclassified	48.4	17.0	45.5	23.4	77.0	0.895	1.000
Actinomycetales unclassified	46.5	22.6	40.6	36.9	51.5	0.140	0.484
Luteolibacter	27.4	23.3	40.1	39.0	91.5	0.561	0.901
Cryobacterium	40.8	26.7	39.8	45.8	63.0	0.384	0.780
Aridibacter unclassified	50.8	30.4	39.7	35.8	63.5	0.399	0.780
Sphingomonadaceae unclassified	47.4	23.1	39.0	18.9	66.0	0.476	0.874
Myxococcales unclassified	25.4	21.8	35.8	35.7	89.0	0.654	0.942
Gp6 unclassified	17.8	12.3	35.6	55.8	80.0	1.000	1.000
Oxalobacteraceae unclassified	46.4	27.0	34.4	26.6	58.0	0.257	0.578
Mycobacterium	7.1	4.7	33.8	31.4	140.5	0.002	0.052
Bacteroidetes unclassified	21.6	20.5	33.1	28.4	102.5	0.246	0.578
Granulicella unclassified	6.7	16.5	32.9	76.1	79.0	0.975	1.000
Clostridium sensu stricto	5.7	4.9	32.9	56.0	120.5	**0.035**	0.240
Bradyrhizobium	14.0	8.6	32.8	22.1	121.0	**0.033**	0.240
Acidobacteria Gp1 unclassified	2.8	3.1	31.4	63.3	74.0	0.762	0.963
Marmoricola	49.5	15.0	30.1	27.6	38.5	**0.031**	0.240
Gemmatimonas	56.0	42.5	30.0	30.6	53.5	0.170	0.494
Noviherbaspirillum	80.0	34.3	29.9	32.7	20.5	**0.002**	0.052
Rhizobiales unclassified	24.5	18.0	28.5	26.2	74.5	0.792	0.963
Burkholderia	4.0	6.1	26.2	53.7	92.0	0.537	0.901

Polaromonas	22.3	20.7	24.8	21.1	85.5	0.792	0.963
Alphaproteobacteria unclassified	5.9	6.0	24.5	31.3	110.0	0.119	0.484
Novosphingobium	24.0	15.3	23.7	23.3	70.5	0.635	0.942
Spirosoma	46.0	31.2	23.6	25.8	50.5	0.124	0.484
Gp3 unclassified	12.1	10.7	23.4	28.6	88.5	0.672	0.942
Pseudomonas	27.7	30.7	22.9	30.9	68.0	0.544	0.901
Actinobacteria unclassified	11.4	8.5	22.7	16.0	117.5	**0.050**	0.300
Arenimonas	26.0	18.3	22.6	22.1	71.5	0.672	0.942
Sinobacteraceae unclassified	14.4	19.3	21.9	28.6	89.0	0.653	0.942
Planctomycetaceae unclassified	4.2	4.4	20.6	19.6	123.0	0.025	0.227
Brevundimonas	15.2	29.2	20.2	23.0	100.0	0.303	0.665
Proteobacteria unclassified	19.0	7.2	20.1	17.9	73.5	0.751	0.963
Gaiella	8.5	6.2	18.3	29.2	79.0	0.979	1.000
candidate division WPS.1 unclassified	8.7	10.0	18.0	17.8	106.5	0.169	0.494
Acidobacteria Gp4 unclassified	23.8	16.7	17.9	15.5	64.0	0.413	0.791
Blastocatella unclassified	20.1	8.0	16.8	35.2	33.0	**0.014**	0.159
Duganella	21.4	14.3	16.7	15.7	58.0	0.256	0.578
Terrimonas	7.7	6.1	16.6	19.4	96.5	0.398	0.780
Nakamurella	19.2	13.8	16.5	9.2	77.5	0.916	1.000
Subdivision3 unclassified	6.7	7.2	15.4	18.5	93.0	0.501	0.874
Opitutus	6.3	6.1	14.9	21.0	98.5	0.340	0.712
Cytophagales unclassified	16.1	10.9	14.6	20.2	54.0	0.178	0.494
Roseomonas	24.5	13.9	14.4	14.7	47.5	0.091	0.410
Acidobacteria Gp3 unclassified	0.8	8.8	14.1	20.5	76.0	0.853	1.000
Dyadobacter	10.1	15.1	13.7	18.6	93.5	0.489	0.874
Cellvibrio	20.4	29.9	13.6	12.7	78.0	0.937	1.000
Acetobacteraceae unclassified	35.4	58.8	13.6	20.7	55.5	0.205	0.526
Gp4 unclassified	4.6	8.2	13.3	40.4	76.5	0.869	1.000
Rhizobium	11.2	6.0	12.2	9.7	78.0	0.937	1.000
Rhodopseudomonas	17.6	7.0	12.1	10.4	51.5	0.140	0.484
Nocardioidaceae unclassified	10.9	9.8	12.1	10.2	80.5	1.000	1.000
Flavisolibacter	38.3	21.4	12.0	13.7	22.5	**0.003**	0.052
Caulobacter	11.3	6.4	11.5	9.7	78.0	0.937	1.000
Conexibacter	8.2	8.6	11.1	15.1	72.0	0.690	0.942
Chryseolinea unclassified	7.8	7.5	11.1	12.3	89.5	0.634	0.942
Roseiarcus	0.1	0.3	10.4	23.7	99.0	0.187	0.494
Pseudoxanthomonas	1.5	2.3	10.0	8.6	134.5	**0.004**	0.052
Deltaproteobacteria unclassified	7.8	5.2	9.9	13.2	73.5	0.751	0.963
Cellulomonas	6.5	5.3	8.6	6.9	91.5	0.560	0.901
Phenylobacterium	7.5	5.9	8.1	9.6	72.0	0.691	0.942
Chloroflexi unclassified	2.6	2.9	7.5	8.5	105.5	0.183	0.494
Micromonosporaceae unclassified	17.0	9.2	7.5	9.4	24.0	**0.003**	0.052
Actinoplanes	5.2	5.7	7.2	14.6	67.0	0.505	0.874
Gp7 unclassified	5.0	7.6	7.1	19.0	70.0	0.592	0.935
Hyphomicrobium	2.0	1.8	6.6	10.7	112.0	0.076	0.367
Cytophaga	9.9	14.6	6.5	10.4	72.5	0.708	0.942

Segetibacter	33.6	30.8	5.8	7.9	25.0	**0.004**	0.052
Moraxellaceae unclassified	3.1	6.6	5.7	14.7	87.5	0.674	0.942
Sphingomonadales unclassified	14.4	9.7	5.7	7.7	37.5	0.025	0.227
Rhizomicrobium unclassified	0.0	0.0	5.3	11.7	95.0	0.169	0.494
Solirubrobacterales unclassified	9.0	11.3	5.2	7.1	66.0	0.473	0.874
Solirubrobacter	2.8	2.6	5.1	7.9	78.0	0.935	1.000
B) Intervention yards baseline vs day-28, Degrees of Freedom = 31	**Mean baseline**	**sd**	**Mean day-28**	**sd**	**Statistic**	**P value**	**P adjust**
Flavobacterium	171.8	145.6	233.0	168.4	80.0	0.552	0.869
Chitinophagaceae unclassified	213.6	72.3	202.1	72.9	48.5	0.326	0.606
Bacteria unclassified	206.0	157.4	180.2	66.4	57.0	0.587	0.870
Sphingomonas	155.8	77.2	159.8	108.3	73.0	0.816	0.970
Massilia	86.9	46.8	141.9	114.9	91.0	0.245	0.584
Hymenobacter	100.1	72.5	114.9	125.2	68.0	1.000	1.000
Ferruginibacter	123.7	69.6	112.4	82.2	60.0	0.698	0.933
Mucilaginibacter	7.9	9.1	94.6	164.6	102.0	**0.018**	0.279
Pedobacter	65.1	44.7	90.4	83.2	70.5	0.570	0.869
Spartobacteria unclassified	27.3	53.0	81.9	90.5	111.0	**0.028**	0.280
Nocardioides	123.5	60.6	76.1	51.6	24.0	**0.024**	0.279
Gammaproteobacteria unclassified	14.9	12.3	64.7	77.2	109.0	**0.036**	0.290
Arthrobacter	89.4	67.4	63.3	79.4	43.0	0.205	0.566
Betaproteobacteria unclassified	30.2	40.5	61.8	92.7	83.0	0.453	0.740
Burkholderiales unclassified	56.1	29.7	61.0	33.0	64.5	0.877	0.970
Chryseobacterium	34.9	60.9	55.1	76.2	95.5	0.162	0.500
Intrasporangiaceae unclassified	98.3	70.3	50.6	30.2	26.0	**0.032**	0.283
Xanthomonadaceae unclassified	65.5	45.2	49.8	37.3	46.5	0.277	0.584
Microbacteriaceae unclassified	44.3	36.7	47.4	36.5	79.5	0.569	0.869
Comamonadaceae unclassified	45.6	20.8	45.5	23.4	68.5	1.000	1.000
Actinomycetales unclassified	53.3	64.1	40.6	36.9	62.5	0.796	0.970
Luteolibacter	24.9	21.6	40.1	39.0	91.5	0.234	0.584
Cryobacterium	28.4	30.7	39.8	45.8	72.0	0.856	0.970
Aridibacter unclassified	44.0	24.2	39.7	35.8	55.5	0.820	0.970
Sphingomonadaceae unclassified	48.6	25.0	39.0	18.9	50.5	0.379	0.632
Myxococcales unclassified	22.3	23.5	35.8	35.7	78.5	0.306	0.584
Gp6 unclassified	21.4	18.3	35.6	55.8	66.0	0.938	0.988
Oxalobacteraceae unclassified	25.7	18.6	34.4	26.6	93.5	0.196	0.560
Mycobacterium	8.1	5.0	33.8	31.4	129.0	**0.002**	0.114
Bacteroidetes unclassified	39.9	24.2	33.1	28.4	45.5	0.255	0.584
Granulicella unclassified	0.8	4.6	32.9	76.1	18.0	0.142	0.455
Clostridium sensu stricto	11.6	20.0	32.9	56.0	84.0	0.052	0.326
Bradyrhizobium	16.0	10.1	32.8	22.1	102.5	0.079	0.370
Acidobacteria Gp1 unclassified	12.1	46.4	31.4	63.3	46.0	0.264	0.584
Marmoricola	73.8	41.7	30.1	27.6	7.0	**0.003**	0.114
Gemmatimonas	43.3	25.1	30.0	30.6	50.0	0.365	0.632
Noviherbaspirillum	57.7	85.2	29.9	32.7	50.5	0.379	0.632
Burkholderia	1.6	2.3	26.2	53.7	80.5	**0.016**	0.279
Polaromonas	23.2	12.5	24.8	21.1	71.0	0.897	0.970

Novosphingobium	32.6	25.5	23.7	23.3	50.5	0.379	0.632
Spirosoma	45.1	28.9	23.6	25.8	33.0	0.074	0.370
Gp3 unclassified	18.4	39.1	23.4	28.6	89.0	0.289	0.584
Pseudomonas	64.4	74.5	22.9	30.9	28.0	**0.041**	0.299
Actinobacteria unclassified	22.8	12.1	22.7	16.0	57.5	0.605	0.880
Arenimonas	33.9	23.4	22.6	22.1	35.5	0.098	0.392
Sinobacteraceae unclassified	5.6	5.9	21.9	28.6	88.0	0.118	0.411
Planctomycetaceae unclassified	16.0	28.2	20.6	19.6	91.0	0.245	0.584
Brevundimonas	15.8	12.6	20.2	23.0	72.5	0.836	0.970
Proteobacteria unclassified	18.6	13.4	20.1	17.9	67.5	1.000	1.000
Gaiella	11.9	12.3	18.3	29.2	63.0	0.887	0.970
candidate division WPS.1 unclassified	6.6	6.0	18.0	17.8	105.5	0.056	0.326
Acidobacteria Gp4 unclassified	26.2	27.4	17.9	15.5	41.0	0.170	0.505
Blastocatella unclassified	17.1	46.0	16.8	35.2	36.0	0.103	0.392
Duganella	22.7	7.5	16.7	15.7	93.0	0.065	0.345
Terrimonas	13.6	6.8	16.6	19.4	90.0	0.093	0.392
Subdivision3 unclassified	4.4	5.9	15.4	18.5	88.0	0.118	0.411
Opitutus	15.9	6.4	14.9	21.0	59.0	0.706	0.933
Cytophagales unclassified	16.1	12.5	14.6	20.2	46.0	0.266	0.584
Roseomonas	23.2	9.9	14.4	14.7	59.0	0.660	0.924
Acidobacteria Gp3 unclassified	8.1	17.3	14.1	20.5	79.0	0.293	0.584
Dyadobacter	14.2	12.0	13.7	18.6	56.0	0.842	0.970
Cellvibrio	36.9	31.5	13.6	12.7	43.2	0.023	0.279
Acetobacteraceae unclassified	14.3	18.7	13.6	20.7	68.0	0.670	0.924
Gp4 unclassified	1.1	1.9	13.3	40.4	53.5	0.270	0.584
Rhizobium	16.0	10.9	12.2	9.7	67.0	0.712	0.933
Rhodopseudomonas	17.3	7.7	12.1	10.4	64.5	0.877	0.970
Nocardioidaceae unclassified	14.4	11.0	12.1	10.2	53.5	0.733	0.946
Flavisolibacter	23.3	15.0	12.0	13.7	26.0	0.057	0.326
Conexibacter	24.6	40.5	11.1	15.1	49.0	0.338	0.615
Chryseolinea unclassified	7.0	6.6	11.1	12.3	54.0	0.576	0.869
Roseiarcus	0.4	1.1	10.4	23.7	43.2	0.128	0.425
Pseudoxanthomonas	10.2	11.5	10.0	8.6	67.0	0.979	1.000
Cellulomonas	9.9	9.4	8.6	6.9	66.0	0.938	0.988
Phenylobacterium	9.0	3.6	8.1	9.6	62.0	0.776	0.970
Phycicoccus	15.3	9.5	7.6	6.4	19.0	0.012	0.279
Actinoplanes	7.5	6.3	7.2	14.6	55.5	0.875	0.970
Gp7 unclassified	8.2	15.1	7.1	19.0	45.0	0.305	0.584
Hyphomicrobium	2.1	2.7	6.6	10.7	72.5	0.217	0.578
Solirubrobacterales unclassified	20.0	30.2	5.2	7.1	36.0	0.103	0.392
Solirubrobacter	5.7	4.0	5.1	7.9	60.5	0.637	0.910

C) Intervention vs standard, Day 28 **Degrees of Freedom = 23**	**Mean standard**	**sd**	**Mean intervention**	**sd**	**Statistic**	**P value**	**P adjust***
Observed OTU richness	484.0	99.7	588.7	128.7	2.3	**0.029**	**0.04**
Chao richness index	533.0	134.9	670.9	156.9	2.4	**0.027**	**0.04**
Shannon total bacterial community	5.2	0.4	5.6	0.4	2.2	**0.040**	**0.04**
CLASS LEVEL RICHNESS							
Actinobacteria richness	72.5	16.2	75.8	16.4	0.5	0.626	0.939
Sphingobacteriia richness	67.4	17.8	74.4	17.2	1.0	0.333	0.777
Alphaproteobacteria richness	80.5	16.3	83.5	14.6	0.5	0.640	0.939
Betaproteobacteria richness	13.0	2.2	12.9	1.6	-0.1	0.939	0.939
Gammaproteobacteria richness	19.3	5.9	28.3	6.5	3.6	**0.002**	**0.024**
Flavobacteriia richness	13.0	2.2	12.9	1.6	-0.1	0.939	0.939
Cytophagia richness	39.7	15.5	28.6	16.7	-1.7	0.101	0.364
Acidobacteria Gp4 richness	13.0	2.2	12.9	1.6	-0.1	0.939	0.939
Deltaproteobacteria richness	9.8	5.1	14.1	8.0	1.7	0.104	0.364
Spartobacteria richness	13.0	2.2	12.9	1.6	-0.1	0.939	0.939
Bacilli richness	1.2	1.9	1.6	2.2	0.4	0.665	0.939
Gemmatimonadetes richness	13.0	2.2	12.9	1.6	-0.1	0.939	0.939
Acidobacteria Gp1 richness	3.4	3.5	11.3	20.3	1.5	0.150	0.419
Verrucomicrobiae richness	3.4	2.4	6	4.1	2.1	0.050	0.349
CLASS LEVEL DIVERSITY							
Actinobacteria Shannon	3.6	0.2	3.6	0.3	-0.2	0.850	0.850
Sphingobacteriia Shannon	3.3	0.3	3.6	0.3	2.7	**0.016**	0.074
Alphaproteobacteria Shannon	3.7	0.2	3.8	0.2	0.8	0.416	0.529
Betaproteobacteria Shannon	1.5	0.1	1.6	0.2	1.9	0.077	0.135
Gammaproteobacteria Shannon	2.3	0.3	2.6	0.3	2.6	**0.016**	0.074
Flavobacteriia Shannon	1.5	0.1	1.6	0.2	1.9	0.077	0.135
Cytophagia Shannon	3.1	0.4	2.6	0.6	-2.8	**0.010**	0.074
Acidobacteria Gp4 Shannon	1.5	0.1	1.6	0.2	1.9	0.077	0.135
Deltaproteobacteria Shannon	1.8	0.7	2.2	0.6	1.5	0.163	0.253
Spartobacteria Shannon	1.5	0.1	1.6	0.2	1.9	0.077	0.135
Bacilli Shannon	0.3	0.6	0.4	0.6	0.6	0.579	0.676
Gemmatimonadetes Shannon	1.5	0.1	1.6	0.2	1.9	0.077	0.135
Acidobacteria Gp1 Shannon	0.8	0.8	0.9	1.4	0.4	0.689	0.742
Verrucomicrobiae Shannon	0.9	0.6	1.2	0.7	1.0	0.316	0.442

*Benjamini-Hochberg correction

Table S4. Comparisons of bacterial richness and Shannon diversity on skin before the intervention period (Baseline A-C) and after the intervention period (Day-28 D-F) among three daycare groups (Intervention, standard and nature-oriented). Data is shown at total bacterial community, phylum and class levels (mean±standard deviation = sd). Analysis of covariance (ANCOVA) or Kruskal-Wallis test was used depending on Shapiro-Wilk test of normality. Tukey's HSD post hoc test was used when normality assumption was true and Dunn's test when normality assumption was violated. The upper part shows (**A**) **baseline** ANCOVA and Kruskal-Wallis tests and (**B**) post-hoc tests Tukey HSD and (**C**) Dunn's test. The lower part shows (**D**) **day-28** ANCOVA and Kruskal-Wallis tests and (**E**) post-hoc tests Tukey HSD and (**F**) Dunn's test. **Bold** font indicates significant differences ($p \leq 0.05$).

A) Analysis of covariance	Intervention		Standard		Nature		ANCOVA^a		Shapiro-Wilk		Kruskal-Wallis	
Baseline	**mean**	**sd**	**mean**	**sd**	**mean**	**sd**	**F**	**P value**	**W**	**P value**	**X^2**	**P value**
Total bacterial community												
Observed OTU richness	52.8	29.3	56.6	31.7	65.9	39.6	1.1	0.347	1.0	0.099	1.3	0.531
Chao richness index	60.3	42.2	61.9	40.4	78.5	55.9	1.1	0.333	0.9	**0.005**	1.0	0.592
shannon	3.3	0.7	3.6	0.6	3.6	0.7	1.2	0.306	0.9	**0.001**	1.6	0.445
DIVERSITY PHYLUM												
Firmicutes Shannon	1.9	0.9	2.2	0.8	2.2	0.6	0.8	0.455	1.0	0.967	1.3	0.509
Proteobacteria Shannon	2.1	0.8	2.2	0.7	2.4	0.9	0.6	0.540	0.9	**0.007**	1.3	0.527
Actinobacteria Shannon	2.0	0.8	2.2	0.6	2.3	0.9	1.4	0.243	1.0	0.247	1.8	0.407
Bacteroidetes Shannon	1.2	0.9	1.2	0.9	1.4	1.0	0.3	0.736	0.9	**0.000**	0.7	0.722
DIVERSITY CLASS												
Bacilli Shannon	1.7	0.8	1.9	0.6	1.9	0.4	1.1	0.333	1.0	0.756	1.5	0.472
Gammaproteobacteria Shannon	1.5	0.7	1.4	0.7	1.3	0.6	0.6	0.572	1.0	**0.011**	1.2	0.547
Betaproteobacteria Shannon	1.0	0.8	1.2	0.7	1.5	0.7	2.2	0.117	1.0	0.053	3.4	0.179
Alphaproteobacteria Shannon	0.5	0.8	0.6	0.9	1.2	1.1	3.6	**0.033**	0.9	**0.000**	5.9	0.053
Clostridia Shannon	0.4	0.8	0.6	0.9	0.4	0.8	0.4	0.665	0.7	**0.000**	1.1	0.575
Bacteroidia Shannon	0.7	0.8	0.8	0.8	0.8	0.8	0.1	0.881	0.9	**0.000**	0.3	0.844
Fusobacteriia Shannon	0.4	0.6	0.5	0.7	0.4	0.7	0.1	0.899	0.7	**0.000**	0.4	0.832
Negativicutes Shannon	0.3	0.5	0.4	0.5	0.2	0.4	0.5	0.585	0.8	**0.000**	0.9	0.642
RICHNESS PHYLUM												
Firmicutes richness	16.3	15.3	16.0	10.4	14.9	8.8	0.1	0.936	0.9	**0.000**	0.3	0.852
Proteobacteria richness	14.2	10.7	13.4	8.2	20.1	14.6	2.2	0.120	0.9	**0.007**	2.4	0.295
Actinobacteria richness	12.1	8.8	14.4	12.0	18.3	14.6	2.0	0.147	0.9	**0.002**	1.3	0.512
Bacteroidetes richness	5.5	4.7	5.6	4.7	7.6	6.5	1.0	0.365	0.9	**0.001**	1.0	0.600
CLASS												
Bacilli richness	11.5	9.8	11.5	7.8	10.8	5.5	0.0	0.958	0.9	**0.000**	0.4	0.833
Gammaproteobacteria richness	6.9	4.8	5.6	3.5	6.0	3.6	0.5	0.599	1.0	0.115	0.2	0.897
Betaproteobacteria richness	4.5	3.7	4.5	2.4	7.1	5.2	3.1	**0.050**	0.9	**0.003**	3.8	0.149
Alphaproteobacteria richness	2.6	4.1	2.9	4.6	6.6	8.0	3.8	**0.027**	0.9	**0.000**	4.1	0.130
Clostridia richness	3.5	11.1	2.7	3.6	2.8	5.9	0.1	0.949	0.4	**0.000**	1.8	0.406

Bacteroidia richness	3.0	3.7	3.1	3.3	3.4	3.1	0.1	0.941	0.9	**0.000**	0.4	0.829
Fusobacteriia richness	1.6	2.0	2.2	3.1	1.6	2.0	0.4	0.661	0.8	**0.000**	0.0	0.989
Negativicutes richness	1.2	1.6	1.5	1.7	1.2	1.5	0.2	0.811	0.9	**0.000**	0.5	0.764

B) POST-HOC TUKEY's HSD	**Intervention vs Standard**		**Nature vs Standard**		**Nature vs Intervention**	
Baseline	**Mean difference**	**P value**	**Mean difference**	**P value**	**Mean difference**	**P value**
Total bacterial community						
Observed OTU richness	-3.843	0.922	9.302	0.688	13.144	0.329
Chao richness index	16.587	0.993	16.587	0.542	18.192	0.332
Shannon index	-0.546	0.561	0.056	0.973	0.284	0.350
DIVERSITY PHYLUM						
Firmicutes Shannon	-0.239	0.618	0.013	0.999	0.251	0.531
Proteobacteria Shannon	-0.087	0.935	0.162	0.832	0.249	0.522
Actinobacteria Shannon	-0.226	0.632	0.139	0.871	0.365	0.247
Bacteroidetes Shannon	-0.011	0.999	0.187	0.834	0.199	0.737
DIVERSITY CLASS						
Bacilli Shannon	-0.209	0.595	0.060	0.967	0.269	0.365
Gammaproteobacteria Shannon	0.148	0.752	-0.040	0.984	-0.188	0.582
Betaproteobacteria Shannon	-0.157	0.774	0.282	0.524	0.439	0.101
Alphaproteobacteria Shannon	-0.090	0.946	0.589	0.164	0.678	**0.030**
Clostridia Shannon	-0.235	0.654	-0.217	0.751	0.018	0.997
Bacteroidia Shannon	-0.074	0.951	0.036	0.991	0.110	0.877
Fusobacteriia Shannon	-0.094	0.889	-0.069	0.952	0.025	0.990
Negativicutes Shannon	-0.130	0.649	-0.164	0.584	-0.034	0.966
RICHNESS PHYLUM						
Firmicutes richness	0.314	0.997	-1.056	0.972	-1.370	0.930
Proteobacteria richness	0.771	0.972	6.683	0.200	5.911	0.151
Actinobacteria richness	-2.214	0.795	3.921	0.569	6.135	0.132
Bacteroidetes richness	-0.157	0.995	1.913	0.559	2.070	0.361
RICHNESS CLASS						
Bacilli richness	-0.543	1.000	-0.722	0.969	-0.679	0.959
Gammaproteobacteria richness	1.243	0.618	0.357	0.969	-0.886	0.747
Betaproteobacteria richness	-0.514	1.000	2.611	0.142	2.625	0.054
Alphaproteobacteria richness	-0.329	0.978	3.683	0.124	4.011	**0.027**
Clostridia richness	0.743	0.962	0.063	1.000	-0.679	0.962
Bacteroidia richness	-0.114	0.994	0.246	0.979	0.360	0.933
Fusobacteriia richness	-0.643	0.650	-0.603	0.742	0.040	0.998
Negativicutes richness	-0.829	0.791	-0.278	0.876	0.051	0.993

C) POST-HOC DUNN'S TEST	**Intervention vs Standard**		**Nature vs Standard**		**Nature vs Intervention**	
Baseline	**Dunn statistic**	**P value**	**Dunn statistic**	**P value**	**Dunn statistic**	**P value**
Total bacterial community						
Observed OTU richness	0.425	0.671	0.659	0.671	1.268	0.614
Chao richness index	0.374	0.708	0.629	0.708	1.177	0.708
Shannon index	0.748	0.649	0.455	0.649	1.371	0.511
DIVERSITY PHYLUM						
Firmicutes Shannon	1.154	0.405	0.125	0.900	1.104	0.405

Proteobacteria Shannon	0.257	0.797	0.586	0.797	0.996	0.797
Actinobacteria Shannon	0.271	0.786	0.801	0.635	1.274	0.608
Bacteroidetes Shannon	0.268	0.788	0.529	0.788	0.939	0.788
DIVERSITY CLASS						
Bacilli Shannon	0.672	0.752	0.212	0.832	0.992	0.752
Gammaproteobacteria Shannon	0.780	0.653	0.317	0.751	1.238	0.647
Betaproteobacteria Shannon	0.559	0.576	0.922	0.535	1.737	0.247
Alphaproteobacteria Shannon	0.413	0.679	1.533	0.188	2.324	0.060
Clostridia Shannon	1.256	0.627	0.806	0.630	0.383	0.702
Bacteroidia Shannon	0.554	0.869	0.108	0.914	0.735	0.869
Fusobacteriia Shannon	0.541	0.920	0.400	0.920	0.101	0.920
Negativicutes Shannon	0.804	0.632	0.829	0.632	0.138	0.890
RICHNESS PHYLUM						
Firmicutes richness	0.618	0.805	0.015	0.988	0.655	0.805
Proteobacteria richness	0.012	0.990	1.148	0.376	1.390	0.376
Actinobacteria richness	0.537	0.686	0.405	0.686	1.079	0.686
Bacteroidetes richness	0.346	0.730	0.639	0.730	1.158	0.730
Bacilli richness	0.234	0.886	0.144	0.886	0.430	0.886
RICHNESS CLASS						
Gammaproteobacteria richness	0.581	0.860	0.176	0.860	0.418	0.860
Betaproteobacteria richness	0.478	0.633	1.074	0.424	1.834	0.200
Alphaproteobacteria richness	0.537	0.591	1.100	0.407	1.930	0.161
Clostridia richness	0.963	0.503	0.364	0.716	1.495	0.405
Bacteroidia richness	0.499	0.844	0.197	0.844	0.784	0.844
Fusobacteriia richness	0.063	0.950	0.116	0.950	0.073	0.950
Negativicutes richness	0.723	0.776	0.285	0.776	0.439	0.776

D) Analysis of covariance Day 28	**Intervention**		**Standard**		**Nature**		**ANCOVA[a]**		**Shapiro-Wilk**		**Kruskal-Wallis**	
Total bacterial community	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**F**	**P value**	**W**	**P value**	**X^2**	**P value**
Observed OTU richness	62.3	39.7	40.8	14.9	69.1	37.8	2.6	0.087	0.9	**0.000**	4.6	0.102
Chao richness index	75.4	73.5	42.4	16.3	82.0	53.2	1.8	0.168	0.8	**0.000**	4.3	0.115
shannon	3.6	0.6	3.1	0.6	3.7	0.6	3.7	**0.030**	1.0	0.927	5.4	0.066
DIVERSITY PHYLUM												
Firmicutes Shannon	2.1	0.6	1.9	0.6	2.0	0.9	0.3	0.747	1.0	0.029	0.9	0.652
Proteobacteria Shannon	2.4	0.7	1.8	0.7	2.5	0.7	4.3	**0.018**	1.0	0.067	9.4	**0.009**
Actinobacteria Shannon	2.0	1.0	1.8	0.7	2.4	0.9	2.0	0.150	1.0	0.276	4.6	0.102
Bacteroidetes Shannon	1.3	0.9	1.0	0.7	1.5	0.8	1.8	0.181	1.0	0.139	2.7	0.260
DIVERSITY CLASS												
Bacilli Shannon	1.9	0.5	1.6	0.6	1.6	0.8	1.3	0.275	1.0	0.296	1.9	0.391
Gammaproteobacteria Shannon	1.6	0.7	1.1	0.7	1.4	0.7	2.7	0.073	0.9	**0.006**	6.4	**0.040**
Betaproteobacteria Shannon	1.3	0.8	0.9	0.6	1.5	0.7	2.7	0.077	1.0	**0.044**	8.7	**0.013**
Alphaproteobacteria Shannon	0.9	1.0	0.2	0.6	1.0	1.1	3.1	0.054	0.9	**0.002**	6.7	**0.036**
Clostridia Shannon	0.3	0.6	0.5	0.7	0.6	1.0	1.1	0.331	0.8	**0.000**	2.7	0.261
Bacteroidia Shannon	0.7	0.8	0.6	0.6	0.7	0.9	0.1	0.886	0.8	**0.000**	0.2	0.910
Fusobacteriia Shannon	0.6	0.7	0.4	0.5	0.5	0.6	0.4	0.677	0.9	**0.000**	0.8	0.680
Negativicutes Shannon	0.2	0.4	0.2	0.4	0.3	0.4	0.3	0.756	0.8	**0.000**	1.3	0.521
RICHNESS PHYLUM												

Firmicutes richness	14.8	9.9	14.2	8.3	15.9	12.2	0.1	0.899	0.9	**0.011**	0.0	0.989
Proteobacteria richness	19.9	15.4	9.1	4.6	19.8	13.0	3.4	**0.042**	0.9	**0.000**	9.4	**0.009**
Actinobacteria richness	15.6	16.7	9.3	4.8	19.4	13.1	2.1	0.136	0.8	**0.000**	3.9	0.142
Bacteroidetes richness	6.4	5.7	3.5	2.4	7.0	4.8	2.1	0.138	0.9	**0.000**	3.3	0.188
RICHNESS CLASS												
Bacilli richness	12.2	8.4	10.8	7.5	10.5	7.8	0.4	0.681	0.9	**0.000**	0.6	0.756
Gammaproteobacteria richness	7.8	5.3	4.5	2.8	6.9	5.1	1.8	0.168	0.9	**0.001**	4.4	0.111
Betaproteobacteria richness	6.6	5.9	3.3	2.2	7.0	4.5	2.5	0.090	0.9	**0.000**	8.0	**0.018**
Alphaproteobacteria richness	5.0	7.2	1.0	2.5	5.4	7.5	2.0	0.144	0.8	**0.000**	7.4	**0.025**
Clostridia richness	1.4	2.7	2.4	3.8	3.9	7.4	1.5	0.235	0.6	**0.000**	1.9	0.381
Bacteroidia richness	2.9	2.8	2.1	1.9	3.1	3.6	0.5	0.615	0.9	**0.000**	0.5	0.791
Fusobacteriia richness	2.5	2.5	1.4	1.3	2.0	2.8	0.9	0.409	0.9	**0.000**	1.8	0.401
Negativicutes richness	1.1	1.3	1.0	1.2	1.3	1.2	0.2	0.825	0.9	**0.000**	0.6	0.755

E) POST-HOC TUKEY's HSD day 28	**Intervention vs Standard**		**Nature vs Standard**		**Nature vs Intervention**	
Total bacterial community	**Mean difference**	**P value P adjust***	**Mean difference**	**P value P adjust***	**Mean difference**	**P value**
Observed OTU richness	21.541	0.168	28.283	0.075 0.113	6.742	0.794
Chao richness index	39.563	0.224	39.563	0.159 0.159	6.589	0.924
shannon	0.066	0.087	0.585	**0.024** 0.072	0.153	0.665
DIVERSITY PHYLUM						
Firmicutes Shannon	0.182	0.736 0.736	0.141	0.853 0.853	-0.041	0.980
Proteobacteria Shannon	0.645	**0.027** 0.108	0.720	**0.021** 0.084	0.075	0.934
Actinobacteria Shannon	0.228	0.724 0.736	0.599	0.157 0.209	0.371	0.342
Bacteroidetes Shannon	0.379	0.357 0.714	0.555	0.154 0.209	0.176	0.748
DIVERSITY CLASS						
Bacilli Shannon	0.282	0.410	0.024	0.994	-0.257	0.386
Gammaproteobacteria Shannon	0.551	0.053	0.369	0.309	-0.181	0.651
Betaproteobacteria Shannon	0.400	0.245	0.617	0.061	0.217	0.582
Alphaproteobacteria Shannon	0.731	0.064	0.792	0.063	0.060	0.975
Clostridia Shannon	-0.218	0.681	0.123	0.900	0.341	0.307
Bacteroidia Shannon	0.120	0.890	0.102	0.929	-0.017	0.997
Fusobacteriia Shannon	0.161	0.716	0.034	0.987	-0.127	0.766
Negativicutes Shannon	-0.032	0.970	0.069	0.890	0.101	0.689
RICHNESS PHYLUM						
Firmicutes richness	0.528	0.987 0.987	1.664	0.897	1.136	0.927
Proteobacteria richness	10.785	**0.038** 0.152	10.713	0.060	-0.073	1.000
Actinobacteria richness	6.244	0.363 0.484	10.061	0.110	3.817	0.613
Bacteroidetes richness	2.841	0.199 0.398	3.462	0.130	0.621	0.903
RICHNESS CLASS						
Bacilli richness	1.403	0.859	-0.296	0.994	-1.699	0.752
Gammaproteobacteria richness	3.220	0.117	2.409	0.348	-0.811	0.834
Betaproteobacteria richness	3.313	0.116	3.692	0.100	0.379	0.963
Alphaproteobacteria richness	4.034	0.156	4.421	0.147	0.387	0.978

Clostridia richness	-0.971	0.825	1.563	0.652	2.534	0.196
Bacteroidia richness	0.854	0.667	0.976	0.635	0.122	0.989
Fusobacteriia richness	1.098	0.378	0.615	0.766	-0.483	0.783
Negativicutes richness	0.069	0.985	0.263	0.832	0.194	0.861

F) POST HOC DUNN'S TEST Day 28	**Intervention vs Standard**			**Nature vs Standard**			**Nature vs Intervention**	
Total bacterial community	**Dunn statistic**	**P value**	**P adjust***	**Dunn statistic**	**P value**	**P adjust***	**Dunn statistic**	**P value**
Observed OTU richness	1.608	0.162		2.112	0.104		0.758	0.449
Chao richness index	1.505	0.199		2.064	0.117		0.816	0.415
shannon	1.664	0.144		2.321	0.061		0.949	0.342
DIVERSITY PHYLUM								
Firmicutes Shannon	0.815	0.415	0.415	0.857	0.392	0.392	0.123	0.902
Proteobacteria Shannon	2.579	**0.010**	**0.040**	2.920	**0.004**	**0.014**	0.644	0.520
Actinobacteria Shannon	0.914	0.361	0.415	2.069	**0.039**	0.077	1.489	0.136
Bacteroidetes Shannon	1.173	0.241	0.415	1.632	0.103	0.137	0.664	0.507
DIVERSITY CLASS								
Bacilli Shannon	1.236	0.216	0.413	0.337	0.736	0.954	0.987	0.324
Gammaproteobacteria Shannon	2.530	**0.005**	**0.041**	1.465	0.142	0.378	1.075	0.169
Betaproteobacteria Shannon	1.652	0.099	0.263	2.927	**0.003**	**0.027**	1.701	0.089
Alphaproteobacteria Shannon	2.379	**0.017**	0.069	2.293	0.022	0.087	0.106	0.915
Clostridia Shannon	1.130	0.258	0.413	0.187	0.852	0.954	1.507	0.132
Bacteroidia Shannon	0.433	0.665	0.665	0.246	0.806	0.954	0.190	0.849
Fusobacteriia Shannon	0.637	0.524	0.665	0.057	0.954	0.954	0.790	0.429
Negativicutes Shannon	0.439	0.660	0.665	0.528	0.598	0.954	1.141	0.254
RICHNESS PHYLUM								
Firmicutes richness	0.146	0.884	0.884	0.064	0.949	0.949	0.088	0.930
Proteobacteria richness	2.717	**0.007**	**0.026**	2.829	**0.005**	**0.019**	0.378	0.705
Actinobacteria richness	0.965	0.334	0.446	1.941	0.052	0.094	1.276	0.202
Bacteroidetes richness	1.359	0.174	0.349	1.808	0.071	0.094	0.669	0.504
RICHNESS CLASS								
Bacilli richness	0.412	0.680	0.777	0.216	0.829	0.864	0.729	0.466
Gammaproteobacteria richness	2.096	**0.036**	0.103	1.300	0.194	0.516	0.785	0.432
Betaproteobacteria richness	2.068	**0.039**	0.103	2.802	**0.005**	**0.041**	1.080	0.280
Alphaproteobacteria richness	2.607	**0.009**	0.073	2.262	0.024	0.095	0.189	0.850
Clostridia richness	0.486	0.627	0.777	0.688	0.491	0.849	1.390	0.165

[a] Degree of Freedom between groups = 2 and within groups = 58

*Benjamini-Hochberg correction

Table S5. Before-after comparisons **(**Wilcoxon-Signed Rank test) for bacterial diversity on skin at total bacterial community, and phylum and class levels among children in (**A**) intervention (n = 29), (**B**) standard (n = 14) and (**C**) nature-oriented daycare centers (n = 19) (Mean ± Standard Deviation = sd). **Bold** font indicates significant differences (p ≤ 0.05).

A) **Intervention**	**Mean before**	**sd before**	**Mean after**	**sd after**	**Statistic**	**P value**	**P adjust***
Observed OTU richness	53.3	29.1	63.5	41.0	239	0.110	
Chao richness index	59.9	40.1	77.5	75.8	257	0.105	
Shannon	3.3	0.8	3.6	0.6	268	0.059	
DIVERSITY PHYLUM							
Firmicutes Shannon	1.9	0.8	2.1	0.6	231	0.319	
Proteobacteria Shannon	2.2	0.8	2.4	0.7	233	0.296	
Actinobacteria Shannon	2.0	0.9	2.0	1.0	187	0.780	
Bacteroidetes Shannon	1.1	0.9	1.4	0.9	198	0.346	
Fusobacteria Shannon	0.5	0.6	0.6	0.7	102	0.486	
DIVERSITY CLASS							
Bacilli Shannon	1.8	0.8	1.9	0.5	225	0.394	0.879
Gammaproteobacteria Shannon	1.6	0.6	1.6	0.7	182	0.879	0.879
Betaproteobacteria Shannon	1.2	0.7	1.3	0.8	208	0.657	0.879
Alphaproteobacteria Shannon	0.6	0.9	1.0	1.0	127	**0.018**	0.144
Clostridia Shannon	0.3	0.4	0.3	0.6	42	0.844	0.879
Bacteroidia Shannon	0.6	0.7	0.7	0.8	97	0.632	0.879
Fusobacteriia Shannon	0.5	0.6	0.6	0.7	102	0.486	0.879
Negativicutes Shannon	0.2	0.4	0.2	0.4	37	0.756	0.879

B) Standard	**Mean before**	**sd before**	**Mean after**	**sd after**	**Statistic**	**P value**
Observed OTU richness	58.9	37.3	44.3	14.7	28	0.235
Chao richness index	69.2	52.8	47.8	19.1	28	0.235
Shannon	3.5	0.8	3.2	0.5	36	0.529
DIVERSITY PHYLUM						
Firmicutes Shannon	2.1	1.1	2.1	0.4	40	0.727
Proteobacteria Shannon	2.1	0.8	2.0	0.6	48	0.889
Actinobacteria Shannon	2.0	0.9	1.6	0.8	27	0.367
Bacteroidetes Shannon	1.2	0.9	1.1	0.7	30	0.505
Fusobacteria Shannon	0.5	0.7	0.6	0.6	25	0.813
DIVERSITY CLASS						
Bacilli Shannon	1.6	0.9	1.8	0.6	50	0.780
Gammaproteobacteria Shannon	1.2	0.6	1.3	0.6	57	0.442
Betaproteobacteria Shannon	1.2	0.7	1.2	0.5	48	0.889
Alphaproteobacteria Shannon	0.4	0.9	0.1	0.3	3	0.281
Clostridia Shannon	0.8	1.2	0.4	0.7	12	0.441
Bacteroidia Shannon	0.7	0.9	0.7	0.7	24	0.906

Fusobacteriia Shannon	0.5	0.7	0.6	0.6	25	0.813
Negativicutes Shannon	0.3	0.4	0.2	0.4	12	0.800
C) Nature-oriented	**Mean before**	**sd before**	**Mean after**	**sd after**	**Statistic**	**P value**
Observed OTU richness	69.5	41.1	73.7	39.2	64	0.864
Chao richness index	84.1	58.5	88.2	56.1	62	0.932
Shannon	3.7	0.8	3.8	0.6	69	0.629
DIVERSITY PHYLUM						
Firmicutes Shannon	2.2	0.6	2.2	0.9	57	0.887
Proteobacteria Shannon	2.4	1.0	2.6	0.8	68	0.670
Actinobacteria Shannon	2.3	0.9	2.6	0.8	74	0.443
Bacteroidetes Shannon	1.5	1.0	1.6	0.8	71	0.551
Fusobacteria Shannon	0.4	0.7	0.5	0.5	30	0.878
DIVERSITY CLASS						
Bacilli Shannon	1.9	0.4	1.7	0.8	49	0.551
Gammaproteobacteria Shannon	1.4	0.6	1.6	0.7	73	0.478
Betaproteobacteria Shannon	1.5	0.7	1.5	0.7	55	0.900
Alphaproteobacteria Shannon	1.3	1.1	1.1	1.1	34	0.724
Clostridia Shannon	0.5	0.8	0.7	1.1	34	0.541
Bacteroidia Shannon	0.8	0.7	0.8	0.9	29	0.756
Fusobacteriia Shannon	0.4	0.7	0.5	0.5	30	0.878
Negativicutes Shannon	0.3	0.5	0.3	0.4	28	0.594

Table S6. Gut bacterial before-after comparisons (Paired t-test) among A) intervention, B) nature-oriented and C) standard daycare children. Relative abundances are shown at order level and diversities at family level [Mean ± Standard Deviation (sd)].

A) Intervention Degrees of Freedom = 22	**Mean before**	**sd before**	**Mean after**	**sd after**	**Statistic**	**P value**	**P adjust***
ORDER RELATIVE ABUNDANCE							
Bacteroidales	1165.3	689.9	1490.9	503.2	2.2	0.039	0.256
Bifidobacteriales	181.1	98.1	190.2	167.8	0.2	0.820	0.888
Burkholderiales	17.5	26.7	17.0	15.1	-0.1	0.941	0.941
Clostridiales	2014.3	490.7	1717.7	401.1	-3.3	**0.003**	**0.043**
Coriobacteriales	45.1	35.3	63.1	66.2	1.6	0.127	0.383
Desulfovibrionales	1.3	3.5	2.8	4.7	1.2	0.236	0.383
Enterobacteriales	14.7	25.9	10.1	18.2	-0.9	0.404	0.478
Erysipelotrichales	11.3	12.5	23.0	29.0	1.8	0.083	0.358
Firmicutes_unclassified	41.1	75.2	22.8	36.2	-1.3	0.201	0.383
Lactobacillales	27.9	40.7	41.8	87.6	0.9	0.404	0.478
Pasteurellales	73.5	274.4	9.7	16.6	-1.1	0.277	0.401
Selenomonadales	94.1	99.5	143.8	166.5	1.3	0.225	0.383
Verrucomicrobiales	136.7	244.1	101.8	170.4	-1.3	0.219	0.383
FAMILY DIVERSITIES							

Bacteroidaceae Shannon	1.4	0.5	1.5	0.5	0.4	0.726	0.726
Bifidobacteriaceae Shannon	0.6	0.4	0.6	0.3	0.8	0.456	0.570
Lachnospiraceae Shannon	2.3	0.3	2.4	0.3	1.7	0.096	0.222
Prevotellaceae Shannon	0.2	0.4	0.1	0.3	-1.6	0.133	0.222
Ruminococcaceae Shannon	1.6	0.5	1.8	0.4	2.8	**0.010**	**0.050**
B) Nature-oriented Degrees of Freedom = 19	**Mean before**	**sd before**	**Mean after**	**sd after**	**Statistic**	**P value**	**P adjust***
ORDER RELATIVE ABUNDANCE							
Bacteroidales	1487.3	629.8	1764.3	840.9	1.6	0.133	
Bifidobacteriales	210.5	191.8	147.5	120.6	-2.1	0.051	
Burkholderiales	12.3	20.6	14.9	17.7	0.5	0.616	
Clostridiales	1910.3	515.2	1664.2	659.9	-1.5	0.147	
Coriobacteriales	42.7	37.8	37.6	39.0	-0.8	0.432	
Desulfovibrionales	1.5	3.9	1.7	3.9	0.2	0.819	
Enterobacteriales	4.4	9.3	15.7	47.2	1.0	0.312	
Erysipelotrichales	17.3	27.3	9.5	9.7	-1.7	0.109	
Firmicutes_unclassified	29.3	53.4	39.4	68.6	1.4	0.177	
Lactobacillales	29.1	44.7	18.9	36.4	-0.7	0.469	
Pasteurellales	17.2	32.8	8.6	12.8	-1.1	0.300	
Selenomonadales	42.8	73.5	65.1	109.0	1.0	0.347	
Verrucomicrobiales	31.9	60.9	39.4	79.8	0.5	0.602	
FAMILY DIVERSITY							
Bacteroidaceae Shannon	1.5	0.3	1.5	0.4	0.0	0.990	
Bifidobacteriaceae Shannon	0.6	0.3	0.5	0.4	-1.8	0.088	
Lachnospiraceae Shannon	2.5	0.4	2.5	0.3	1.2	0.244	
Prevotellaceae Shannon	0.2	0.4	0.3	0.4	1.2	0.254	
Ruminococcaceae Shannon	1.7	0.4	1.8	0.3	1.1	0.292	
C) Standard Degrees of Freedom = 12	**Mean before**	**sd before**	**Mean after**	**sd after**	**Statistic**	**P value**	**P adjust***
ORDER RELATIVE ABUNDANCE							
Bacteroidales	1060.2	791.1	1489.3	630.1	2.0	0.069	0.179
Bifidobacteriales	367.3	233.3	213.6	182.0	-2.1	0.059	0.179
Burkholderiales	1.4	2.6	13.6	11.8	3.4	**0.007**	0.091
Clostridiales	2123.5	642.3	1907.5	623.0	-1.2	0.260	0.483
Coriobacteriales	77.3	71.5	42.5	46.5	-2.6	**0.029**	0.179
Desulfovibrionales	1.3	4.2	2.1	3.3	0.7	0.502	0.670
Enterobacteriales	11.3	15.2	6.9	20.0	-0.5	0.617	0.670
Erysipelotrichales	24.5	25.9	12.6	12.3	-1.7	0.113	0.245
Firmicutes_unclassified	35.6	34.2	44.7	78.4	0.5	0.618	0.670
Lactobacillales	31.4	48.3	4.6	8.3	-2.1	0.060	0.179
Pasteurellales	2.5	5.2	3.1	4.4	0.4	0.718	0.718
Selenomonadales	39.0	65.1	55.1	115.5	0.6	0.580	0.670
Verrucomicrobiales	53.6	120.9	30.4	74.1	-0.5	0.614	0.670
FAMILY DIVERSITY							
Bacteroidaceae Shannon	1.3	0.3	1.5	0.4	2.3	**0.044**	0.219
Bifidobacteriaceae Shannon	0.5	0.3	0.5	0.3	0.1	0.902	0.902
Lachnospiraceae Shannon	2.5	0.2	2.4	0.4	-0.5	0.634	0.793

Prevotellaceae Shannon	0.0	0.1	0.1	0.2	1.3	0.227	0.567
Ruminococcaceae Shannon	1.9	0.4	1.8	0.3	-0.6	0.560	0.793

*Benjamini-Hochberg correction

Table S7. Correlations between diversity changes on skin microbiota and plasma cytokine concentrations.

(**A**) Increase in skin Gammaproteobacterial Alpha diversity during the 28-day intervention period was associated with arise in plasma TGF-β1 concentration when all children (n = 26) were analyzed with linear mixed model. Among the intervention daycare center children (n = 12), (**B**) this diversity increase was also associated with a decrease in plasma IL-17A levels and (**C**) increase in total Treg cell levels. (**D**) Among the nature-oriented daycare center children (n = 10), the high Gammaproteobacterial diversity was associated with an increase in IL-10 expression, while Proteobacterial diversity was associated with a decrease in IL-10 expression. (**E**) Among the standard daycare center children (n = 6), the Gammaproteobacterial diversity change was mostly negative, and it was associated with TGF-β1 plasma concentration. Thus, the change in TGF-β1 plasma concentration was mostly negative. (**F**) Linear mixed-effect model showed that among children in nature-oriented daycare centers (n = 14), the higher abundance of Faecalibacterium prausnitzii (Otu000007) was associated with lower plasma levels of IL-17A and Otu000008 (unknown Faecalibacterium) with higher plasma levels of IL-17A. (**G**) The latter association was observed also within standard daycare children (n = 8). (**H**) Linear mixed-effect model showed that among nature-oriented daycare center children (n = 10), the decrease in IL-17A during the trial was associated with the decrease in the relative abundance of *Dorea* and *Romboutsia*, and increase in *Anaerostipes*.

A) All children: TGF-β1	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Gammaproteobacteria	2.601	0.904	2.877	**0.004**	**0.012**

B) Intervention children: IL-17A	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Gammaproteobacteria	-0.885	0.283	-3.132	**0.002**	**0.003**

C) Treg cells	**Estimate**	**Std. Error**	**t value**	**P value**
Intervention: Gammaproteobacteria	1.238	0.513	2.413	**0.016**
Standard: Gammaproteobacteria	-0.281	0.300	-0.936	0.349

D) Nature-oriented children: IL-10	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Gammaproteobacteria	3.539	0.715	4.947	**7.5 x 10^{-7}**	**2.3 x 10^{-6}**
Proteobacteria	-2.278	0.644	-3.536	**0.0004**	**0.0006**

E) Standard children: TGF-β1	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Gammaproteobacteria	4.388	1.598	2.745	**0.006**	**0.012**

F) Nature-oriented children	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Otu000007	-0.023	0.006	-3.885	**0.000**	**0.004**
Otu000008	0.013	0.004	3.470	**0.001**	**0.009**

G) Standard children	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Otu000008	0.033	0.012	3.067	**0.002**	**0.038**

H) Nature-oriented children: IL-17A	**Estimate**	**Std. Error**	**t value**	**P value**	**P adjusted***
Dorea	0.033	0.011	2.953	**0.003**	**0.027**
Romboutsia	0.0381	0.008	4.794	**1.6 x 10^{-6}**	**5.7 x 10^{-5}**
Anaerostipes	-0.013	0.004	-3.324	**0.0009**	**0.010**

*Benjamini-Hochberg correction

Table S8. Correlation between stool *Faecalibacterium* community composition and plasma cytokine levels.

Community composition of *Faecalibacterium* was associated with the IL-17A concentration in the plasma (n = 55) after but not before the 28-day intervention. No other associations between the measured plasma cytokines and *Faecalibacterium* community composition were found. Non-metric multidimensional scaling (NMDS) with Bray-Curtis metric was used to score the OTUs onto an ordination (NMDS coordinates 1 and 2) and correlation with corresponding cytokine expression levels was assessed using function *envfit* in *vegan* package in R computing environment.

Before	**NMDS 1**	**NMDS 2**	**r^2**	**P-value**	
IL-10	0.292	0.956	0.011	0.794	
IL-17A	-0.517	0.856	0.076	0.179	
TGF-β1	-0.302	0.953	0.045	0.362	
After	**NMDS 1**	**NMDS 2**	**r^2**	**P-value**	**P adjust***
IL-10	-0.950	-0.311	0.048	0.354	0.531
IL-17A	-0.884	-0.468	0.214	**0.015**	**0.045**
TGF-β1	0.918	0.397	0.025	0.585	0.585

*Benjamini-Hochberg correction

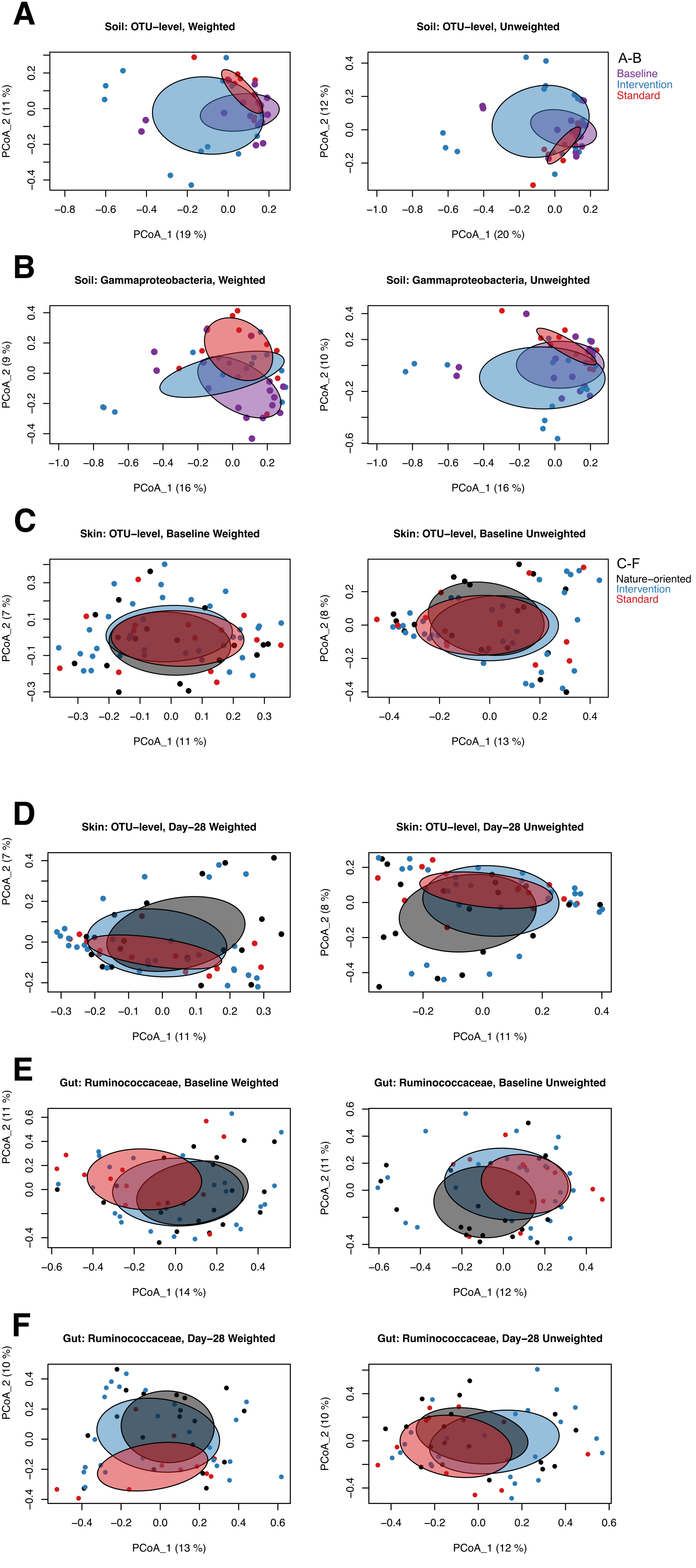
A
Soil: OTU−level, Weighted
PCoA_2 (11 %)
PCoA_1 (19 %)
Soil: OTU−level, Unweighted
PCoA_2 (12 %)
PCoA_1 (20 %)
A-B
Baseline
Intervention
Standard
B
Soil: Gammaproteobacteria, Weighted
PCoA_2 (9 %)
PCoA_1 (16 %)
Soil: Gammaproteobacteria, Unweighted
PCoA_2 (10 %)
PCoA_1 (16 %)
C
Skin: OTU−level, Baseline Weighted
PCoA_2 (7 %)
PCoA_1 (11 %)
Skin: OTU−level, Baseline Unweighted
PCoA_2 (8 %)
PCoA_1 (13 %)
C-F
Nature−oriented
Intervention
Standard
D
Skin: OTU−level, Day−28 Weighted
PCoA_2 (7 %)
PCoA_1 (11 %)
Skin: OTU−level, Day−28 Unweighted
PCoA_2 (8 %)
PCoA_1 (11 %)
E
Gut: Ruminococcaceae, Baseline Weighted
PCoA_2 (11 %)
PCoA_1 (14 %)
Gut: Ruminococcaceae, Baseline Unweighted
PCoA_2 (11 %)
PCoA_1 (12 %)
F
Gut: Ruminococcaceae, Day−28 Weighted
PCoA_2 (10 %)
PCoA_1 (13 %)
Gut: Ruminococcaceae, Day−28 Unweighted
PCoA_2 (10 %)
PCoA_1 (12 %)

Fig. S1. Principal Coordinate Analysis (PCoA) for differences and shifts in bacterial communities A-B) in soil, B-C) on skin and E-F) in the gut. PCoA plots were calculated with dissimilarity indices with Bray-Curtis metric for weighted (abundance data) and unweighted (presence/absence data) data sets. For details of significant differences, please see Table S2. After the intervention period, **(A)** standard and intervention yards had different weighted and unweighted total bacterial and **(B)** Gammaproteobacterial community composition in soil. **(C)** Skin total bacterial community differed before intervention period between children in nature-oriented and standard daycares, **(D)** but not after intervention. In the gut, the sole difference at baseline was found **(E)** between nature-oriented and standard children in Ruminococcaceae community before intervention, while **(F)** after the intervention period Ruminococcaceae community was different additionally between the intervention and standard children.

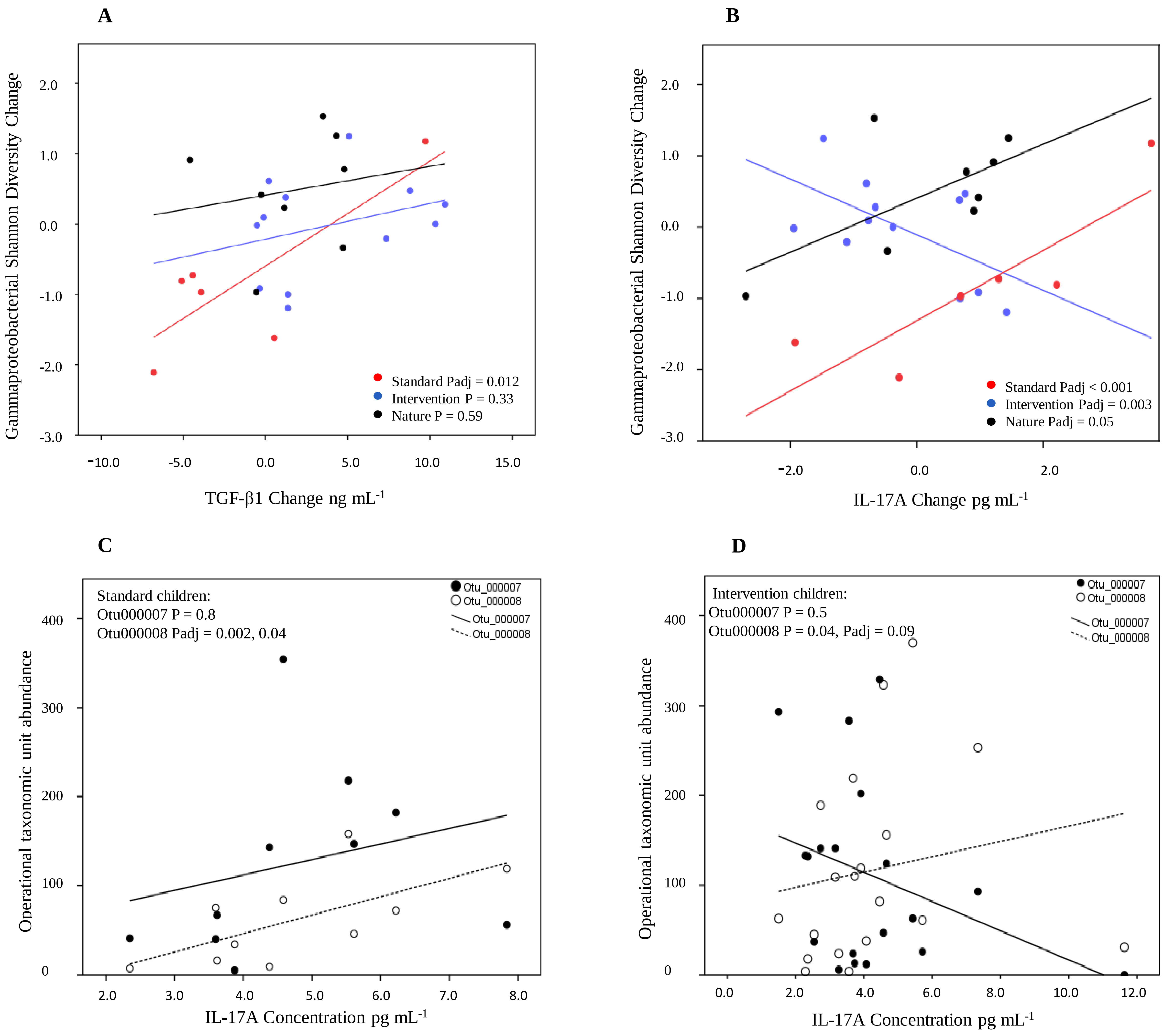
A
Gammaproteobacterial Shannon Diversity Change
2.0
1.0
0.0
-1.0
-2.0
-3.0
-10.0
-5.0
0.0
5.0
10.0
15.0
TGF-β1 Change ng mL-1
● Standard Padj = 0.012
● Intervention P = 0.33
● Nature P = 0.59
B
Gammaproteobacterial Shannon Diversity Change
2.0
1.0
0.0
-1.0
-2.0
-3.0
-2.0
0.0
2.0
IL-17A Change pg mL-1
● Standard Padj < 0.001
● Intervention Padj = 0.003
● Nature Padj = 0.05
C
Standard children:
Otu000007 P = 0.8
Otu000008 Padj = 0.002, 0.04
● Otu_000007
○ Otu_000008
Otu_000007
Otu_000008
Operational taxonomic unit abundance
400
300
200
100
0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
IL-17A Concentration pg mL-1
D
Intervention children:
Otu000007 P = 0.5
Otu000008 P = 0.04, Padj = 0.09
● Otu_000007
○ Otu_000008
Otu_000007
Otu_000008
Operational taxonomic unit abundance
400
300
200
100
0
0.0
2.0
4.0
6.0
8.0
10.0
12.0
IL-17A Concentration pg mL-1

Fig. S2. Associations between change in A-B) skin Gammaproteobacterial diversity and C-D) gut Faecalibacterium OTUs, and immune markers. Skin Gammaproteobacterial diversity change was associated with plasma **(A)** TGF-β1 (ng mL^{-1}) and **(B)** IL-17A (pg mL^{-1}) change among children in standard, intervention and nature-oriented daycares. **(C)** Among standard and **(D)** intervention children, *Faecalibacterium* Otu000008 was associated with an increase in IL-17A concentration (results from end of trial). Skin alpha diversity (Shannon index) and immune markers were measured on days 0 and 28 (change = day 28 – day 0).