# Supplementary Information

# Impact of Medium- and Long-Chain Triacylglycerols and *sn*-2 Palmitate on Temperament Development in Term Infants: Potential Role of Gut *Bifidobacterium*

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**Table S1.** Demographic characteristics of participants

| | Novel-F | Contr-F | BF | *p* |
|---|---|---|---|---|
| | n = 65 | n = 46 | n = 66 | |
| **Birth characteristics** | | | | |
| Gestational age, weeks | 39.1±1.3 | 39.4±1.4 | 40.3±1.4 | <0.001 |
| Male infants, n (%) | 36 (55.4%) | 27 (58.7%) | 38 (57.6%) | 0.936 |
| Vaginal delivery, n (%) | 26 (40.0%) | 28 (60.9%) | 25 (37.9%) | 0.035 |
| Weight, g | 3291±390 | 3294±388 | 3429±336 | 0.063 |
| Length, cm | 50.2±1.3 | 50.4±1.2 | 50.5±1.6 | 0.419 |
| **Baseline** | | | | |
| $Z_{w/a}$ | 0.09±1.00 | −0.02±0.92 | 0.18±0.89 | 0.518 |
| $Z_{l/a}$ | 0.21±0.97 | 0.14±0.85 | 0.17±0.75 | 0.919 |
| $Z_{w/l}$ | −0.33±0.85 | −0.29±1.25 | −0.08±1.00 | 0.348 |
| Infectious diseases, n (%) | 4 (6.2%) | 1 (2.2%) | 2 (3.0%) | 0.557 |
| **Endpoint** | | | | |
| $Z_{w/a}$ | 0.26±0.77 | −0.26±0.76 | 0.14±0.90 | 0.004 |
| $Z_{l/a}$ | 0.26±0.97 | −0.09±0.92 | −0.05±1.00 | 0.095 |
| $Z_{w/l}$ | 0.14±0.92 | −0.92±0.98 | 0.37±1.15 | 0.048 |
| Infectious diseases, n (%) | 3 (4.6%) | 3 (6.5%) | 2 (3.0%) | 0.536 |
| **Maternal characteristics** | | | | |
| Age, years | 28.9±4.9 | 28.6±4.9 | 27.6±4.4 | 0.259 |
| Primipara, n (%) | 18 (27.7%) | 16 (34.8%) | 28 (42.4%) | 0.210 |
| Education, completed senior high school, n (%) | 19 (29.2%) | 26 (56.5%) | 33 (50.0%) | 0.008 |
| **Socio-economic conditions** | | | | |
| Living space per capita ($m^2$) | 30.51±10.72 | 30.96±9.92 | 34.78±9.79 | 0.051 |
| **Daily formula intake, mL** | | | | |
| Baseline | 676±70 | 648±80 | / | 0.058 |
| Endpoint | 924±102 | 897±118 | / | 0.219 |

Mean ± SD for continuous variables and *n* (%) for categorical variables. One-way ANOVA or *t* test was used to compare continuous variables, and chi-square test or Fisher's exact tests was used for categorical variables, as appropriate. Abbreviations: $Z_{w/a}$, weight-for-age z-scores; $Z_{l/a}$, length-for-age z-scores; $Z_{w/l}$, weight-for-length z-scores.

**Table S2.** Relative abundance of gut microbiome at genus level during the intervention (%)

| Genus | Time Point | IG | CG | BG | $p_{\text{Baseline}}$ | $p^1$ | $p^2$ | $p^3$ |
|---|---|---|---|---|---|---|---|---|
| *Bifidobacterium* | Baseline | 56.45±22.03 | 63.24±23.24 | 53.64±27.32 | 0.164 | **0.011** | 0.759 | **0.004** |
| | Endpoint | 69.20±16.17 | 60.18±27.67 | 68.28±20.67 | | | | |
| *Streptococcus* | Baseline | 14.16±19.39 | 10.44±19.18 | 14.98±18.68 | 0.067 | 0.183 | 0.202 | 0.867 |
| | Endpoint | 3.77±5.56 | 5.88±12.61 | 9.42±10.53 | | | | |
| *Escherichia-Shigella* | Baseline | 8.31±10.26 | 6.27±11.58 | 8.95±14.13 | 0.249 | 0.454 | 0.736 | 0.282 |
| | Endpoint | 7.13±8.98 | 7.53±15.60 | 6.98±13.21 | | | | |
| *Klebsiella* | Baseline | 3.59±8.79 | 2.92±7.69 | 8.03±20.53 | 0.214 | 0.758 | 0.189 | 0.125 |
| | Endpoint | 1.84±5.40 | 2.21±8.92 | 2.35±11.08 | | | | |
| *Enterococcus* | Baseline | 2.45±3.08 $^{a}$ | 3.96±5.51 $^{a}$ | 1.54±4.24 $^{b}$ | **< 0.001** | 0.468 | 0.919 | 0.405 |
| | Endpoint | 3.62±4.87 | 6.21±9.91 | 2.47±4.69 | | | | |
| *Lactobacillus* | Baseline | 1.95±4.98 | 1.93±3.42 | 1.52±3.48 | 0.146 | 0.423 | 0.947 | 0.381 |
| | Endpoint | 2.44±6.83 | 1.32±3.64 | 2.04±5.00 | | | | |
| *Collinsella* | Baseline | 1.39±3.92 | 1.87±6.66 | 1.44±5.72 | 0.331 | 0.773 | 0.280 | 0.193 |
| | Endpoint | 2.18±4.28 | 2.87±8.03 | 0.97±3.75 | | | | |
| *unclassified_f_Enterobacteriaceae* | Baseline | 2.18±9.02 $^{a}$ | 1.34±3.27 $^{ab}$ | 0.99±3.25 $^{b}$ | **0.015** | 0.276 | 0.102 | 0.676 |
| | Endpoint | 0.47±2.13 | 0.86±3.61 | 0.95±3.21 | | | | |
| *Blautia* | Baseline | 2.56±6.70 | 0.59±2.29 | 0.39±2.69 | 0.055 | **0.002** | **0.048** | 0.156 |
| | Endpoint | 0.78±1.68 | 1.96±6.51 | 0.38±2.45 | | | | |
| *Veillonella* | Baseline | 1.23±4.01 | 1.11±4.50 | 1.01±4.89 | 0.769 | 0.392 | 0.873 | 0.470 |
| | Endpoint | 2.67±10.42 | 1.03±3.74 | 2.18±7.15 | | | | |

Data were expressed as mean±SD. $p_{Baseline}$ indicated baseline comparisons among the three groups using the Kruskal-Wallis test. Genera with significant differences were further analyzed by Bonferroni-corrected post hoc pairwise comparisons; values with different superscript letters (a, b) indicated significant differences at baseline. Linear mixed-effect models were used to examine the changes of genera during the two-month intervention, with fixed effects including time × group, gender, mode of delivery, gestational age, maternal education, and change in $Z_{w/a}$, with subjects included as random effects. *p*-values indicated the significant differences of the time × group interaction between the IG and CG ($p^1$), IG and BG ($p^2$), and CG and BG ($p^3$).

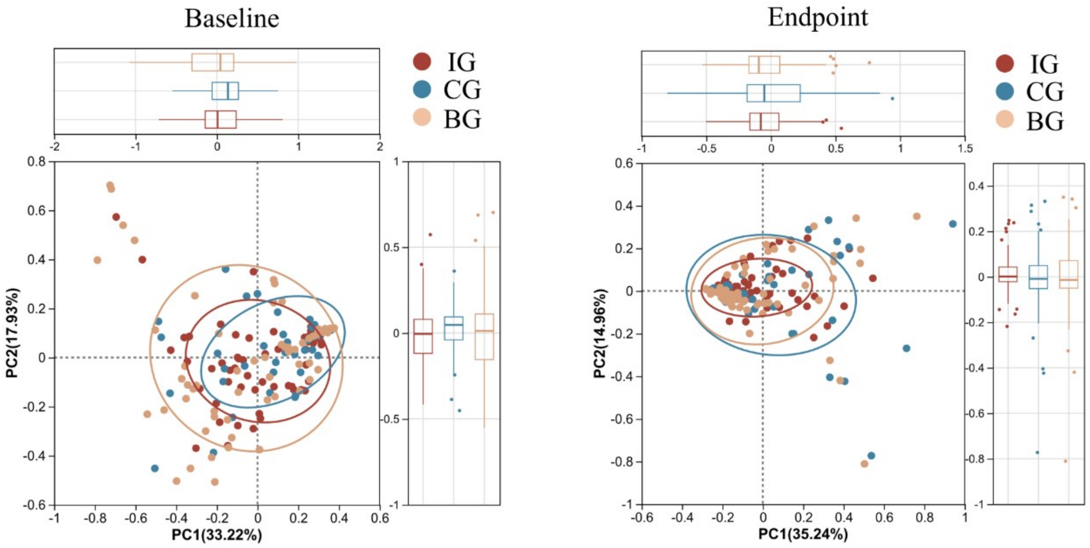

**Figure S1**. Beta diversity of the gut microbiome at the genus level. PCoA plots showed the microbial communities based on weighted UniFrac distance across groups. Box plots on the axes represented the distribution of values for PC1 and PC2. Differences in beta diversity between groups were assessed using the Adonis test and the results indicated no significant differences among the three groups at both baseline ($p = 0.077$) and endpoint ($p = 0.139$).