Electronic Supplementary Material (ESI) for Food & Function.
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**Table S1: Diet composition**

| | Sn2PA | Sn2PDHA | Sn2PARA |
|---|---|---|---|
| | g/100 g | g/100 g | g/100 g |
| Protein | 19.6 | 19.6 | 19.6 |
| Carbohydrate | 61.9 | 61.9 | 61.9 |
| Fat | 10.0 | 10.0 | 10.0 |
| Ingredient | g | g | g |
| Casein | 180 | 180 | 180 |
| L-Cystine | 2.7 | 2.7 | 2.7 |
| Corn Starch | 357.73 | 357.73 | 357.73 |
| Sucrose | 90 | 90 | 90 |
| maltodextrin 10 | 118.8 | 118.8 | 118.8 |
| Cellulose,BW 200 | 45 | 45 | 45 |
| sn2PA fat | 93 | 83.7 | 83.7 |
| DHA oil | | 9.3 | |
| ARA oil | | | 9.3 |
| Mineral Mix S10022G | 31.5 | 31.5 | 31.5 |
| t-Butylhydroquinone | 0.0126 | 0.0126 | 0.0126 |
| Vitamin Mix V10037 | 9.0 | 9.0 | 9.0 |
| Choline Bitartrate | 2.25 | 2.25 | 2.25 |
| **Total** | **930** | **930** | **930** |

**Table S2: Fatty acid composition (g/100g total fatty acid) of oils and fats in animal feeds**

| **Fatty acids** | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** |
|---|---|---|---|
| C12:0 | 0.3 | 0.2 | 0.2 |
| C14:0 | 1.1 | 1.6 | 1.1 |
| C16:0 | 34.8 | 33.2 | 32.4 |
| C18:0 | 3.4 | 3.2 | 4.1 |
| C18:1n-9 | 50.3 | 47.3 | 47.1 |
| C18:2n-6 | 8.5 | 7.7 | 8.3 |
| C18:3n-3 | 0.1 | 0.0 | 0.3 |
| C20:4*n*-6 | 0 | 0.0 | 4.7 |
| C22:6*n*-3 | 0 | 4.5 | 0.0 |
| Others | 1.6 | 2.3 | 1.7 |

**Table S3: Sequences of Real-time PCR primers**

| **Genes** | **Direction** | **Sequence (5'-3')** |
|---|---|---|
| GAPDH | Forward | TCTCTGCTCCTCCCTGTTCT |
| | Reverse | TACGGCCAAATCCGTTCACA |
| *Fas* | Forward | TCTGATCAGTGGCCTCCTTAAC |
| | Reverse | CAGTGCTGAGATGTGGGAATAC |
| *Srebp-1c* | Forward | TGGAGCGAGCATTGAACTGT |
| | Reverse | GTGGTAGCCATGCTGGAACT |
| *PPARα* | Forward | TACCACTATGGAGTCCACGCATGT |
| | Reverse | TTGCAGCTTCGATCACACTTGTCG |

GAPDH: glyceraldehyde-3-phosphate dehydrogenase; *Fas*: fatty acid synthase; *Srebp-1c*: sterol regulatory element-binding protein 1; *PPARα:* peroxisome proliferator-activated receptor α.

**Table S4: Feed intake and growth during the 6-week experimental period**

| | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** | *P* |
|---|---|---|---|---|
| Final weight(g) | $423^{a}$ ± 14.6 | $424^{a}$ ± 25.7 | $410^{a}$ ± 21.3 | 0.32 |
| Epididymal fat (g) | $7.11^{a}$ ± 1.10 | $5.67^{b}$ ± 0.85 | $5.35^{b}$ ± 0.85 | 0.001 |
| Perirenal fat (g) | $6.94^{a}$ ± 1.09 | $6.54^{a}$ ± 1.22 | $6.71^{a}$ ± 1.13 | 0.76 |
| Food intake (g/d per rat) | $19.4^{a}$ ± 0.8 | $18.8^{a}$ ± 0.4 | $18.6^{a}$ ± 0.5 | 0.34 |

The results are the mean ± SD of 9 animals per group. $^{a,b}$ Mean values within a row with unlike superscript letters were significantly different ($P < 0.05$; ANOVA followed by post hoc Tukey's multiple comparison test).

**Table S5: Fatty acid compositions (g/100g total fatty acid) in the liver of rats.**

| | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** | *P* |
|---|---|---|---|---|
| C14:0 | $0.67^{a} \pm 0.13$ | $0.72^{a} \pm 0.12$ | $0.59^{a} \pm 0.07$ | 0.08 |
| C16:0 | $26.53^{a} \pm 0.58$ | $26.69^{a,b} \pm 0.89$ | $24.74^{c} \pm 0.98$ | 0.002 |
| C16:1*n*-9 | $3.58^{a} \pm 0.45$ | $2.66^{b} \pm 0.43$ | $2.28^{b,c} \pm 0.39$ | 0.0003 |
| C18:0 | $8.48^{a} \pm 0.40$ | $7.69^{a} \pm 0.88$ | $8.89^{a} \pm 1.19$ | 0.09 |
| C18:1*n*-9 | $43.0^{a} \pm 2.56$ | $36.8^{a} \pm 3.80$ | $37.3^{a} \pm 5.61$ | 0.06 |
| C18:2*n*-6 | $4.73^{a} \pm 0.81$ | $7.06^{b} \pm 0.57$ | $6.84^{b,c} \pm 1.08$ | 0.0004 |
| C20:4*n*-6 | $9.92^{a} \pm 1.53$ | $6.89^{b} \pm 1.13$ | $15.2^{c} \pm 2.84$ | < 0.0001 |
| C20:5*n*-3 | $0.43^{a} \pm 0.05$ | $1.48^{b} \pm 0.18$ | $0.3^{a} \pm 0.03$ | < 0.0001 |
| C22:6*n*-3 | $0.87^{a} \pm 0.11$ | $7.88^{b} \pm 1.28$ | $0.49^{a,c} \pm 0.06$ | < 0.0001 |
| Others | $1.7^{a} \pm 0.21$ | $2.1^{a,b} \pm 0.33$ | $3.3^{b,c} \pm 0.26$ | 0.03 |

The results are the mean ± SD of 9 animals per group. $^{a,b,c}$ Mean values within a row with unlike superscript letters were significantly different ($P < 0.05$; ANOVA followed by post hoc Tukey's multiple comparison test).

**Table S6: Fatty acid compositions (g/100g total fatty acid) in the brain of rats.**

| | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** | *P* |
|---|---|---|---|---|
| C14:0 | $0.50^{a} \pm 0.12$ | $0.59^{a} \pm 0.09$ | $0.44^{a} \pm 0.08$ | 0.11 |
| C16:0 | $25.7^{a} \pm 1.00$ | $25.2^{a} \pm 0.80$ | $25.7^{a} \pm 0.81$ | 0.56 |
| C16:1 *n*-9 | $0.56^{a} \pm 0.08$ | $0.49^{a} \pm 0.08$ | $0.63^{a} \pm 0.05$ | 0.21 |
| C18:0 | $19.1^{a} \pm 1.14$ | $18.7^{a} \pm 1.26$ | $19.2^{a} \pm 0.72$ | 0.69 |
| C18:1*n*-9 | $22.2^{a} \pm 1.09$ | $22.8^{a,b} \pm 0.85$ | $20.7^{c} \pm 0.65$ | 0.003 |
| C18:2*n*-6 | $0.76^{a} \pm 0.07$ | $1.58^{b} \pm 0.24$ | $1.02^{c} \pm 0.16$ | < 0.0001 |
| C18:3*n*-3 | $0.53^{a} \pm 0.07$ | $0.59^{a} \pm 0.09$ | $0.59^{a} \pm 0.07$ | 0.36 |
| C20:4*n*-6 | $6.00^{a} \pm 0.41$ | $5.11^{a,b} \pm 0.85$ | $8.24^{c} \pm 0.97$ | < 0.0001 |
| C22:5*n*-3 | $0.16^{a} \pm 0.04$ | $0.18^{a} \pm 0.03$ | $0.14^{a} \pm 0.05$ | 0.38 |
| C22:6*n*-3 | $12.6^{a} \pm 0.48$ | $14.5^{b} \pm 0.74$ | $12.3^{a,c} \pm 0.86$ | 0.0001 |
| Others | $11.8^{a} \pm 2.36$ | $10.2^{a} \pm 1.59$ | $11.0^{a} \pm 1.54$ | 0.54 |

The results are the mean ± SD of 9 animals per group. $^{a,b,c}$Mean values within a row with unlike superscript letters were significantly different ($P < 0.05$; ANOVA followed by post hoc Tukey's multiple comparison test).

**Table S7: Fatty acid compositions (g/100g total fatty acid) in the epididymal adipose tissue of rats.**

| | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** | *P* |
|---|---|---|---|---|
| C14:0 | $1.25^{a} \pm 0.13$ | $1.54^{b} \pm 0.12$ | $1.28^{a,c} \pm 0.07$ | 0.0007 |
| C16:0 | $27.31^{a} \pm 0.35$ | $29.39^{b} \pm 0.76$ | $27.04^{a,c} \pm 0.75$ | < 0.0001 |
| C16:1*n*-9 | $5.18^{a} \pm 0.64$ | $3.35^{b} \pm 0.43$ | $3.75^{b,c} \pm 0.89$ | 0.0008 |
| C18:0 | $2.20^{a} \pm 0.14$ | $3.07^{b} \pm 0.21$ | $2.94^{b,c} \pm 0.29$ | < 0.0001 |
| C18:1*n*-9 | $55.03^{a} \pm 0.80$ | $51.71^{b} \pm 0.69$ | $52.66^{b,c} \pm 1.15$ | < 0.0001 |
| C18:2*n*-6 | $5.98^{a} \pm 0.40$ | $7.14^{b} \pm 0.40$ | $8.14^{c} \pm 0.45$ | < 0.0001 |
| C18:3*n*-3 | $0.11^{a} \pm 0.01$ | $0.15^{b} \pm 0.01$ | $0.15^{b,c} \pm 0.01$ | 0.0002 |
| C20:4*n*-6 | $0.12^{a} \pm 0.01$ | $0.23^{a} \pm 0.02$ | $0.55^{b} \pm 0.02$ | 0.0005 |
| C22:5*n*-3 | $0.0^{a}$ | $0.45^{b} \pm 0.01$ | $0.0^{a}$ | < 0.0001 |
| C22:6*n*-3 | $0.0^{a}$ | $0.98^{b} \pm 0.05$ | $0.0^{a}$ | < 0.0001 |
| Others | $2.82^{a} \pm 0.24$ | $1.99^{a} \pm 0.17$ | $3.49^{a} \pm 0.36$ | 0.12 |

The results are the mean ± SD of 9 animals per group. $^{a,b,c}$ Mean values within a row with unlike superscript letters were significantly different ($P < 0.05$; ANOVA followed by post hoc Tukey's multiple comparison test).

**Table S8: Fatty acid compositions (g/100g total fatty acid) in the perirenal adipose of rats.**

| | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** | *P* |
|---|---|---|---|---|
| C14:0 | $1.25^{a} \pm 0.07$ | $1.55^{b} \pm 0.11$ | $1.33^{a,c} \pm 0.15$ | 0.0011 |
| C16:0 | $27.84^{a} \pm 0.65$ | $29.63^{b} \pm 0.40$ | $27.77^{a,c} \pm 1.05$ | 0.0008 |
| C16:1*n*-9 | $4.26^{a} \pm 0.78$ | $3.23^{b} \pm 0.33$ | $3.60^{a,b} \pm 0.68$ | 0.0348 |
| C18:0 | $2.58^{a} \pm 0.27$ | $3.26^{b} \pm 0.19$ | $3.34^{b,c} \pm 0.43$ | < 0.0001 |
| C18:1*n*-9 | $55.88^{a} \pm 0.60$ | $52.00^{b} \pm 0.54$ | $53.92^{c} \pm 0.97$ | < 0.0001 |
| C18:2*n*-6 | $5.53^{a} \pm 0.39$ | $6.80^{b} \pm 0.38$ | $7.29^{b,c} \pm 0.65$ | < 0.0001 |
| C18:3*n*-3 | $0.12^{a} \pm 0.01$ | $0.16^{b} \pm 0.01$ | $0.17^{b,c} \pm 0.02$ | < 0.0001 |
| C20:4*n*-6 | $0.11^{a} \pm 0.01$ | $0.13^{a} \pm 0.01$ | $0.61^{b} \pm 0.01$ | 0.0021 |
| C22:5*n*-3 | $0.0^{a}$ | $0.27^{b} \pm 0.01$ | $0.0^{a}$ | < 0.0001 |
| C22:6*n*-3 | $0.0^{a}$ | $0.78^{b} \pm 0.05$ | $0.0^{a}$ | < 0.0001 |
| Others | $2.43^{a} \pm 0.16$ | $2.19^{a} \pm 0.32$ | $1.97^{a} \pm 0.36$ | 0.09 |

The results are the mean ± SD of 9 animals per group. $^{a,b,c}$ Mean values within a row with unlike superscript letters were significantly different ($P < 0.05$; ANOVA followed by post hoc Tukey's multiple comparison test).

**Table S9: Richness and diversity indexes relative to each fecal sample. (OTU cutoff of 0.03)**

| | **Sn2PA** | **Sn2PDHA** | **Sn2PARA** | *P1[*] | *P2 |
|---|---|---|---|---|---|
| Reads | 53691 ± 10340 | 46295 ± 12024 | 62740 ± 10448 | 0.46 | 0.34 |
| OTUs | 449 ± 10 | 421 ± 19 | 358 ± 39 | 0.08 | 0.0071 |
| Coverage (%) | 99.87 ± 0.03 | 99.80 ± 0.04 | 99.87 ± 0.03 | 0.12 | 0.96 |
| Ace | 495 ± 6 | 499 ± 16 | 436 ± 32 | 0.73 | 0.037 |
| Chao1 | 504 ± 15 | 515 ± 34 | 432 ± 35 | 0.67 | 0.031 |
| Shannon indices | 4.27 ± 0.097 | 3.80 ± 0.13 | 2.45 ± 0.39 | 0.008 | 0.0014 |
| Simpson indices | 0.03 ± 0.005 | 0.07 ± 0.01 | 0.33 ± 0.11 | 0.0098 | 0.10 |

[*] *P1* value for the indexes were determined by student's t-test between sn2PA and sn2PDHA groups.

[*] *P2* value for the indexes were determined by student's t-test between sn2PA and sn2PARA groups.

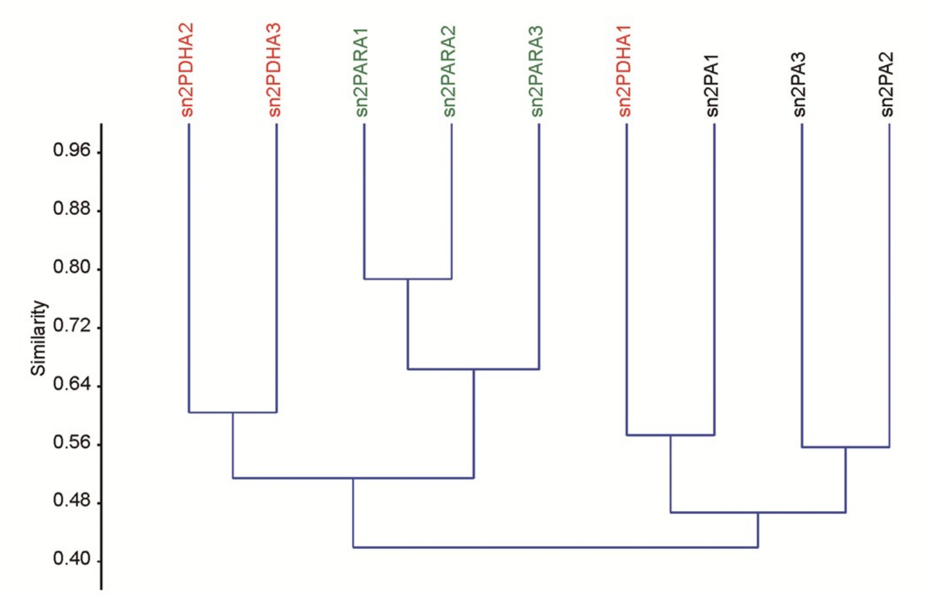

Fig. S1 Clustering analysis of fecal microbiota.

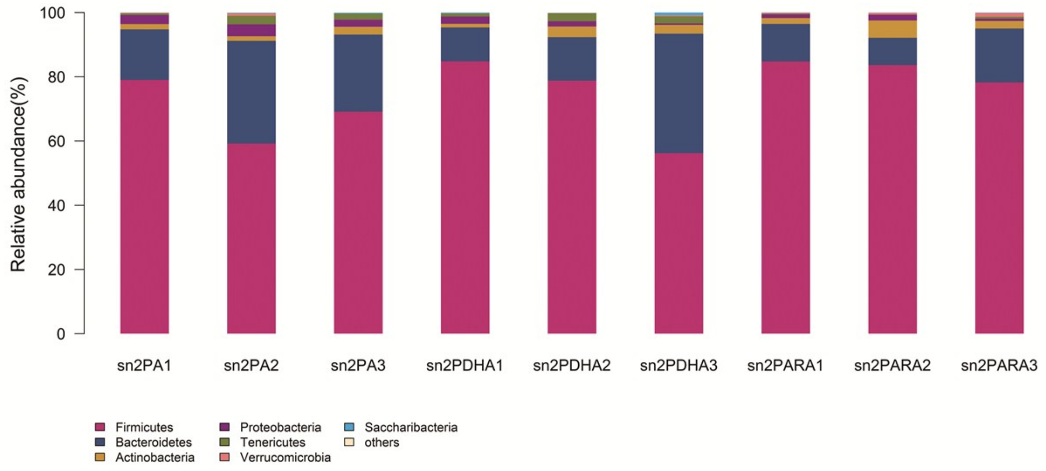

Fig.S2 Fecal bacterial population at the phylum level. The ones with an abundance less than 1% in the phyla were combined as “others”.

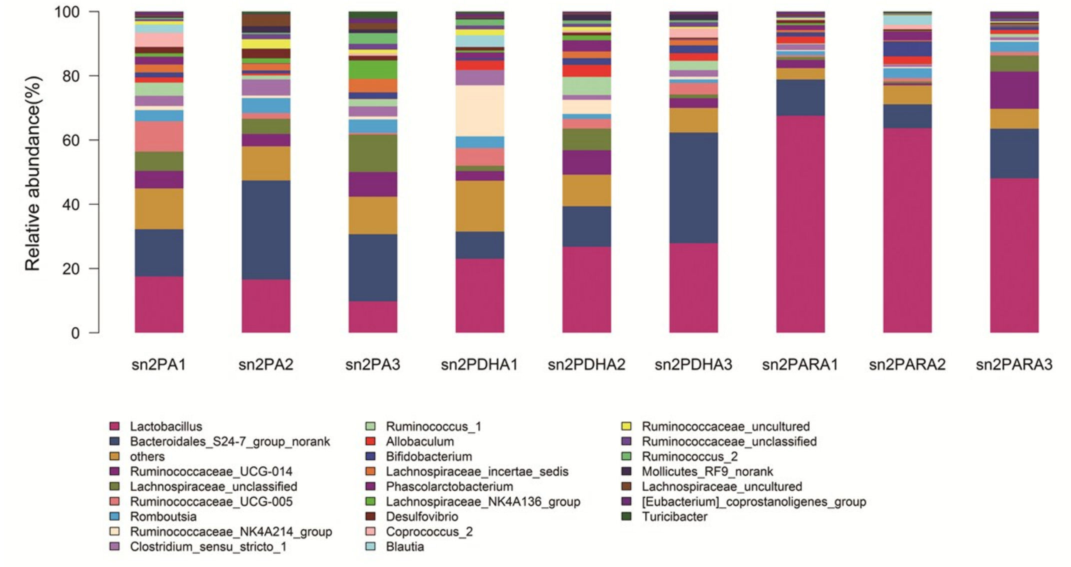

Fig. S3 Fecal bacterial population at the genus level. Relative abundance of different bacterial genus within the different communities. Sequences that could not be classified into any known group were assigned as “Unclassified bacteria” and “No_Rank”. The ones with an abundance less than 1% in the genera were combined as “others”.