

Table S1: Primers used for PCR

| Gene | FORWARD PRIMER | REVERSE PRIMER | ACCESSION NUMBER |
|---------------|---------------------------|------------------------|------------------|
| ACTIN | CCCTAAGGCCAACCGTGAAA | CATACAGGGACAACACAGCCT | NM_031144.3 |
| HPRT1 | TAGGTCCATTCCCTATGACTGTAGA | TGGCCTGTATCCAACACTTC | XM_008773659.2 |
| RPS18 | TCCACAGGAGGCCTACAC | CTCTTGGTGAGGTCAATGTCTG | XM_002727833.5 |
| Fasn | TAAGCGGTCTGGAAAGCTGA | CACCAGTGTTCCTCGG | NM_017332.1 |
| Lipe (HLS) | GTGTGTGAGCGCCTATTCAG | GCAGGCAATGGGGTCTTATG | NM_012859.1 |
| LPL | ACTCAAAGTTAGGCCAGCT | GGCCCAGCAACATTATCCAG | NM_012598.2 |
| PPAR γ | TCAGCTCTGTGAACGGGAT | GCACTGCCTATGAGCACTTC | NM_013124.3 |

Table S2: Fatty acid composition (% total fatty acids) of dam liver, mesenteric adipose tissue and mammary gland at weaning.

| | Liver | | Mesenteric fat | | Mammary gland | |
|---------------|------------|--------------|----------------|---------------|---------------|---------------|
| Maternal diet | C | LA | C | LA | C | LA |
| SFA | 37.6 (1.9) | 39.8 (0.5) | 25.3 (0.3) | 26.9 (0.2)* | 32.0 (2.3) | 37.1 (1.6) |
| MUFA | 47.8 (3.4) | 29.5 (4.5)* | 59.1 (0.8) | 33.0 (0.7)*** | 54.5 (1.4) | 25.9 (1.5)*** |
| n-6 PUFA | 11.4 (4.2) | 28.0 (3.7)** | 14.4 (1.0) | 38.8 (0.9)*** | 12.0 (1.0) | 35.6 (0.2)*** |
| 18:2 n-6 | 4.8 (1.6) | 16.2 (1.3)* | 13.8 (1.0) | 36.3 (1.0)*** | 9.6 (1.4) | 31.5 (0.8)*** |
| 20:4 n-6 | 5.8 (2.4) | 9.2 (3.6) | 0.3 (0.0) | 1.0 (0.1)*** | 1.5 (0.4) | 2.3 (0.4) |
| n-3 PUFA | 3.2 (1.2) | 2.8 (0.9) | 1.2 (0.1) | 1.2 (0.0) | 1.5 (0.1) | 1.3 (0.0)* |
| n-6/n-3 | 3.6 | 11.71* | 12.5 | 31.4*** | 8.1 | 28.3*** |

* P<0.05, ** P<0.01, *** P<0.001

Table S3: Fatty acid composition (% total fatty acids) of offspring liver and mesenteric adipose tissue at weaning.

| | Liver | | Mesenteric fat | |
|---------------|------------|---------------|----------------|---------------|
| Maternal diet | C | LA | C | LA |
| SFA | 40.7 (2.0) | 35.3 (0.4) | 37.6 (0.5) | 35.6 (0.9) |
| MUFA | 39.5 (0.8) | 20.8 (2.1)** | 54.5 (0.7) | 28.9 (0.7)*** |
| n-6 PUFA | 13.7 (1.2) | 38.8 (1.5)*** | 6.6 (0.2) | 34.0 (1.5)*** |
| 18:2 n-6 | 5.0 (0.3) | 20.8 (0.4)*** | 5.7 (0.1) | 31.5 (1.5)*** |
| 20:4 n-6 | 7.4 (0.6) | 13.4 (1.0)** | 0.6 (0.1) | 1.3 (0.1)** |
| n-3 PUFA | 5.8 (0.5) | 5.0 (0.4) | 1.2 (0.1) | 1.4 (0.1) |
| n-6/n-3 | 2.4 | 7.8*** | 5.7 | 24.8*** |

* P<0.05, ** P<0.01, *** P<0.001

Table S4: Microbiota family relative abundances in the rat caecum at 3 months of age

| | C-C | | C-LA | | LA-C | | LA-LA | | Maternal diet | Weaning diet | Maternal x weaning diet |
|---|-------|----------|-------|----------|-------|----------|-------|----------|---------------|--------------|-------------------------|
| <i>Actinobacteria, Bifidobacteriaceae</i> | 0.11 | (0.05) | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | ns | ns | ns |
| <i>Actinobacteria, Sporichthyaceae</i> | 0.01 | (0.00) | 0.01 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | 0.01 | ns | ns |
| <i>Actinobacteria, Micrococcaceae</i> | 0.18 | (0.04) | 0.21 | (0.05) | 0.21 | (0.08) | 0.51 | (0.27) | ns | ns | ns |
| <i>Actinobacteria, Atopobiaceae</i> | 0.55 | (0.32) | 0.02 | (0.01) | 0.03 | (0.01) | 0.02 | (0.01) | ns | ns | ns |
| <i>Actinobacteria, Eggethellaceae</i> | 0.09 | (0.02) | 0.07 | (0.01) | 0.07 | (0.02) | 0.06 | (0.02) | ns | ns | ns |
| <i>Bacteroidetes, Bacterioidaceae</i> | 0.65 | (0.27) a | 10.15 | (3.72) b | 1.43 | (0.57) a | 1.22 | (0.18) a | 0.02 | 0.009 | 0.007 |
| <i>Bacteroidetes, Muribaculaceae</i> | 2.93 | (1.02) | 0.66 | (0.20) | 2.47 | (0.33) | 2.15 | (0.10) | ns | 0.05 | ns |
| <i>Bacteroidetes, Prevotellaceae</i> | 0.54 | (0.37) | 0.00 | (0.00) | 0.03 | (0.02) | 5.21 | (2.42) | ns | ns | ns |
| <i>Bacteroidetes, Rikenellaceae</i> | 3.59 | (1.76) | 0.01 | (0.01) | 3.99 | (2.40) | 3.84 | (0.54) | ns | ns | ns |
| <i>Bacteroidetes, Tannerellaceae</i> | 4.22 | (1.67) | 6.84 | (2.02) | 11.99 | (2.23) | 9.22 | (2.07) | 0.03 | ns | ns |
| <i>Firmicutes, Enterococcaceae</i> | 0.02 | (0.01) | 0.00 | (0.00) | 0.01 | (0.01) | 0.01 | (0.01) | ns | ns | ns |
| <i>Firmicutes Lactobacillaceae</i> | 1.46 | (0.25) a | 0.21 | (0.04) b | 0.22 | (0.07) b | 0.53 | (0.23) b | 0.04 | 0.03 | 0.002 |
| <i>Firmicutes Streptococcaceae</i> | 0.03 | (0.02) | 0.03 | (0.00) | 0.02 | (0.01) | 0.08 | (0.04) | ns | ns | ns |
| <i>Firmicutes Christensenellaceae</i> | 0.22 | (0.05) a | 0.96 | (0.09) b | 0.39 | (0.12) a | 0.25 | (0.09) a | 0.01 | 0.008 | 0.007 |
| <i>Firmicutes Clostridiaceae</i> | 8.64 | (1.61) a | 0.39 | (0.15) b | 2.29 | (0.75) b | 3.53 | (1.49) b | ns | 0.02 | 0.003 |
| <i>Firmicutes Clostridiales vadinBB60 group</i> | 0.01 | (0.01) | 0.00 | (0.00) | 0.01 | (0.01) | 0.00 | (0.00) | ns | ns | ns |
| <i>Firmicutes Defluviitaleaceae</i> | 0.02 | (0.02) | 0.00 | (0.00) | 0.00 | (0.00) | 0.02 | (0.01) | ns | ns | ns |
| <i>Firmicutes Eubacteriaceae</i> | 0.01 | (0.01) | 0.03 | (0.01) | 0.01 | (0.01) | 0.00 | (0.00) | ns | ns | 0.03 |
| <i>Firmicutes Family XIII</i> | 0.41 | (0.11) | 0.61 | (0.04) | 0.57 | (0.21) | 0.43 | (0.14) | ns | ns | ns |
| <i>Firmicutes Lachnospiraceae</i> | 32.00 | (4.80) a | 49.46 | (3.28) b | 31.07 | (1.69) a | 20.17 | (2.77) a | 0.001 | ns | 0.002 |
| <i>Firmicutes Peptococcaceae</i> | 1.26 | (0.47) | 0.83 | (0.25) | 0.73 | (0.11) | 0.86 | (0.17) | ns | ns | ns |
| <i>Firmicutes Peptostreptococcaceae</i> | 26.23 | (4.66) | 9.82 | (7.99) | 13.67 | (2.80) | 20.68 | (3.91) | ns | ns | 0.03 |
| <i>Firmicutes Ruminococcaceae</i> | 10.13 | (3.01) | 7.53 | (0.94) | 16.48 | (2.81) | 17.78 | (3.20) | 0.01 | ns | ns |
| <i>Firmicutes Erysipelotrichaceae</i> | 3.78 | (1.61) | 2.80 | (0.15) | 2.35 | (0.29) | 1.49 | (0.18) | ns | ns | ns |
| <i>Proteobacteria, Rhodospirillaceae</i> | 0.04 | (0.01) | 0.01 | (0.01) | 0.11 | (0.05) | 0.08 | (0.02) | 0.05 | ns | ns |
| <i>Proteobacteria, Desulfovibrionaceae</i> | 2.43 | (1.67) | 8.10 | (2.84) | 10.99 | (3.35) | 11.30 | (1.04) | 0.03 | ns | ns |
| <i>Proteobacteria, Desulfuromonadaceae</i> | 0.01 | (0.01) | 0.00 | (0.00) | 0.01 | (0.01) | 0.01 | (0.01) | ns | ns | ns |
| <i>Proteobacteria, Geobacteraceae</i> | 0.02 | (0.01) | 0.01 | (0.01) | 0.03 | (0.02) | 0.01 | (0.00) | ns | ns | ns |

| | | | | | | | | | | | |
|---|------|----------|------|----------|------|-----------|------|-----------|------|----|-------|
| <i>Proteobacteria, Burkholderiaceae</i> | 0.15 | (0.04) | 0.50 | (0.13) | 0.32 | (0.08) | 0.22 | (0.08) | ns | ns | 0.02 |
| <i>Proteobacteria, Enterobacteriaceae</i> | 0.01 | (0.01) | 0.02 | (0.01) | 0.01 | (0.01) | 0.01 | (0.00) | ns | ns | ns |
| <i>Proteobacteria, Halomonadaceae</i> | 0.01 | (0.01) | 0.01 | (0.00) | 0.01 | (0.01) | 0.00 | (0.00) | ns | ns | ns |
| <i>Tenericutes, Mollicutes RF39</i> | 0.02 | (0.01) a | 0.37 | (0.04) b | 0.27 | (0.13) ab | 0.12 | (0.02) ab | ns | ns | 0.007 |
| <i>Verrucomicrobia, Akkermansiaceae</i> | 0.19 | (0.09) | 0.33 | (0.06) | 0.16 | (0.08) | 0.06 | (0.01) | 0.05 | ns | ns |

a,b,c: P<0.05

Table S5: Caecal microbiota family relative abundances at 6 months of age

| | C-C | | C-LA | | LA-C | | LA-LA | | Maternal diet | Weaning diet | Maternal x weaning diet |
|--|-------|-----------|-------|----------|-------|-----------|-------|----------|---------------|--------------|-------------------------|
| <i>Actinobacteria. Bifidobacteriaceae</i> | 0.01 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | 0.03 | (0.02) | ns | ns | ns |
| <i>Actinobacteria. Sporichthyaceae</i> | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | ns | ns | ns |
| <i>Actinobacteria. Micrococcaceae</i> | 0.24 | (0.06) | 0.35 | (0.10) | 0.55 | (0.10) | 0.53 | (0.18) | 0.05 | ns | ns |
| <i>Actinobacteria. Atopobiaceae</i> | 0.00 | (0.00) | 0.02 | (0.00) | 0.03 | (0.01) | 0.02 | (0.00) | ns | ns | ns |
| <i>Actinobacteria. Eggethellaceae</i> | 0.03 | (0.01) | 0.07 | (0.03) | 0.05 | (0.02) | 0.06 | (0.01) | ns | ns | ns |
| <i>Bacteroidetes. Bacterioidaceae</i> | 0.95 | (0.08) | 1.53 | (0.22) | 1.20 | (0.17) | 1.05 | (0.19) | ns | ns | 0.05 |
| <i>Bacteroidetes. Muribaculaceae</i> | 2.38 | (0.30) | 3.39 | (0.45) | 2.01 | (0.41) | 1.64 | (0.21) | 0.007 | ns | ns |
| <i>Bacteroidetes. Prevotellaceae</i> | 2.07 | (0.29) | 2.56 | (0.45) | 2.15 | (0.36) | 4.04 | (1.16) | ns | ns | ns |
| <i>Bacteroidetes. Rikenellaceae</i> | 1.71 | (0.35) | 4.01 | (1.50) | 3.08 | (1.00) | 3.02 | (0.66) | ns | ns | ns |
| <i>Bacteroidetes. Tannerellaceae</i> | 7.82 | (0.84) ab | 14.49 | (3.15) a | 11.13 | (1.36) ab | 7.14 | (1.26) b | ns | ns | 0.01 |
| <i>Firmicutes. Enterococcaceae</i> | 0.01 | (0.01) | 0.01 | (0.01) | 0.02 | (0.01) | 0.01 | (0.00) | 0.01 | ns | ns |
| <i>Firmicutes. Lactobacillaceae</i> | 0.39 | (0.08) | 0.22 | (0.05) | 0.58 | (0.11) | 0.65 | (0.11) | 0.002 | ns | ns |
| <i>Firmicutes. Streptococcaceae</i> | 0.02 | (0.00) | 0.04 | (0.01) | 0.05 | (0.01) | 0.05 | (0.02) | ns | ns | ns |
| <i>Firmicutes. Christensenellaceae</i> | 0.22 | (0.03) | 0.36 | (0.09) | 0.38 | (0.08) | 0.34 | (0.09) | ns | ns | ns |
| <i>Firmicutes. Clostridiaceae</i> | 0.73 | (0.28) | 0.88 | (0.58) | 0.11 | (0.09) | 0.80 | (0.71) | ns | ns | ns |
| <i>Firmicutes. Clostridiales vadinBB60 group</i> | 0.07 | (0.03) | 0.03 | (0.01) | 0.00 | (0.00) | 0.05 | (0.02) | ns | ns | 0.03 |
| <i>Firmicutes. Deffluviitaleaceae</i> | 0.03 | (0.01) | 0.02 | (0.02) | 0.01 | (0.01) | 0.02 | (0.01) | ns | ns | ns |
| <i>Firmicutes. Eubacteriaceae</i> | 0.01 | (0.00) | 0.01 | (0.01) | 0.02 | (0.01) | 0.01 | (0.00) | ns | ns | ns |
| <i>Firmicutes. Family XIII</i> | 0.31 | (0.06) | 0.46 | (0.10) | 0.43 | (0.12) | 0.56 | (0.26) | ns | ns | ns |
| <i>Firmicutes. Lachnospiraceae</i> | 39.20 | (0.59) | 30.36 | (1.60) | 39.00 | (4.25) | 33.66 | (2.88) | ns | 0.02 | ns |
| <i>Firmicutes. Peptococcaceae</i> | 0.26 | (0.05) | 1.02 | (0.43) | 0.62 | (0.09) | 0.47 | (0.08) | ns | ns | ns |
| <i>Firmicutes. Peptostreptococcaceae</i> | 7.21 | (2.30) | 3.74 | (1.99) | 1.33 | (0.68) | 10.46 | (3.61) | ns | ns | 0.02 |
| <i>Firmicutes. Ruminococcaceae</i> | 23.46 | (1.22) | 25.70 | (4.41) | 24.04 | (2.23) | 27.38 | (5.00) | ns | ns | ns |
| <i>Firmicutes. Erysipelotrichaceae</i> | 0.45 | (0.09) | 0.55 | (0.19) | 1.11 | (0.21) | 0.89 | (0.27) | 0.02 | ns | ns |
| <i>Proteobacteria. Rhodospirillaceae</i> | 0.19 | (0.06) | 0.18 | (0.03) | 0.16 | (0.05) | 0.12 | (0.04) | ns | ns | ns |
| <i>Proteobacteria. Desulfovibrionaceae</i> | 11.60 | (2.88) | 8.96 | (2.64) | 10.88 | (2.17) | 6.21 | (1.23) | ns | ns | ns |
| <i>Proteobacteria. Desulfuromonadaceae</i> | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | ns | ns | ns |

| | | | | | | | | | | | |
|---|------|--------|------|--------|------|--------|------|--------|----|----|------|
| <i>Proteobacteria. Geobacteraceae</i> | 0.00 | (0.00) | 0.01 | (0.01) | 0.00 | (0.00) | 0.00 | (0.00) | ns | ns | ns |
| <i>Proteobacteria. Burkholderiaceae</i> | 0.21 | (0.05) | 0.29 | (0.06) | 0.28 | (0.04) | 0.12 | (0.02) | ns | ns | 0.02 |
| <i>Proteobacteria. Enterobacteriaceae</i> | 0.01 | (0.01) | 0.03 | (0.01) | 0.02 | (0.01) | 0.05 | (0.03) | ns | ns | ns |
| <i>Proteobacteria. Halomonadaceae</i> | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | 0.00 | (0.00) | ns | ns | ns |
| <i>Tenericutes. Mollicutes RF39</i> | 0.19 | (0.05) | 0.22 | (0.14) | 0.57 | (0.20) | 0.40 | (0.21) | ns | ns | ns |
| <i>Verrucomicrobia. Akkermansiaceae</i> | 0.02 | (0.01) | 0.06 | (0.02) | 0.12 | (0.06) | 0.13 | (0.08) | ns | ns | ns |

a,b,c P<0.05