**Supplemental Table S1.** *Maternal gut microbial diversity*

|  |  |  |  |
| --- | --- | --- | --- |
| Variables | Total(n=51) | Males(n=22) | Females(n=29) |
| Diversity | 　 | 　 | 　 |
| Observed\_OTUs | 447 (115) | 460.5 (145.25) | 431 (134.5) |
| Chao1 | 651 (192.1961) | 694.6431 (248.1962) | 622.6 (158.5299) |
| Shannon | 4.5565 (0.403) | 4.5694 (0.3798) | 4.5456 (0.4896) |

Values are presented as median (interquartile range).

**Supplemental Table S2.** *The proportions of maternal gut microbiota at the phylum and genus levels*

|  |  |  |  |
| --- | --- | --- | --- |
| Variables | Total(n=51) | Males(n=22) | Females(n=29) |
| Phylum | 　 | 　 | 　 |
| Actinobacteria | 0.1362 (0.1349) | 0.1446 (0.125) | 0.1241 (0.1329) |
| Bacteroidetes | 0.1887 (0.1387) | 0.1412 (0.1601) | 0.2018 (0.1501) |
| Firmicutes | 0.6467 (0.1389) | 0.6878 (0.1293) | 0.6082 (0.0985) |
| Proteobacteria | 0.0083 (0.0117) | 0.007 (0.0079) | 0.0103 (0.0116) |
| Genus | 　 | 　 | 　 |
| *Actinomyces* | 0.0006 (0.0006) | 0.0007 (0.0006) | 0.0005 (0.0007) |
| *Rothia* | 0.0001 (0.0003) | 0.0001 (0.0002) | 0.0001 (0.0004) |
| *Bifidobacterium* | 0.1082 (0.0996) | 0.1123 (0.1078) | 0.1082 (0.1261) |
| *Coriobacteriaceae unclassified* | 0.0003 (0.0014) | 0.0003 (0.0021) | 0.0002 (0.0013) |
| *Adlercreutzia* | 0.0002 (0.0012) | 0.0003 (0.0012) | 0.0002 (0.0012) |
| *Collinsella* | 0.0164 (0.0442) | 0.0188 (0.0523) | 0.013 (0.0384) |
| *Eggerthella* | 0.0008 (0.0023) | 0.0005 (0.0026) | 0.0011 (0.0022) |
| *Bacteroides* | 0.1178 (0.1391) | 0.1085 (0.1322) | 0.151 (0.1766) |
| *Parabacteroides* | 0.0071 (0.0117) | 0.0067 (0.0077) | 0.0074 (0.0163) |
| *Prevotella* | 0.0001 (0.0074) | 0.0003 (0.0116) | 0.0001 (0.0016) |
| *Rikenellaceae unclassified* | 0.0035 (0.0078) | 0.0036 (0.0069) | 0.0032 (0.0097) |
| *Alistipes* | 0.0001 (0.001) | 0.0003 (0.0013) | 0 (0.001) |
| *Barnesiellaceae unclassified* | 0.0007 (0.0035) | 0.0006 (0.0034) | 0.0007 (0.0038) |
| *Odoribacter* | 0.0007 (0.0012) | 0.0006 (0.0006) | 0.0008 (0.0014) |
| *Granulicatella* | 0.0001 (0.0002) | 0.0001 (0.0002) | 0.0001 (0.0004) |
| *Lactobacillus* | 0.0003 (0.0008) | 0.0003 (0.0007) | 0.0003 (0.0016) |
| *Lactococcus* | 0.0001 (0.0003) | 0.0001 (0.0003) | 0.0001 (0.0003) |
| *Streptococcus* | 0.016 (0.0292) | 0.0119 (0.0164) | 0.0185 (0.0451) |
| *Turicibacter* | 0.0001 (0.0006) | 0.0003 (0.0006) | 0.0001 (0.0006) |
| *Christensenellaceae unclassified* | 0.0002 (0.0009) | 0.0004 (0.0012) | 0 (0.0006) |
| *G 02d06* | 0.0001 (0.0005) | 0 (0.0004) | 0.0001 (0.0006) |
| *Clostridiaceae Clostridium* | 0.0032 (0.0061) | 0.0026 (0.0065) | 0.0042 (0.0063) |
| *SMB53* | 0.003 (0.0058) | 0.0031 (0.0052) | 0.0027 (0.007) |
| *Lachnospiraceae unclassified* | 0.0859 (0.0711) | 0.0691 (0.0658) | 0.0946 (0.0731) |
| *Anaerostipes* | 0.0026 (0.0066) | 0.0031 (0.006) | 0.0015 (0.0067) |
| *Blautia* | 0.1062 (0.0588) | 0.1207 (0.0629) | 0.0944 (0.0655) |
| *Lachnospiraceae Clostridium* | 0.0004 (0.0009) | 0.0004 (0.0008) | 0.0004 (0.0009) |
| *Coprococcus* | 0.0211 (0.0256) | 0.0231 (0.0213) | 0.0197 (0.0306) |
| *Dorea* | 0.0232 (0.0194) | 0.0236 (0.0181) | 0.0232 (0.0202) |
| *Lachnobacterium* | 0.0004 (0.0012) | 0.0007 (0.0016) | 0.0002 (0.0011) |
| *Lachnospira* | 0.0059 (0.012) | 0.0065 (0.0095) | 0.0052 (0.0125) |
| *Roseburia* | 0.0075 (0.0211) | 0.0137 (0.0301) | 0.0065 (0.0151) |
| *Lachnospiraceae Ruminococcus* | 0.0281 (0.033) | 0.0245 (0.0324) | 0.0302 (0.0319) |
| *Ruminococcaceae unclassified* | 0.0241 (0.0369) | 0.0241 (0.0623) | 0.0252 (0.03) |
| *Butyricicoccus* | 0.003 (0.004) | 0.0028 (0.0039) | 0.003 (0.0042) |
| *Faecalibacterium* | 0.0353 (0.0669) | 0.0286 (0.0446) | 0.0499 (0.0861) |
| *Oscillospira* | 0.0147 (0.0172) | 0.0174 (0.0239) | 0.0113 (0.0164) |
| *Ruminococcus* | 0.0464 (0.1142) | 0.0928 (0.1034) | 0.0174 (0.1) |
| *Dialister* | 0.0005 (0.0053) | 0.0016 (0.0116) | 0.0003 (0.0009) |
| *Phascolarctobacterium* | 0.0028 (0.008) | 0.0031 (0.0102) | 0.0028 (0.0071) |
| *Veillonella* | 0.0002 (0.0022) | 0.0001 (0.0008) | 0.0006 (0.0065) |
| *Mogibacteriaceae unclassified* | 0.0018 (0.0036) | 0.0025 (0.0039) | 0.0016 (0.0034) |
| *Erysipelotrichaceae unclassified* | 0.0048 (0.0121) | 0.0053 (0.0113) | 0.0044 (0.0154) |
| *Erysipelotrichaceae Clostridium* | 0.0005 (0.0027) | 0.0004 (0.0028) | 0.0006 (0.0025) |
| *Coprobacillus* | 0.0004 (0.0015) | 0.0006 (0.0036) | 0.0004 (0.0014) |
| *Holdemania* | 0.0001 (0.0003) | 0.0002 (0.0003) | 0.0001 (0.0002) |
| *Eubacterium* | 0.0027 (0.0059) | 0.0023 (0.0353) | 0.0033 (0.005) |
| *cc 115* | 0.0002 (0.0013) | 0.0003 (0.0012) | 0.0001 (0.0018) |
| *Sutterella* | 0.0024 (0.0049) | 0.0016 (0.0038) | 0.0029 (0.0063) |
| *Bilophila* | 0.0009 (0.0021) | 0.0007 (0.0016) | 0.0012 (0.0021) |
| *Trabulsiella* | 0.0011 (0.005) | 0.0006 (0.0013) | 0.0021 (0.0051) |
| *unassigned* | 0.0076 (0.0133) | 0.0084 (0.0197) | 0.0066 (0.0113) |

Values are presented as median (interquartile range).

**Supplemental Table S3.** *Correlation between phylum of maternal microbiota and newborn anthropometrics*

|  |  |  |  |
| --- | --- | --- | --- |
| Variables | Height SDS | Weight SDS | Head circumference SDS |
| *r* | *p* value | *r* | *p* value | *r* | *p* value |
| Males | 　 | 　 | 　 | 　 | 　 | 　 |
| Actinobacteria | -0.221  | 0.322  | 0.073  | 0.747  | -0.072  | 0.749  |
| Bacteroidetes | 0.037  | 0.869  | 0.112  | 0.619  | -0.243  | 0.275  |
| Firmicutes | 0.104  | 0.644  | -0.212  | 0.344  | 0.295  | 0.183  |
| Proteobacteria | -0.037  | 0.871  | 0.033  | 0.885  | 0.355  | 0.105  |
| Females | 　 | 　 | 　 | 　 | 　 | 　 |
| Actinobacteria | -0.155  | 0.423  | 0.007  | 0.970  | 0.055  | 0.778  |
| Bacteroidetes | 0.037  | 0.850  | -0.077  | 0.690  | -0.177  | 0.359  |
| Firmicutes | 0.000  | 0.998  | 0.102  | 0.597  | 0.132  | 0.495  |
| Proteobacteria | -0.159  | 0.410  | -0.254  | 0.183  | -0.251  | 0.189  |

*r* Values indicate Spearman’s rank correlation coefficients.

SDS: standard deviation score

**Supplemental Table S4.** *The concentrations of SCFAs (μmol/g) in maternal stool*

|  |  |  |  |
| --- | --- | --- | --- |
| Variables | Total(n=51) | Males(n=22) | Females(n=29) |
| Acetate | 13.2101 (11.402) | 11.8935 (13.9822) | 13.4124 (10.5469) |
| Propionate | 8.3711 (4.6422) | 8.2957 (5.0118) | 8.3711 (4.9085) |
| Isobutyrate | 0.4764 (0.6748) | 0.4787 (0.8834) | 0.4619 (0.5699) |
| Butyrate | 3.485 (2.7268) | 3.9757 (3.4219) | 3.3759 (2.3978) |
| Isovalerate | 0.1536 (0.3672) | 0.1585 (0.41) | 0.1498 (0.3256) |
| Valerate | 0.2459 (0.5144) | 0.2556 (0.481) | 0.2459 (0.5854) |
| Hexanoate | 0.0209 (0.0354) | 0.0213 (0.1057) | 0.0206 (0.0311) |

Values are presented as median (interquartile range).

**Supplemental Table S5.** *Correlation between maternal SCFAs in stool and newborn anthropometrics*

|  |  |  |  |
| --- | --- | --- | --- |
| Variables | Height SDS | Weight SDS | Head circumference SDS |
| *r* | *p* value | *r* | *p* value | *r* | *p* value |
| Males | 　 | 　 | 　 | 　 | 　 | 　 |
| Acetate | -0.006  | 0.980  | -0.276  | 0.214  | 0.167  | 0.459  |
| Propionate | 0.249  | 0.265  | -0.200  | 0.371  | 0.023  | 0.921  |
| Isobutyrate | 0.064  | 0.778  | -0.354  | 0.106  | -0.115  | 0.611  |
| Butyrate | 0.005  | 0.982  | -0.357  | 0.102  | 0.286  | 0.197  |
| Isovalerate | -0.007  | 0.975  | -0.251  | 0.261  | -0.138  | 0.540  |
| Valerate | 0.069  | 0.759  | -0.181  | 0.420  | 0.045  | 0.844  |
| Hexanoate | -0.025  | 0.913  | 0.040  | 0.859  | 0.463  | **0.030**  |
| Females | 　 | 　 | 　 | 　 | 　 | 　 |
| Acetate | -0.158  | 0.413  | -0.037  | 0.849  | 0.058  | 0.764  |
| Propionate | -0.099  | 0.610  | -0.083  | 0.668  | -0.019  | 0.921  |
| Isobutyrate | -0.003  | 0.987  | -0.231  | 0.229  | -0.349  | 0.064  |
| Butyrate | -0.086  | 0.657  | -0.121  | 0.531  | -0.058  | 0.764  |
| Isovalerate | -0.038  | 0.844  | -0.127  | 0.512  | -0.265  | 0.165  |
| Valerate | 0.048  | 0.804  | 0.009  | 0.962  | -0.028  | 0.887  |
| Hexanoate | 0.448  | **0.015**  | 0.161  | 0.405  | 0.052  | 0.790  |

*r* Values indicate Spearman’s rank correlation coefficients.

Significant *p* values (*p* < 0.05) are shown in bold.

SCFAs: short-chain fatty acids

SDS: standard deviation score