*Article*

# Gut Microbiota and Endothelial Dysfunction Markers in Obese Mexican Children and Adolescents

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# Supplementary material

**Table S1. Dietary diversity of the studied children and adolescents by phenotypic classification.**

| Group | Mean diversity score (range 0–7) | % with low diversity | % with middle diversity | % with high diversity |
|---|---|---|---|---|
| | | 0–2 food groups | 3–4 food groups | 5–7 food groups |
| Children (105) | | | | |
| Normal weight (46) | 6.87 | 26.71 | 31.68 | 41.61 |
| Obesity (59) | 6.75 | 21.18 | 32.45 | 42.37 |
| Adolescents (57) | | | | |
| Normal weight (25) | 6.88 | 26.29 | 34.86 | 38.86 |
| Obesity (32) | 6.53 | 32.59 | 25.00 | 42.41 |

Food groups: (1) starchy staples; (2) legumes; (3) dairy; (4) meat; (5) vitamin A-rich fruits and vegetables; (6) other fruits and vegetables or fruit juices; and (7) foods made with oil, fat, or butter. 6 children and 4 adolescents could not participate for dietary diversity study.

**Table S2. Diversity indexes for children and adolescents.**

| Diversity index | | | | |
|---|---|---|---|---|
| Children | Normal weight* | Obesity* | $p$-value | $q$-value |
| Observed | 4,015.55 | 4,007.79 | 0.6995 | 1.0 |
| Chao1 | 7,424.22 | 7,636.18 | 0.4472 | 1.0 |
| Shannon | 4.53 | 4.61 | 0.4946 | 1.0 |
| Simpson | 0.94 | 0.95 | 0.4615 | 1.0 |
| Adolescents | Normal weight* | Obesity* | $p$ value | $q$ value |
| Observed | 3,569.93 | 3,412.79 | 0.3876 | 1.0 |
| Chao1 | 6,209.36 | 5,912.67 | 0.3876 | 1.0 |
| Shannon | 4.48 | 4.62 | 0.4904 | 1.0 |
| Simpson | 0.94 | 0.95 | 0.0827 | 1.0 |

$p$-values were calculated by Mann-Whitney test for unequal variances. $p$-values corrected by Benjamini-Hochberg, 1995 method and generated FDR value ($q$-value). $p < 0.05$ and $q < 0.05$ are considered statistically significant. Where * shows mean values

**Table S3. Significant level of bacterial phylum in children.**

| Taxa | Normal weight* | Obesity* | *P*-value | *q*-value |
|---|---|---|---|---|
| Children | | | | |
| p_Actinobacteria | 7.93% | 9.10% | 0.1314 | 0.6906 |
| p_Bacteroidetes | 33.22% | 25.59% | 0.0493 | 0.6906 |
| p_Firmicutes | 55.55% | 61.09% | 0.0543 | 0.6906 |
| p_Proteobacteria | 2.05% | 3.41% | 0.2444 | 0.6906 |
| p_Tenericutes | 0.10% | 0.19% | 0.5328 | 0.7991 |
| Others | 1.00% | 0.67% | 0.7170 | 1.0000 |
| Adolescents | | | | |
| p_Actinobacteria | 4.34% | 10.04% | 0.0025 | 0.0740 |
| p_Bacteroidetes | 32.63% | 26.83% | 0.3270 | 0.9771 |
| p_Firmicutes | 58.91% | 59.58% | 0.9248 | 0.9850 |
| p_Proteobacteria | 2.13% | 2.06% | 0.4723 | 0.9836 |
| p_Tenericutes | 0.09% | 0.04% | 0.6454 | 0.9836 |
| Others | 0.40% | 0.67% | 0.7930 | 1.0000 |

*p*-values corrected by Benjamini-Hochberg, 1995 method and generated FDR value (q-value). $p < 0.05$ and $q < 0.05$ are considered statistically significant. The name of a higher taxon level was added before its taxon abbreviation "p", phylum. * shows mean values.

**Table S4. Linear discriminant analysis (LDA) effect size (LEfSe) analysis for children.**

| Taxa | Group | LDA score | *p*-value |
|---|---|---|---|
| p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_*Lactobacillus* | Obese children | 3.7495 | 0.0402 |
| p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Succinivibrionaceae;g_*Succinivibrio* | Obese children | 3.7613 | 0.0194 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_*Clostridium* | Obese children | 2.4784 | 0.0256 |
| p_Elusimicrobia;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiaceae | Obese children | 2.1828 | 0.0053 |
| p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae | Obese children | 3.1561 | 0.0194 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae | Obese children | 3.8233 | 0.0363 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_*SMB53* | Obese children | 2.1799 | 0.0180 |
| p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_*Dickeya* | Obese children | 2.0485 | 0.0429 |
| p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales | Obese children | 3.3284 | 0.0196 |
| p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Candidatus *portiera* | Obese children | 2.2739 | 0.0429 |
| p_Tenericutes;c_Mollicutes;o_Acholeplasmatales;f_Acholeplasmataceae;g_*Acholeplasma* | Normal weight children | 2.4934 | 0.0493 |
| p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_*Nocardioides* | Normal weight children | 2.2210 | 0.0226 |
| p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales | Normal weight children | 2.1983 | 0.0104 |
| p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Conexibacteraceae | Normal weight children | 2.4045 | 0.0226 |

The threshold on the logarithmic LDA score for discriminative features was set to 2.0. The name of a higher taxon level was added before its taxon abbreviation. "p", phylum; "c", class; "o", order; "f", family; "g", genus. "LDA" Linear discriminant analysis. *p* < 0.05 are considered statistically significant.

**Table S5. Linear discriminant analysis (LDA) effect size (LEfSe) analysis for adolescents.**

| Taxa | Group | LDA score | *p*-value |
|---|---|---|---|
| p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_*Adlercreutzia* | Obese adolescents | 2.2280 | 0.0041 |
| p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_*Bradyrhizobium* | Obese adolescents | 2.3751 | 0.0499 |
| p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_*Bifidobacterium* | Obese adolescents | 4.2532 | 0.0210 |
| p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae | Obese adolescents | 2.6803 | 0.0160 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_*Blautia* | Obese adolescents | 4.2739 | 0.0436 |
| p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_*Collinsella* | Obese adolescents | 4.0767 | 0.0018 |
| p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae | Obese adolescents | 3.1937 | 0.0035 |
| p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_*Lactococcus* | Obese adolescents | 2.7848 | <0.001 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_*Coprococcus* | Obese adolescents | 3.9461 | 0.0202 |
| p_Cyanobacteria;c_Chloroplast;o_Streptophyta | Obese adolescents | 2.2671 | 0.0303 |
| p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Paraprevotellaceae;g_*Prevotella* | Obese adolescents | 2.7781 | 0.0309 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mogibacteriaceae | Obese adolescents | 2.8203 | 0.0024 |
| p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae | Obese adolescents | 2.2309 | 0.0040 |
| p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_*Propionicimonas* | Obese adolescents | 3.2475 | 0.0394 |
| p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g_*Gemella* | Obese adolescents | 2.6242 | 0.0058 |
| p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_*Stenotrophomonas* | Obese adolescents | 3.1971 | 0.0132 |
| p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_*Paludibacter* | Normal weight adolescents | 3.0903 | 0.0403 |
| p_Tenericutes;c_Mollicutes;o_Acholeplasmatales;f_Acholeplasmataceae;g_*Acholeplasma* | Normal weight adolescents | 2.9836 | 0.0481 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_*Megamonas* | Normal weight adolescents | 3.6010 | 0.0361 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_*Lachnospira* | Normal weight adolescents | 3.2791 | 0.0316 |
| p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_*Anaerovibrio* | Normal weight adolescents | 2.9063 | 0.0481 |
| p_Firmicutes;c_Clostridia;o_SHA_98 | Normal weight adolescents | 2.1641 | 0.0249 |
| p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_*Fusobacterium* | Normal weight adolescents | 2.2006 | 0.0321 |
| p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae | Normal weight adolescents | 2.4231 | 0.0024 |

The threshold on the logarithmic LDA score for discriminative features was set to 2.0. The name of a higher taxon level was added before its taxon abbreviation. "p", phylum; "c", class; "o", order; "f", family; "g", genus. "LDA" Linear discriminant analysis. *p* < 0.05 are considered statistically significant.

**Table S6. Taxonomic composition of gut microbiota with different metadata in obese children.**

| Variable | Feature | Coefficient | *p*-value | *q*-value |
|---|---|---|---|---|
| VCAM-1 | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae | <-0.00010 | <0.001 | 0.060 |
| E-selectin | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae | 0.00019 | 0.005 | 0.219 |
| E-selectin | o_Bacteroidales;f_S24-7 | 0.00010 | 0.005 | 0.219 |
| ICAM-1 | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_*Oscillospira* | 0.00012 | 0.003 | 0.152 |
| ICAM-1 | p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae | 0.00060 | <0.001 | <0.001 |
| ICAM-1 | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_*SMB53* | -0.00007 | <0.001 | 0.003 |
| ICAM-1 | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae | -0.00040 | <0.001 | 0.013 |
| ICAM-1 | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_*Ruminococcus* | 0.00040 | <0.001 | 0.020 |
| ICAM-1 | p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_*Bradyrhizobium* | -0.00004 | 0.003 | 0.156 |

A positive coefficient means gut microbial abundance increases with respective variable, while a negative coefficient means gut microbial abundance decreases with respective variable. For readability the kingdom label is not present. "ICAM-1", intercellular adhesion molecule-1; "VCAM-1", vascular cell adhesion molecule. The name of a higher taxon level was added before its taxon abbreviation. "p", phylum; "c", class; "o", order; "f". family; "g", genus.


**Table S7. Taxonomic composition of gut microbiota with different metadata in obese adolescents.**

| Variable | Feature | Coefficient | *p*-value | q-value |
|---|---|---|---|---|
| Cholesterol | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_*Ruminococcus* | 0.00114 | 0.0040 | 0.192 |
| HDL | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mogibacteriaceae | 0.00103 | 0.0060 | 0.239 |
| LDL | p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_*Parvimonas* | -0.00033 | 0.0012 | 0.146 |
| ICAM-1 | p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f__Bacteroidaceae;g_*Bacteroides* | 0.00110 | 0.0001 | 0.102 |

A positive coefficient means gut microbial abundance increases with respective variable, while a negative coefficient means gut microbial abundance decreases with respective variable. For readability the kingdom label is not present. "HDL", high-density lipoprotein," LDL", low-density protein, "ICAM-1", intercellular adhesion molecule-1. The name of a higher taxon level was added before its taxon abbreviation. "p", phylum; "c", class; "o", order; "f". family; "g", genus.

**Table S8.** List of bacterial taxa with their OTUs ID in normal weight children for Figure S1.

| No. | OTUs ID | Bacteria | No. | OTUs ID | Bacteria |
|---|---|---|---|---|---|
| 1 | 10496 | Lachnospiraceae | 46 | 370154 | Ruminococcaceae |
| 2 | 12246 | *Bacteroides* | 47 | 409732 | *Blautia* |
| 3 | 12426 | *Bilophila* | 48 | 508984 | Lachnospiraceae |
| 4 | 14479 | Ruminococcaceae | 49 | 519765 | Lachnospiraceae |
| 5 | 14550 | Erysipelotrichaceae | 50 | 523782 | *Coprococcus* |
| 6 | 15355 | *Blautia* | 51 | 529740 | *Roseburia* |
| 7 | 22335 | Rikenellaceae | 52 | 529940 | Ruminococcaceae |
| 8 | 179384 | Lachnospiraceae | 53 | 530094 | Ruminococcaceae |
| 9 | 182107 | Lachnospiraceae | 54 | 531582 | *Blautia* |
| 10 | 188887 | *Bacteroides* | 55 | 532771 | Lachnospiraceae |
| 11 | 190358 | Ruminococcaceae | 56 | 535549 | *Bacteroides* |
| 12 | 190975 | Barnesiellaceae | 57 | 548233 | *Clostridiales* |
| 13 | 192406 | Ruminococcaceae | 58 | 548503 | Lachnospiraceae |
| 14 | 193041 | *Blautia* | 59 | 552380 | *Ruminococcus* |
| 15 | 194341 | *Bacteroides* | 60 | 556835 | *Phascolarctobacterium* |
| 16 | 194395 | Barnesiellaceae | 61 | 560535 | Ruminococcaceae |
| 17 | 194909 | *Bacteroides* | 62 | 570507 | *Blautia* |
| 18 | 195222 | Ruminococcaceae | 63 | 577170 | *Bacteroides* |
| 19 | 198145 | *Blautia* | 64 | 579561 | *Blautia* |
| 20 | 208739 | *Faecalibacterium* | 65 | 580008 | Erysipelotrichaceae |
| 21 | 210371 | Ruminococcaceae | 66 | 580629 | *Bacteroides* |
| 22 | 264552 | *Dialister* | 67 | 581003 | *Clostridiales* |
| 23 | 267718 | *Faecalibacterium* | 68 | 583089 | *Blautia* |
| 24 | 287951 | *Clostridiales* | 69 | 591891 | Lachnospiraceae |
| 25 | 297150 | Lachnospiraceae | 70 | 593422 | *Blautia* |
| 26 | 301910 | Lachnospiraceae | 71 | 659361 | *Roseburia* |
| 27 | 316761 | *Bacteroides* | 72 | 696563 | *Blautia* |
| 28 | 318970 | *Blautia* | 73 | 700298 | *Dorea* |
| 29 | 322380 | Ruminococcaceae | 74 | 702414 | Lachnospiraceae |
| 30 | 325244 | Lachnospiraceae | 75 | 708680 | *Clostridiales* |
| 31 | 337167 | Ruminococcaceae | 76 | 712677 | Peptostreptococcaceae |
| 32 | 347115 | *Blautia* | 77 | 727140 | *Clostridiales* |
| 33 | 351231 | *Bacteroides* | 78 | 804526 | *Blautia* |
| 34 | 355837 | Ruminococcaceae | 79 | 851865 | Ruminococcaceae |
| 35 | 358410 | Ruminococcaceae | 80 | 875709 | Lachnospiraceae |
| 36 | 359359 | Ruminococcaceae | 81 | 1105552 | Lachnospiraceae |
| 37 | 360158 | Lachnospiraceae | 82 | 1106861 | *Coprococcus* |
| 38 | 361966 | *Faecalibacterium* | 83 | 1107327 | Lachnospiraceae |
| 39 | 362968 | Ruminococcaceae | 84 | 1111458 | Peptostreptococcaceae |
| 40 | 365496 | *Bacteroides* | 85 | 2198356 | *Bacteroides* |
| 41 | 365717 | *Faecalibacterium* | 86 | 2388088 | *Phascolarctobacterium* |
| 42 | 368117 | Ruminococcaceae | 87 | 3678349 | *Streptococcus* |
| 43 | 369027 | Lachnospiraceae | 88 | 4338624 | *Sutterella* |
| 44 | 369109 | Ruminococcaceae | 89 | 4476780 | Rikenellaceae |
| 45 | 369555 | *Ruminococcus* | | | |

Table S9. List of bacterial taxa with their OTUs ID in normal weight adolescents for Figure S2.

| No. | OTUs ID | Bacteria | No. | OTUs ID | Bacteria |
|---|---|---|---|---|---|
| 1 | 583 | *Dialister* | 25 | 521982 | Rikenellaceae |
| 2 | 1060 | *Prevotella* | 26 | 523782 | *Coprococcus* |
| 3 | 8103 | Ruminococcaceae | 27 | 527751 | Lachnospiraceae |
| 4 | 9799 | Bifidobacteriaceae | 28 | 529940 | Ruminococcaceae |
| 5 | 10094 | Lachnospiraceae | 29 | 530094 | Ruminococcaceae |
| 6 | 10254 | Ruminococcaceae | 30 | 531582 | *Blautia* |
| 7 | 10888 | *Ruminococcus* | 31 | 548503 | Lachnospiraceae |
| 8 | 178664 | *Clostridiales* | 32 | 552380 | *Ruminococcus* |
| 9 | 180082 | *Parabacteroides* | 33 | 560535 | Ruminococcaceae |
| 10 | 182431 | Ruminococcaceae | 34 | 570507 | Lachnospiraceae |
| 11 | 190358 | Ruminococcaceae | 35 | 577170 | *Bacteroides* |
| 12 | 192365 | *Coprococcus* | 36 | 579561 | *Blautia* |
| 13 | 195222 | Ruminococcaceae | 37 | 580629 | *Bacteroides* |
| 14 | 198866 | *Parabacteroides* | 38 | 583089 | *Blautia* |
| 15 | 228199 | *Ruminococcus* | 39 | 591891 | Lachnospiraceae |
| 16 | 264552 | *Dialister* | 40 | 593422 | *Blautia* |
| 17 | 272587 | *Dialister* | 41 | 700298 | Lachnospiraceae |
| 18 | 287951 | *Clostridiales* | 42 | 702414 | Lachnospiraceae |
| 19 | 325244 | Lachnospiraceae | 43 | 708680 | *Clostridiales* |
| 20 | 368117 | Ruminococcaceae | 44 | 712677 | *Clostridiales* |
| 21 | 369027 | Lachnospiraceae | 45 | 851865 | Ruminococcaceae |
| 22 | 369555 | *Ruminococcus* | 46 | 1105552 | Lachnospiraceae |
| 23 | 370086 | Ruminococcaceae | 47 | 4314092 | *Prevotella* |
| 24 | 370154 | Ruminococcaceae | | | |

Table S10. List of bacterial taxa with their OTUs ID in obese children for Figure S3.

| No. | OTUs ID | Bacteria | No. | OTUs ID | Bacteria |
|-----|---------|----------|-----|---------|----------|
| 1 | 335 | *Phascolarctobacterium* | 46 | 362214 | *Bifidobacterium* |
| 2 | 1899 | *Peptococcus* | 47 | 362968 | Ruminococcaceae |
| 3 | 4007 | *Peptococcus* | 48 | 365496 | *Bacteroides* |
| 4 | 6529 | *Lactobacillus* | 49 | 365717 | *Faecalibacterium* |
| 5 | 7389 | *Haemophilus* | 50 | 369027 | Lachnospiraceae |
| 6 | 8433 | Clostridiales | 51 | 370086 | Ruminococcaceae |
| 7 | 9453 | *Prevotella* | 52 | 370154 | Ruminococcaceae |
| 8 | 11321 | *Phascolarctobacterium* | 53 | 403701 | *Dialister* |
| 9 | 11423 | *Bacteroides* | 54 | 517282 | *Blautia* |
| 10 | 12345 | *Phascolarctobacterium* | 55 | 521982 | Clostridiales |
| 11 | 13188 | *Prevotella* | 56 | 522364 | *Prevotella* |
| 12 | 13949 | Ruminococcaceae | 57 | 523782 | *Coprococcus* |
| 13 | 14550 | Erysipelotrichaceae | 58 | 524371 | *Prevotella* |
| 14 | 19296 | *Bacteroides* | 59 | 524884 | *Eubacterium* |
| 15 | 19314 | *Parabacteroides* | 60 | 529940 | Ruminococcaceae |
| 16 | 21736 | *Phascolarctobacterium* | 61 | 530094 | Ruminococcaceae |
| 17 | 22231 | *Haemophilus* | 62 | 531582 | *Blautia* |
| 18 | 22619 | *Peptococcus* | 63 | 531928 | Clostridiales |
| 19 | 22894 | Ruminococcaceae | 64 | 560535 | Ruminococcaceae |
| 20 | 24722 | *Bacteroides* | 65 | 567846 | Bifidobacterium |
| 21 | 41229 | *Sutterella* | 66 | 570507 | *Blautia* |
| 22 | 130864 | *Lactobacillus* | 67 | 574111 | *Prevotella* |
| 23 | 157424 | *Phascolarctobacterium* | 68 | 580008 | Erysipelotrichaceae |
| 24 | 179261 | *Sutterella* | 69 | 583746 | *Dialister* |
| 25 | 180082 | *Parabacteroides* | 70 | 587753 | Coriobacteriaceae |
| 26 | 183480 | Rikenellaceae | 71 | 591891 | Lachnospiraceae |
| 27 | 183603 | *Bacteroides* | 72 | 593422 | *Blautia* |
| 28 | 190358 | Ruminococcaceae | 73 | 639310 | *Bifidobacterium* |
| 29 | 190975 | Barnesiellaceae | 74 | 700298 | *Dorea* |
| 30 | 193723 | Bacteroidales | 75 | 702414 | Lachnospiraceae |
| 31 | 194395 | Barnesiellaceae | 76 | 708680 | Clostridiales |
| 32 | 195222 | Ruminococcaceae | 77 | 712677 | Peptostreptococcaceae |
| 33 | 196604 | *Catenibacterium* | 78 | 716286 | *Lactobacillus* |
| 34 | 198866 | *Parabacteroides* | 79 | 804526 | *Blautia* |
| 35 | 202162 | Ruminococcaceae | 80 | 849535 | *Prevotella* |
| 36 | 208739 | Faecalibacterium | 81 | 850218 | Phascolarctobacterium |
| 37 | 215331 | *Peptococcus* | 82 | 851865 | Ruminococcaceae |
| 38 | 230403 | *Bacteroides* | 83 | 875709 | Lachnospiraceae |
| 39 | 235591 | *Lactobacillus* | 84 | 1105328 | *Blautia* |
| 40 | 236308 | *Lactobacillus* | 85 | 1105552 | Lachnospiraceae |
| 41 | 269937 | *Prevotella* | 86 | 1106861 | *Coprococcus* |
| 42 | 293883 | *Phascolarctobacterium* | 87 | 1107327 | Lachnospiraceae |
| 43 | 309133 | Enterococcaceae | 88 | 1111458 | Peptostreptococcaceae |
| 44 | 339685 | *Peptococcus* | 89 | 4226929 | *Bacteroides* |
| 45 | 361966 | *Faecalibacterium* | | | |

Table S11. List of bacterial taxa with their OTUs ID in obese adolescents for Figure S4.

| No. | OTUs ID | Bacteria | No. | OTUs ID | Bacteria |
|-----|---------|----------|-----|---------|----------|
| 1 | 1002 | *Sphingomonas* | 51 | 362214 | *Bifidobacterium* |
| 2 | 1184 | *Collinsella* | 52 | 362968 | Ruminococcaceae |
| 3 | 4568 | *Bradyrhizobium* | 53 | 363794 | *Collinsella* |
| 4 | 5337 | Clostridiaceae | 54 | 365496 | *Bacteroides* |
| 5 | 6613 | Bradyrhizobium | 55 | 365717 | *Faecalibacterium* |
| 6 | 7367 | *Prevotella* | 56 | 368175 | *Collinsella* |
| 7 | 7786 | Clostridiales | 57 | 369109 | Ruminococcaceae |
| 8 | 9022 | *Lactobacillus* | 58 | 370154 | Ruminococcaceae |
| 9 | 9328 | *Collinsella* | 59 | 383885 | *Lactobacillus* |
| 10 | 10094 | Lachnospiraceae | 60 | 469663 | *Atopobium* |
| 11 | 10254 | Ruminococcaceae | 61 | 470382 | Clostridiales |
| 12 | 10278 | *Lactobacillus* | 62 | 471180 | Bifidobacterium |
| 13 | 10560 | *Collinsella* | 63 | 529940 | Ruminococcaceae |
| 14 | 11912 | Clostridiaceae | 64 | 530094 | Ruminococcaceae |
| 15 | 12479 | *Lactobacillus* | 65 | 531582 | *Blautia* |
| 16 | 12723 | Lachnospiraceae | 66 | 556835 | *Phascolarctobacterium* |
| 17 | 12734 | Ruminococcaceae | 67 | 560336 | *Bacteroides* |
| 18 | 12974 | *Lactobacillus* | 68 | 560535 | Ruminococcaceae |
| 19 | 13485 | *Bifidobacterium* | 69 | 566154 | Coriobacteriaceae |
| 20 | 29566 | *Sneathia* | 70 | 567846 | *Bifidobacterium* |
| 21 | 128300 | *Lactobacillus* | 71 | 568118 | *Prevotella* |
| 22 | 130468 | *Lactobacillus* | 72 | 570507 | *Blautia* |
| 23 | 130864 | *Lactobacillus* | 73 | 579608 | *Streptococcus* |
| 24 | 133372 | *Parvimonas* | 74 | 583089 | *Blautia* |
| 25 | 137183 | Bifidobacteriaceae | 75 | 584347 | *Actinomyces* |
| 26 | 177679 | S24-7 | 76 | 589071 | *Bacteroides* |
| 27 | 183988 | Clostridiales | 77 | 593422 | *Blautia* |
| 28 | 188956 | *Blautia* | 78 | 663885 | *Prevotella* |
| 29 | 190358 | Ruminococcaceae | 79 | 696563 | *Blautia* |
| 30 | 191112 | Lachnospiraceae | 80 | 708680 | Clostridiales |
| 31 | 195222 | Ruminococcaceae | 81 | 712047 | Clostridiaceae |
| 32 | 197060 | Clostridiaceae | 82 | 712677 | Clostridiales |
| 33 | 198915 | *Blautia* | 83 | 826270 | *Bradyrhizobium* |
| 34 | 208739 | *Faecalibacterium* | 84 | 826382 | Lachnospiraceae |
| 35 | 225846 | *Dialister* | 85 | 840914 | *Prevotella* |
| 36 | 236308 | *Lactobacillus* | 86 | 844589 | S24-7 |
| 37 | 272516 | *Adlercreutzia* | 87 | 851726 | *Megasphaera* |
| 38 | 292921 | *Prevotella* | 88 | 851865 | Ruminococcaceae |
| 39 | 296420 | Clostridiaceae | 89 | 858535 | Coriobacteriaceae |
| 40 | 318990 | Lachnospiraceae | 90 | 866365 | Caulobacteraceae |
| 41 | 322367 | Clostridiaceae | 91 | 934235 | Rhizobiales |
| 42 | 338273 | Clostridiaceae | 92 | 986513 | *Clostridium* |
| 43 | 338381 | *Prevotella* | 93 | 1105328 | *Blautia* |
| 44 | 344114 | Clostridiales | 94 | 1105552 | Lachnospiraceae |
| 45 | 354905 | *Lactobacillus* | 95 | 1106861 | *Coprococcus* |
| 46 | 357046 | Rikenellaceae | 96 | 1109964 | Sphingomonadaceae |
| 47 | 358798 | Lachnospiraceae | 97 | 1111458 | Peptostreptococcaceae |
| 48 | 359359 | Ruminococcaceae | 98 | 1656781 | *Prevotella* |
| 49 | 360158 | Lachnospiraceae | 99 | 64179 | *Sphingomonas* |
| 50 | 360518 | *Bacteroides* | | | |
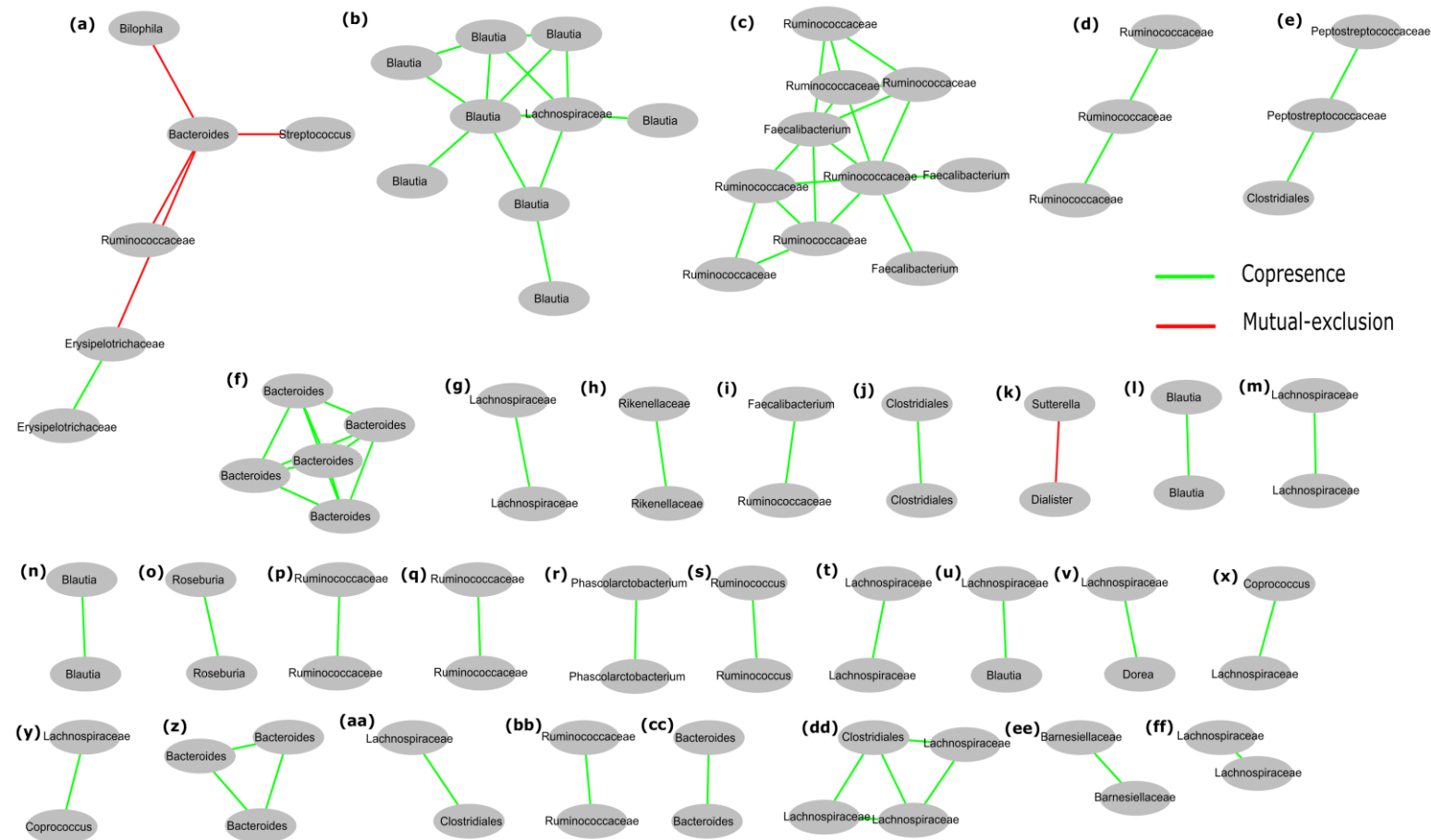
**Figure S1.** Significant co-occurrence analysis between gut microbiota in normal weight Mexican children (**a-ff**). This graphic shows the interesting interaction between different bacterial communities; copresence (positive interaction; *green lines*). This analysis was performed using *otu_table.biom* file in CoNet plugin tool and generated co-occurrence networks were visualized by Cytoscape (v3.6.1) software as described in Material and methods. Each node indicates a microbial clade (bacterial taxon) belonging to a unique OTUs number. Edges (lines) are connecting two nodes, represent significant correlations (*p* < .05; *q* < 0.05; *R* > 0.8). In this graphics some bacteria names are shown more than one time e.g. Ruminococcaceae etc., however they belong to different OTUs number. Bacteria names and corresponding OTUs number are shown in Table S8, and the significant interaction values are shown in Table S12.
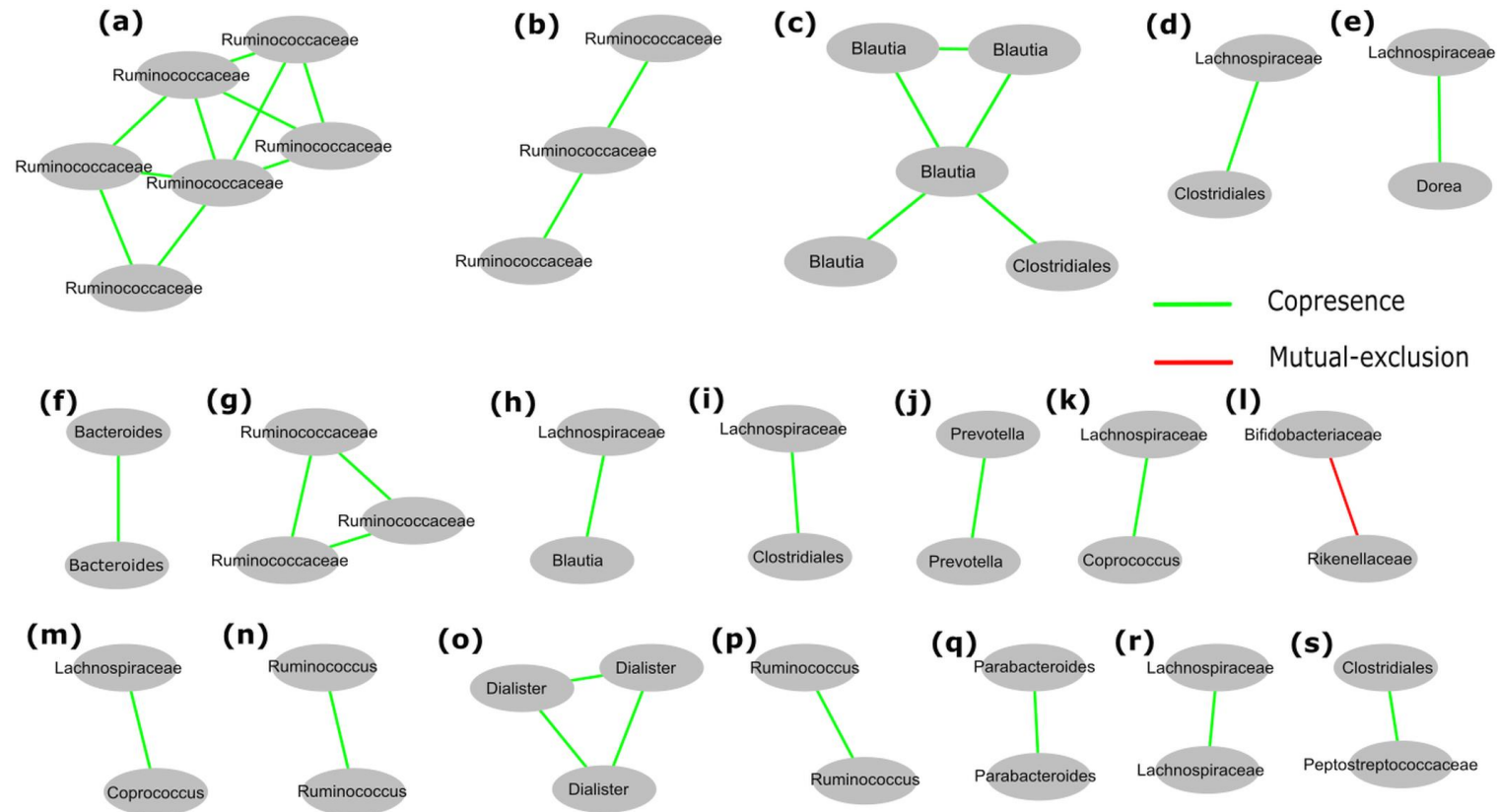
**Figure S2.** Significant co-occurrence analysis between gut microbiota in normal weight Mexican adolescents (**a-s**). This graphic shows the interesting interaction between different bacterial communities; copresence (positive interaction; *green lines*). This analysis was performed using *otu_table.biom* file in CoNet plugin tool and generated co-occurrence networks were visualized by Cytoscape (v3.6.1) software as described in Material and methods. Each node indicates a microbial clade (bacterial taxon) belonging to a unique OTUs number. Edges (lines) are connecting two nodes, represent significant correlations ($p < .05$; $q < 0.05$; $R > 0.8$). In this graphics some bacteria names are shown more than one time e.g. Ruminococcaceae etc., however they belong to different OTUs number. Bacteria names and corresponding OTUs number are shown in Table S9, and the significant interaction values are shown in Table S12.
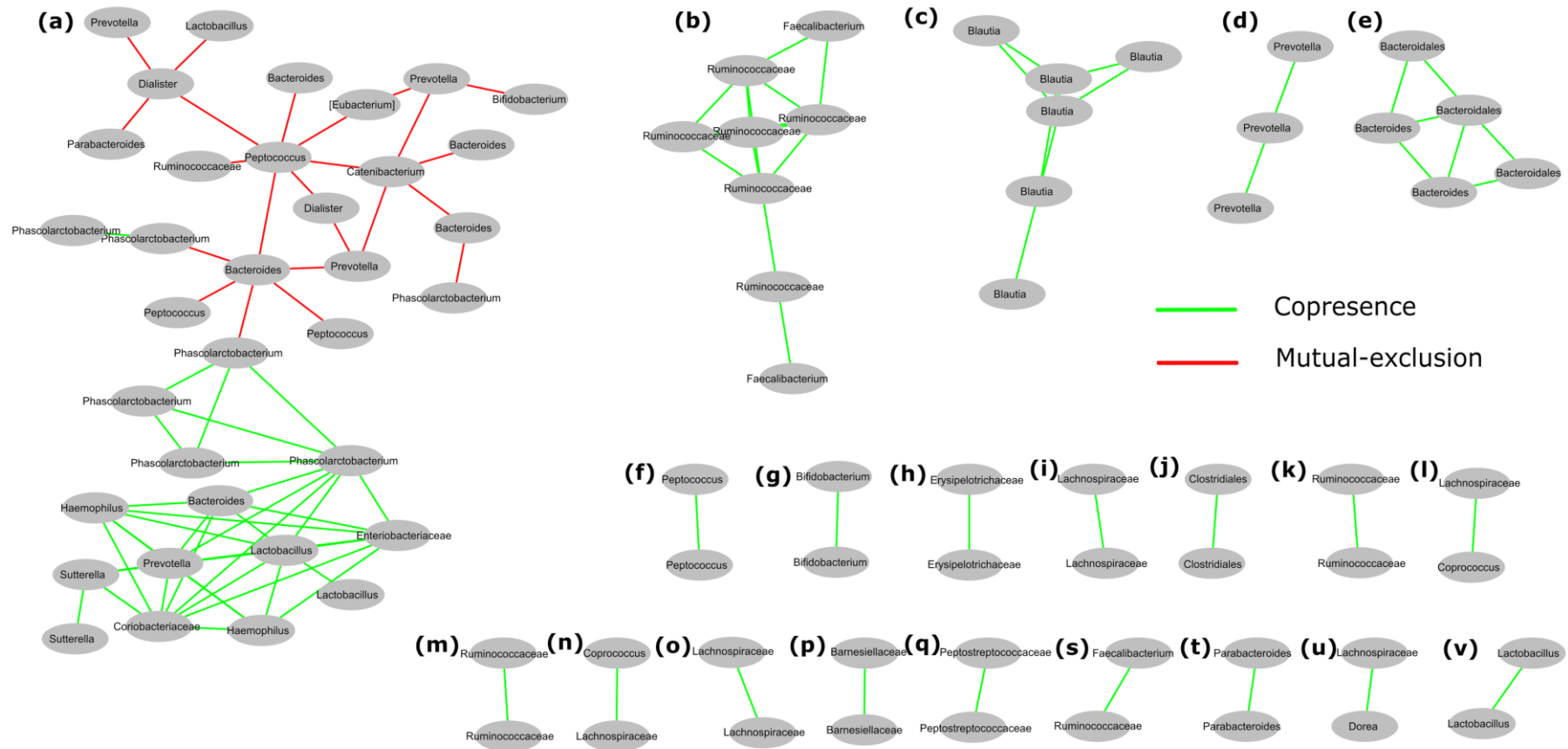
**Figure S3.** Significant co-occurrence analysis between gut microbiota in obese Mexican children (**a-v**). This graphic shows the interesting interaction between different bacterial communities; copresence (positive; *green lines*). This analysis was performed using *otu_table.biom* file in CoNet plugin tool and generated co-occurrence networks were visualized by Cytoscape (v3.6.1) software as described in Material and methods. Each node indicates a microbial clade (bacterial taxon) belonging to a unique OTUs number. Edges (lines) are connecting two nodes, represent significant correlations ($p < .05$; $q < 0.05$; $R > 0.8$). In this graphics some bacteria names are shown more than one time e.g. Ruminococcaceae etc., however they belong to different OTUs number. Bacteria names and corresponding OTUs number are shown in Table S10, and the significant interaction values are shown in Table S12.
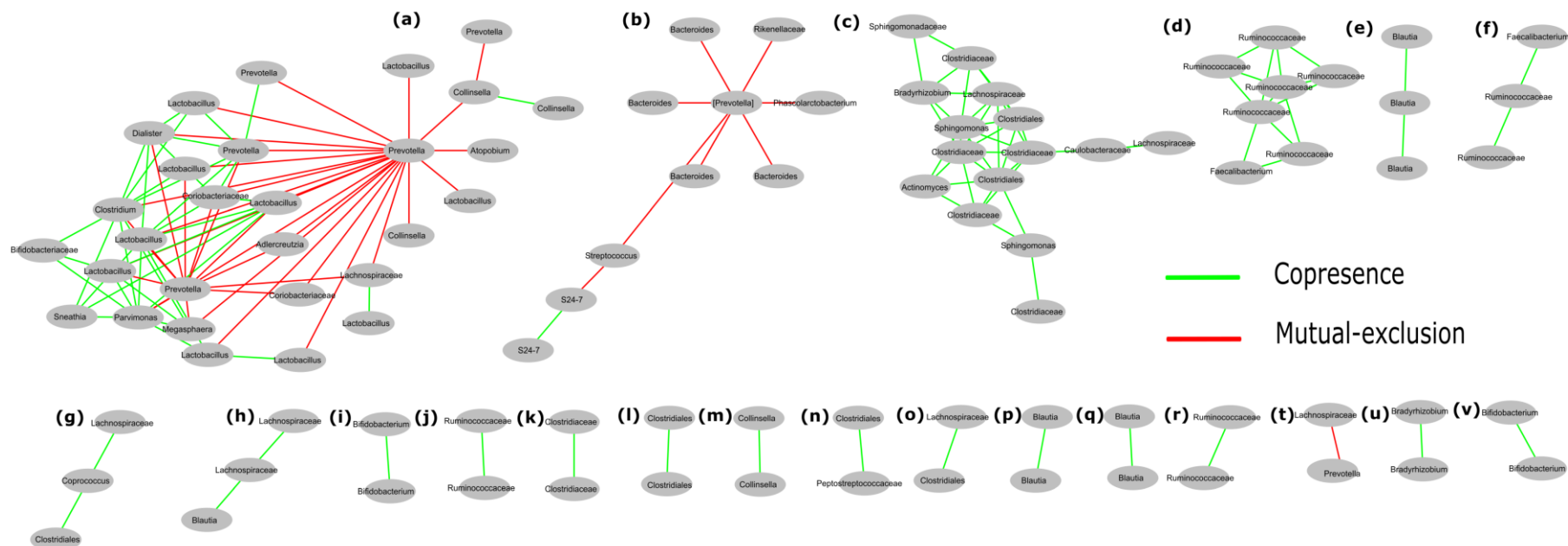
**Figure S4.** Significant co-occurrence analysis between gut microbiota in obese Mexican adolescents (**a-v**). This graphic shows the interesting interaction between different bacterial communities; copresence (positive interaction; *green lines*). This analysis was performed using *otu_table.biom* file in CoNet plugin tool and generated co-occurrence networks were visualized by Cytoscape (v3.6.1) software as described in Material and methods. Each node indicates a microbial clade (bacterial taxon) belonging to a unique OTUs number. Edges (lines) are connecting two nodes, represent significant correlations ($p < .05$; $q < 0.05$; $R > 0.8$). In this graphics some bacteria names are shown more than one time e.g. Ruminococcaceae etc., however they belong to different OTUs number. Bacteria names and corresponding OTUs number are shown in Table S11, and the significant interaction values are shown in Table S12.

-----end-of-text-----