Supplementary Table S2. Discriminatory OTUs found to be significantly different (q-value<0.05) in relative abundance in infant stool samples at 6 months based on maternal group B *Streptococcus* status, after adjusting for maternal race, prenatal antifungal use and intrapartum antibiotics. Data are ordered by *P*-value.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **OTUa** | **Order** | **Family** | **Genus** | **Estimateb** | ***P*-value** |  |  |  |  |
| 3537197 | Clostridiales | *Lachnospiraceae* | *Anaerostipes* | 1.53 | 1.33623E-42 |  |  |  |  |
| 174499 | Clostridiales | *Lachnospiraceae* |  | -8.84 | 3.51407E-27 |  |  |  |  |
| 186981 | Bacteroidales | *[Barnesiellaceae]* |  | -5.46 | 3.00536E-19 |  |  |  |  |
| 111135 | Burkholderiales | *Alcaligenaceae* | *Sutterella* | -8.21 | 9.80951E-16 |  |  |  |  |
| New.CleanUp.ReferenceOTU60232 | Clostridiales | *Veillonellaceae* | *Acidaminococcus* | 2.91 | 7.56572E-14 |  |  |  |  |
| 357930 | Clostridiales | *Veillonellaceae* | *Dialister* | 2.85 | 2.97403E-13 |  |  |  |  |
| New.ReferenceOTU205 |   |  |  | 2.71 | 4.99258E-12 |  |  |  |  |
| New.CleanUp.ReferenceOTU7382 | Verrucomicrobiales | *Verrucomicrobiaceae* | *Akkermansia* | 2.66 | 2.03523E-10 |  |  |  |  |
| New.CleanUp.ReferenceOTU25328 | Clostridiales | *Lachnospiraceae* |  | -1.83 | 2.65871E-10 |  |  |  |  |
| 301253 | Bacteroidales | *Prevotellaceae* | *Prevotella* | -4.75 | 4.3444E-10 |  |  |  |  |
| New.CleanUp.ReferenceOTU108388 | Clostridiales | *Ruminococcaceae* | *Ruminococcus* | 2.43 | 6.21831E-10 |  |  |  |  |
| 174911 | Clostridiales | *Lachnospiraceae* |  | -4.45 | 7.96386E-10 |  |  |  |  |
| 12297 | Actinomycetales |  |  | 5.58 | 9.53672E-10 |  |  |  |  |
| New.CleanUp.ReferenceOTU121171 | Verrucomicrobiales | *Verrucomicrobiaceae* | *Akkermansia* | -2.22 | 2.68295E-09 |  |  |  |  |
| New.CleanUp.ReferenceOTU81053 | Erysipelotrichales | *Erysipelotrichaceae* | *[Eubacterium]* | 2.35 | 5.79176E-09 |  |  |  |  |
| 3805726 | Clostridiales | *[Mogibacteriaceae]* |  | 2.35 | 6.63844E-09 |  |  |  |  |
| New.ReferenceOTU233 |   |  |  | 4.02 | 7.33926E-09 |  |  |  |  |
| New.CleanUp.ReferenceOTU164632 | Clostridiales | *Veillonellaceae* | *Acidaminococcus* | 1.43 | 8.88497E-09 |  |  |  |  |
| 186735 | Clostridiales | *Lachnospiraceae* | *Blautia* | 2.74 | 1.83476E-08 |  |  |  |  |
| 4425495 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 2.8 | 1.9597E-08 |  |  |  |  |
| New.CleanUp.ReferenceOTU183131 | Clostridiales | *Veillonellaceae* |  | 2.6 | 2.75025E-08 |  |  |  |  |
| 323135 | Clostridiales | *Ruminococcaceae* | *Ruminococcus* | 4.62 | 3.1665E-08 |  |  |  |  |
| 185575 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | -7.48 | 4.14083E-08 |  |  |  |  |
| 130103 | Clostridiales | *Lachnospiraceae* | *Dorea* | -6.08 | 5.32722E-08 |  |  |  |  |
| New.CleanUp.ReferenceOTU14560 | Verrucomicrobiales | *Verrucomicrobiaceae* | *Akkermansia* | -3.31 | 5.93437E-08 |  |  |  |  |
| New.CleanUp.ReferenceOTU42881 | Lactobacillales |  |  | 2.62 | 6.61314E-08 |  |  |  |  |
| 193654 | Clostridiales | *Lachnospiraceae* |  | 6.25 | 9.88886E-08 |  |  |  |  |
| New.CleanUp.ReferenceOTU121640 | Erysipelotrichales | *Erysipelotrichaceae* |  | -2.42 | 9.90629E-08 |  |  |  |  |
| New.CleanUp.ReferenceOTU89170 | Clostridiales | *Lachnospiraceae* |  | 4.17 | 1.01193E-07 |  |  |  |  |
| 2046330 | Clostridiales | *Lachnospiraceae* |  | -6.1 | 1.37729E-07 |  |  |  |  |
| New.CleanUp.ReferenceOTU134498 | Enterobacteriales | *Enterobacteriaceae* |  | -2.02 | 1.48212E-07 |  |  |  |  |
| 180468 | Clostridiales | *Ruminococcaceae* | *Oscillospira* | -5.16 | 1.50916E-07 |  |  |  |  |
| 2264285 | Lactobacillales | *Enterococcaceae* |  | 3.46 | 1.83189E-07 |  |  |  |  |
| 4353757 | Pasteurellales | *Pasteurellaceae* |  | 5.73 | 1.84006E-07 |  |  |  |  |
| New.CleanUp.ReferenceOTU91178 | Clostridiales | *Veillonellaceae* |  | 1.94 | 2.24826E-07 |  |  |  |  |
| New.CleanUp.ReferenceOTU32176 | Erysipelotrichales | *Erysipelotrichaceae* | *Coprobacillus* | 2.62 | 2.5551E-07 |  |  |  |  |
| New.CleanUp.ReferenceOTU30224 |   |  |  | 1.7 | 3.60491E-07 |  |  |  |  |
| 346003 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | 5.14 | 4.50411E-07 |  |  |  |  |
| New.CleanUp.ReferenceOTU41721 | Lactobacillales | *Enterococcaceae* |  | 2.17 | 4.72798E-07 |  |  |  |  |
| New.ReferenceOTU678 | Clostridiales |  |  | -2.73 | 6.9137E-07 |  |  |  |  |
| 194297 | Clostridiales | *Ruminococcaceae* | *Ruminococcus* | 4.59 | 7.05575E-07 |  |  |  |  |
| 1820513 | Burkholderiales | *Alcaligenaceae* | *Sutterella* | -4.71 | 1.19951E-06 |  |  |  |  |
| 187126 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | 2 | 1.27573E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU167237 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | 6.89 | 1.34901E-06 |  |  |  |  |
| 4405104 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | 6.55 | 1.39292E-06 |  |  |  |  |
| 130289 | Clostridiales | *Lachnospiraceae* |  | 1.96 | 1.40859E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU73467 |   |  |  | 2.69 | 1.65231E-06 |  |  |  |  |
| 189548 | Clostridiales | *Lachnospiraceae* |  | -5.61 | 1.75374E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU162740 | Coriobacteriales | *Coriobacteriaceae* | *Collinsella* | 2.93 | 2.33519E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU134782 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | 1.81 | 3.30321E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU84312 | Lactobacillales | *Streptococcaceae* | *Streptococcus* | 1.37 | 4.39616E-06 |  |  |  |  |
| New.ReferenceOTU798 | Clostridiales |  |  | 4.82 | 5.31541E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU112926 | Clostridiales | *Lachnospiraceae* |  | -2.42 | 5.48849E-06 |  |  |  |  |
| 191792 | Clostridiales | *Ruminococcaceae* |  | 7.73 | 5.67113E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU75622 | Clostridiales | *Clostridiaceae* | *SMB53* | 3.12 | 6.12185E-06 |  |  |  |  |
| 192070 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 3.29 | 7.59851E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU129851 | Clostridiales | *Lachnospiraceae* |  | 4.08 | 8.02826E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU19554 | Clostridiales |  |  | -1.96 | 8.34359E-06 |  |  |  |  |
| New.CleanUp.ReferenceOTU91099 | Clostridiales | *Lachnospiraceae* | *Roseburia* | 2.39 | 1.07811E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU60707 | Clostridiales | *Lachnospiraceae* | *Lachnospira* | -1.97 | 1.13251E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU189610 | Clostridiales |  |  | -1.88 | 1.15012E-05 |  |  |  |  |
| 1055212 | Lactobacillales | *Enterococcaceae* | *Enterococcus* | 2.4 | 1.38054E-05 |  |  |  |  |
| 344154 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | -2.96 | 1.42176E-05 |  |  |  |  |
| 4377715 | Clostridiales | *Lachnospiraceae* | *Epulopiscium* | -2.06 | 1.44464E-05 |  |  |  |  |
| 495017 | Bacteroidales | *Porphyromonadaceae* | *Porphyromonas* | 1.64 | 1.54812E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU194188 |  |  |  | -3.34 | 1.73988E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU58476 | Bacteroidales | *Porphyromonadaceae* | *Parabacteroides* | 3.75 | 1.86079E-05 |  |  |  |  |
| 163494 | Clostridiales | *Lachnospiraceae* |  | 5.67 | 1.97796E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU106994 | Clostridiales | *Lachnospiraceae* |  | 1.76 | 1.98108E-05 |  |  |  |  |
| 4459750 | Clostridiales | *Veillonellaceae* | *Veillonella* | 1.74 | 2.01525E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU139461 | Clostridiales | *Lachnospiraceae* |  | 3.07 | 2.08234E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU157995 | Clostridiales | *Lachnospiraceae* |  | 2.96 | 2.32264E-05 |  |  |  |  |
| 23625 | GMD14H09 |  |  | -1.41 | 2.36377E-05 |  |  |  |  |
| 191683 | Clostridiales | *Lachnospiraceae* |  | -2.66 | 2.39346E-05 |  |  |  |  |
| 291870 | Clostridiales | *Lachnospiraceae* | *Blautia* | 2.1 | 2.54921E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU176786 |  |  |  | 4.96 | 2.61063E-05 |  |  |  |  |
| 359314 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | 1.42 | 2.61686E-05 |  |  |  |  |
| 185802 | Clostridiales | *Ruminococcaceae* |  | -3.22 | 2.75298E-05 |  |  |  |  |
| 336559 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 3.92 | 2.83368E-05 |  |  |  |  |
| 4472551 | Clostridiales | *Lachnospiraceae* | *Blautia* | 4.81 | 2.92776E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU106051 | Clostridiales | *Lachnospiraceae* |  | 5.01 | 3.13136E-05 |  |  |  |  |
| 297182 | Clostridiales | *Lachnospiraceae* | *Dorea* | 1.08 | 3.20215E-05 |  |  |  |  |
| 4416614 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 3.31 | 3.80318E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU53451 | Clostridiales | *Lachnospiraceae* |  | 2.01 | 3.87936E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU25549 | Clostridiales | *Lachnospiraceae* |  | -2.11 | 4.15872E-05 |  |  |  |  |
| 556126 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 3.59 | 4.23069E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU83878 | Clostridiales |  |  | -2.95 | 4.29239E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU187168 | Clostridiales | *Veillonellaceae* | *Veillonella* | 1.68 | 4.4962E-05 |  |  |  |  |
| New.ReferenceOTU504 | Clostridiales | *Ruminococcaceae* |  | 4.75 | 4.54376E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU190437 | Clostridiales |  |  | 1.93 | 4.54598E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU14620 | Clostridiales |  |  | 1.61 | 4.75024E-05 |  |  |  |  |
| 195207 | Clostridiales | *Lachnospiraceae* | *Roseburia* | 2.19 | 5.32088E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU164338 | Erysipelotrichales | *Erysipelotrichaceae* | *Coprobacillus* | 1.87 | 5.35198E-05 |  |  |  |  |
| 4380971 | Clostridiales | *Clostridiaceae* | *Clostridium* | -4.79 | 5.51957E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU65149 | Clostridiales | *Lachnospiraceae* | *Epulopiscium* | 4.42 | 5.71787E-05 |  |  |  |  |
| 14124 | Clostridiales | *Lachnospiraceae* | *Epulopiscium* | 4.46 | 5.8581E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU79706 |   |  |  | 1.88 | 6.16428E-05 |  |  |  |  |
| 4382457 | Erysipelotrichales | *Erysipelotrichaceae* | *[Eubacterium]* | 2.53 | 6.25566E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU121349 | Enterobacteriales | *Enterobacteriaceae* |  | 2.05 | 6.38421E-05 |  |  |  |  |
| 4361101 | Clostridiales | *Lachnospiraceae* |  | 4.23 | 6.59734E-05 |  |  |  |  |
| 3244896 | Lactobacillales | *Streptococcaceae* | *Streptococcus* | 4.01 | 6.97773E-05 |  |  |  |  |
| 357168 | Clostridiales | *Lachnospiraceae* | *Blautia* | -4.5 | 6.97971E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU132670 | Clostridiales | *Lachnospiraceae* |  | 3.62 | 7.59869E-05 |  |  |  |  |
| 1146349 | Clostridiales | *Lachnospiraceae* | *Epulopiscium* | 3.8 | 7.79796E-05 |  |  |  |  |
| 198011 | Clostridiales | *Lachnospiraceae* |  | 3.64 | 7.85581E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU84432 | Erysipelotrichales | *Erysipelotrichaceae* | *[Eubacterium]* | 4.37 | 8.46858E-05 |  |  |  |  |
| 185763 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | -4.99 | 8.58616E-05 |  |  |  |  |
| 4452634 | Clostridiales | *Clostridiaceae* | *Clostridium* | -7.11 | 9.35313E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU93102 | Clostridiales | *Lachnospiraceae* |  | 4.57 | 9.46433E-05 |  |  |  |  |
| New.CleanUp.ReferenceOTU39542 | Clostridiales | *Lachnospiraceae* |  | 2.68 | 0.000110851 |  |  |  |  |
| New.ReferenceOTU371 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 3.15 | 0.000117725 |  |  |  |  |
| New.CleanUp.ReferenceOTU48746 |  |  |  | 3.92 | 0.000120876 |  |  |  |  |
| 139279 | Actinomycetales |  |  | 2.94 | 0.000128423 |  |  |  |  |
| New.CleanUp.ReferenceOTU83896 | Clostridiales | *Lachnospiraceae* | *Lachnospira* | 2.68 | 0.000131778 |  |  |  |  |
| 173965 | Coriobacteriales | *Coriobacteriaceae* | *Adlercreutzia* | 5.59 | 0.000131902 |  |  |  |  |
| 4193309 | Clostridiales | *Clostridiaceae* | *Clostridium* | 4.92 | 0.000133057 |  |  |  |  |
| 306299 | Clostridiales | *Lachnospiraceae* |  | 2.78 | 0.000136813 |  |  |  |  |
| 230421 | Clostridiales | *Ruminococcaceae* |  | -3.12 | 0.000138867 |  |  |  |  |
| 186416 | Clostridiales | *Lachnospiraceae* |  | 4.38 | 0.000139526 |  |  |  |  |
| 176980 | Clostridiales | *Lachnospiraceae* | *Dorea* | 7.31 | 0.000143122 |  |  |  |  |
| 572254 | Clostridiales | *Lachnospiraceae* |  | -5.7 | 0.000147902 |  |  |  |  |
| 193969 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | 2.4 | 0.000148454 |  |  |  |  |
| New.ReferenceOTU20 |   |  |  | 1.46 | 0.000163289 |  |  |  |  |
| New.CleanUp.ReferenceOTU79974 | Clostridiales |  |  | 2.12 | 0.000171421 |  |  |  |  |
| New.CleanUp.ReferenceOTU26279 |   |  |  | 3.61 | 0.000178067 |  |  |  |  |
| New.CleanUp.ReferenceOTU124490 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | 1.31 | 0.000178265 |  |  |  |  |
| 145009 | Lactobacillales | *Streptococcaceae* | *Streptococcus* | 2.5 | 0.000180072 |  |  |  |  |
| 191476 | Clostridiales | *Lachnospiraceae* | *[Ruminococcus]* | -3.32 | 0.000180345 |  |  |  |  |
| 840376 | Clostridiales | *Ruminococcaceae* |  | 7.23 | 0.000185984 |  |  |  |  |
| New.ReferenceOTU957 | Clostridiales |  |  | 3.69 | 0.000189874 |  |  |  |  |
| 4435402 | Clostridiales | *Veillonellaceae* | *Megasphaera* | -1.72 | 0.000193353 |  |  |  |  |
| New.ReferenceOTU797 | Bacteroidales | *Porphyromonadaceae* | *Parabacteroides* | -2.38 | 0.000202331 |  |  |  |  |
| New.CleanUp.ReferenceOTU8967 | Clostridiales |  |  | 3.66 | 0.000207849 |  |  |  |  |
| 4377091 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | 2.58 | 0.000216592 |  |  |  |  |
| 4178726 | Clostridiales | *Lachnospiraceae* |  | 4.16 | 0.000234664 |  |  |  |  |
| New.CleanUp.ReferenceOTU179614 | Verrucomicrobiales | *Verrucomicrobiaceae* | *Akkermansia* | 1.64 | 0.000236058 |  |  |  |  |
| New.CleanUp.ReferenceOTU109345 | Erysipelotrichales | *Erysipelotrichaceae* | *[Eubacterium]* | -4 | 0.000236387 |  |  |  |  |
| 186077 | Clostridiales | *Lachnospiraceae* | *Roseburia* | -1.46 | 0.00024851 |  |  |  |  |
| 199279 | Clostridiales | *Lachnospiraceae* | *Roseburia* | -1.75 | 0.000257221 |  |  |  |  |
| New.CleanUp.ReferenceOTU78398 | Clostridiales | *Lachnospiraceae* |  | 2.58 | 0.000275697 |  |  |  |  |
| New.ReferenceOTU326 | Clostridiales |  |  | 2.16 | 0.00027809 |  |  |  |  |
| New.CleanUp.ReferenceOTU112685 | Clostridiales | *Lachnospiraceae* | *Blautia* | 2.69 | 0.000282631 |  |  |  |  |
| 183656 | Clostridiales | *Lachnospiraceae* |  | 3.28 | 0.000284114 |  |  |  |  |
| New.CleanUp.ReferenceOTU8277 | Clostridiales | *Clostridiaceae* | *SMB53* | 2.22 | 0.000285245 |  |  |  |  |
| New.CleanUp.ReferenceOTU13639 | Lactobacillales | *Enterococcaceae* |  | 4.34 | 0.00028673 |  |  |  |  |
| 299837 | Clostridiales | *Ruminococcaceae* | *Faecalibacterium* | 2.39 | 0.000293966 |  |  |  |  |
| New.CleanUp.ReferenceOTU162085 | Clostridiales | *Lachnospiraceae* |  | 2.39 | 0.00029585 |  |  |  |  |
| New.ReferenceOTU1237 | Erysipelotrichales | *Erysipelotrichaceae* | *[Eubacterium]* | -3.93 | 0.000312958 |  |  |  |  |
| 351163 | Clostridiales | *Lachnospiraceae* | *Blautia* | 5.31 | 0.000321374 |  |  |  |  |
| New.CleanUp.ReferenceOTU111557 |  |  |  | -1.9 | 0.000321376 |  |  |  |  |
| New.CleanUp.ReferenceOTU37576 | Clostridiales | *Lachnospiraceae* |  | 4.15 | 0.000329539 |  |  |  |  |
| 194380 | Clostridiales | *Lachnospiraceae* | *Blautia* | 1.91 | 0.000354442 |  |  |  |  |
| New.CleanUp.ReferenceOTU108429 | Clostridiales | *Lachnospiraceae* |  | 2.83 | 0.000357612 |  |  |  |  |
| New.CleanUp.ReferenceOTU19817 | Enterobacteriales | *Enterobacteriaceae* |  | 3.23 | 0.000364472 |  |  |  |  |
| 187178 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | -5.3 | 0.000367198 |  |  |  |  |
| New.ReferenceOTU194 | Clostridiales | *Lachnospiraceae* |  | -4.45 | 0.00038152 |  |  |  |  |
| New.ReferenceOTU1054 | Clostridiales | *Lachnospiraceae* |  | 3 | 0.000387597 |  |  |  |  |
| 470117 | Clostridiales | *Ruminococcaceae* | *Ruminococcus* | 6.92 | 0.000388019 |  |  |  |  |
| 4411295 | Clostridiales | *Lachnospiraceae* |  | -3.54 | 0.0003894 |  |  |  |  |
| 4393057 | Sphingomonadales | *Sphingomonadaceae* | *Sphingobium* | -1.1 | 0.000397935 |  |  |  |  |
| New.CleanUp.ReferenceOTU4113 | Clostridiales | *Veillonellaceae* |  | 2.84 | 0.000399298 |  |  |  |  |
| New.CleanUp.ReferenceOTU13433 | Clostridiales | *Clostridiaceae* | *SMB53* | 1.82 | 0.000406562 |  |  |  |  |
| 195407 | Clostridiales | *Lachnospiraceae* |  | 1.42 | 0.00040851 |  |  |  |  |
| New.CleanUp.ReferenceOTU48503 | Clostridiales |  |  | 2.49 | 0.000418408 |  |  |  |  |
| New.CleanUp.ReferenceOTU82524 | Clostridiales | *Clostridiaceae* | *Clostridium* | 2.93 | 0.000426527 |  |  |  |  |
| 187050 | Clostridiales | *Lachnospiraceae* | *Blautia* | 1.9 | 0.000428309 |  |  |  |  |
| 367092 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | 3.07 | 0.000435888 |  |  |  |  |
| New.CleanUp.ReferenceOTU78890 | Clostridiales | *Ruminococcaceae* | *Oscillospira* | -2.06 | 0.000436431 |  |  |  |  |
| 194287 | Clostridiales | *Lachnospiraceae* | *Blautia* | 2.43 | 0.000438278 |  |  |  |  |
| New.ReferenceOTU1266 | Clostridiales |  |  | 2.35 | 0.00044758 |  |  |  |  |
| New.CleanUp.ReferenceOTU115399 | Clostridiales | *Lachnospiraceae* |  | 1.38 | 0.000450952 |  |  |  |  |
| 4323727 | Clostridiales | *Lachnospiraceae* |  | -2.64 | 0.000496836 |  |  |  |  |
| New.CleanUp.ReferenceOTU168269 | Bifidobacteriales | *Bifidobacteriaceae* | *Bifidobacterium* | -1.2 | 0.000523569 |  |  |  |  |
| 124906 | Clostridiales | *Veillonellaceae* | *Megasphaera* | -1.9 | 0.000529879 |  |  |  |  |
| 3829951 | Clostridiales | *Lachnospiraceae* | *Epulopiscium* | -3.8 | 0.000530699 |  |  |  |  |
| 306499 | Clostridiales | *Lachnospiraceae* |  | 6.26 | 0.000543462 |  |  |  |  |
| New.CleanUp.ReferenceOTU111830 | Clostridiales | *Lachnospiraceae* |  | -2.57 | 0.00054688 |  |  |  |  |
| New.CleanUp.ReferenceOTU50137 | Verrucomicrobiales | *Verrucomicrobiaceae* | *Akkermansia* | 3.6 | 0.000547588 |  |  |  |  |
| New.CleanUp.ReferenceOTU54675 | Clostridiales |  |  | 4.05 | 0.000560859 |  |  |  |  |
| New.ReferenceOTU185 | Clostridiales | *Lachnospiraceae* | *[Ruminococcus]* | 1.81 | 0.000566403 |  |  |  |  |
| New.CleanUp.ReferenceOTU180084 | Clostridiales | *Clostridiaceae* | *Clostridium* | 2.69 | 0.000567877 |  |  |  |  |
| New.CleanUp.ReferenceOTU112391 | Clostridiales | *Veillonellaceae* | *Veillonella* | 2.56 | 0.000572487 |  |  |  |  |
| 409686 | Clostridiales | *Lachnospiraceae* |  | 4.37 | 0.000581738 |  |  |  |  |
| New.CleanUp.ReferenceOTU94526 | Clostridiales | *Lachnospiraceae* |  | 4.03 | 0.000591471 |  |  |  |  |
| New.CleanUp.ReferenceOTU193025 | Clostridiales | *Lachnospiraceae* | *Lachnospira* | -4.43 | 0.000630021 |  |  |  |  |
| 170652 | Clostridiales | *Clostridiaceae* | *Clostridium* | -1.87 | 0.000630177 |  |  |  |  |
| 338994 | Clostridiales | *Lachnospiraceae* |  | -1.95 | 0.000649759 |  |  |  |  |
| 184009 | Clostridiales | *Clostridiaceae* | *SMB53* | 2.33 | 0.000657582 |  |  |  |  |
| New.ReferenceOTU829 | Clostridiales | *Lachnospiraceae* |  | 2.19 | 0.000660159 |  |  |  |  |
| 360636 | Erysipelotrichales | *Erysipelotrichaceae* |  | 4.77 | 0.000662681 |  |  |  |  |
| 337465 | Clostridiales | *Lachnospiraceae* |  | 2.87 | 0.000668961 |  |  |  |  |
| New.CleanUp.ReferenceOTU128118 | Clostridiales |  |  | 2.29 | 0.000674553 |  |  |  |  |
| 187511 | Clostridiales | *Lachnospiraceae* |  | 4.36 | 0.000676673 |  |  |  |  |
| 227083 | Bacillales | *Staphylococcaceae* | *Staphylococcus* | -2.51 | 0.000692856 |  |  |  |  |
| 292145 |   |  |  | -2.39 | 0.000692887 |  |  |  |  |
| New.CleanUp.ReferenceOTU128863 | Clostridiales | *Lachnospiraceae* |  | 2.41 | 0.000694822 |  |  |  |  |
| New.ReferenceOTU103 | Bacteroidales | *Bacteroidaceae* | *Bacteroides* | -5.54 | 0.000696849 |  |  |  |  |
| 184525 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | -2.01 | 0.000703714 |  |  |  |  |
| New.CleanUp.ReferenceOTU73870 | Clostridiales | *Lachnospiraceae* |  | 3.03 | 0.000710258 |  |  |  |  |
| New.CleanUp.ReferenceOTU54185 |  |  |  | 5.07 | 0.000716934 |  |  |  |  |
| 184342 | Clostridiales | *Lachnospiraceae* | *Coprococcus* | -2.2 | 0.00071851 |  |  |  |  |

aGreengenes Database V.13\_5

bParameter estimate interpreted as difference in log mean OTU abundance, comparing infants with GBS+ mothers to infants with GBS- mothers (0: no association, >0: enriched in infants with GBS+ mothers, <0: diminished in infants with GBS+ mothers)