**Supplement 4:** The full list of correlations between relative abundances of all observed bacterial genera (after rarefaction) and the beta PCo1 and PCo2 matrices.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Beta PCo1** | | | **Beta PCo2** | |
|  | **Genus** | **cor.val** | **Genus** | | **cor.val** |
| 1 | Lactobacillus | 0.926 | Faecalibacterium | | -0.598 |
| 2 | Bacteroides | -0.542 | Blautia | | -0.588 |
| 3 | Faecalibacterium | -0.514 | Gardnerella | | 0.559 |
| 4 | Blautia | -0.498 | Agathobacter | | -0.519 |
| 5 | Agathobacter | -0.436 | Bacteroides | | -0.512 |
| 6 | Ruminococcus | -0.426 | Ruminococcus | | -0.51 |
| 7 | Prevotella | -0.41 | Dorea | | -0.446 |
| 8 | Parabacteroides | -0.361 | Corynebacterium | | 0.431 |
| 9 | Dorea | -0.359 | Subdoligranulum | | -0.415 |
| 10 | Subdoligranulum | -0.347 | Coprococcus | | -0.411 |
| 11 | Lachnoclostridium | -0.336 | Lachnospiraceae\_NK4A136\_group | | -0.397 |
| 12 | Coprococcus | -0.335 | Parabacteroides | | -0.392 |
| 13 | Monoglobus | -0.326 | Odoribacter | | -0.369 |
| 14 | Anaerostipes | -0.321 | Monoglobus | | -0.364 |
| 15 | Corynebacterium | -0.319 | Staphylococcus | | 0.355 |
| 16 | Lachnospira | -0.316 | Lachnoclostridium | | -0.342 |
| 17 | Lachnospiraceae\_NK4A136\_group | -0.304 | Alistipes | | -0.34 |
| 18 | Alistipes | -0.301 | Erysipelotrichaceae\_UCG-003 | | -0.339 |
| 19 | Fusicatenibacter | -0.292 | Lachnospira | | -0.327 |
| 20 | Dialister | -0.284 | Lachnospiraceae\_ND3007\_group | | -0.307 |
| 21 | Sutterella | -0.277 | Fusicatenibacter | | -0.306 |
| 22 | Erysipelotrichaceae\_UCG-003 | -0.267 | Butyricicoccus | | -0.303 |
| 23 | Gardnerella | -0.262 | Phascolarctobacterium | | -0.296 |
| 24 | Collinsella | -0.261 | Collinsella | | -0.296 |
| 25 | Odoribacter | -0.255 | UCG-005 | | -0.294 |
| 26 | Colidextribacter | -0.251 | Sutterella | | -0.279 |
| 27 | Phascolarctobacterium | -0.249 | Christensenellaceae\_R-7\_group | | -0.269 |
| 28 | Anaerococcus | -0.249 | Atopobium | | 0.265 |
| 29 | Incertae\_Sedis | -0.244 | Oscillibacter | | -0.262 |
| 30 | UCG-002 | -0.243 | UCG-002 | | -0.259 |
| 31 | Oscillibacter | -0.237 | Tyzzerella | | -0.256 |
| 32 | Roseburia | -0.236 | CAG-56 | | -0.25 |
| 33 | Fenollaria | -0.233 | Incertae\_Sedis | | -0.248 |
| 34 | Mobiluncus | -0.232 | Anaerostipes | | -0.246 |
| 35 | Lachnospiraceae\_ND3007\_group | -0.215 | Family\_XIII\_UCG-001 | | -0.246 |
| 36 | Paraprevotella | -0.209 | Colidextribacter | | -0.24 |
| 37 | Flavonifractor | -0.208 | Roseburia | | -0.239 |
| 38 | UCG-003 | -0.208 | Megasphaera | | 0.237 |
| 39 | Christensenellaceae\_R-7\_group | -0.207 | Bilophila | | -0.217 |
| 40 | Barnesiella | -0.205 | Adlercreutzia | | -0.209 |
| 41 | Holdemanella | -0.205 | UBA1819 | | -0.209 |
| 42 | Finegoldia | -0.201 | UCG-003 | | -0.206 |
| 43 | Staphylococcus | -0.198 | Coprobacter | | -0.203 |
| 44 | Peptococcus | -0.198 | Family\_XIII\_AD3011\_group | | -0.201 |
| 45 | Peptoniphilus | -0.197 | Intestinibacter | | -0.201 |
| 46 | Varibaculum | -0.195 | DNF00809 | | 0.2 |
| 47 | Bilophila | -0.189 | Parasutterella | | -0.193 |
| 48 | Adlercreutzia | -0.188 | Dermabacter | | 0.183 |
| 49 | Fastidiosipila | -0.186 | Paraprevotella | | -0.182 |
| 50 | Family\_XIII\_UCG-001 | -0.179 | Barnesiella | | -0.181 |
| 51 | Family\_XIII\_AD3011\_group | -0.179 | Lachnospiraceae\_UCG-001 | | -0.177 |
| 52 | CAG-352 | -0.179 | DTU089 | | -0.177 |
| 53 | Butyricicoccus | -0.177 | GCA-900066575 | | -0.177 |
| 54 | Lachnospiraceae\_UCG-001 | -0.173 | Ochrobactrum | | 0.175 |
| 55 | Holdemania | -0.172 | Defluviitaleaceae\_UCG-011 | | -0.174 |
| 56 | Lachnospiraceae\_UCG-004 | -0.171 | Senegalimassilia | | -0.174 |
| 57 | Atopobium | -0.17 | Rothia | | 0.165 |
| 58 | CAG-56 | -0.169 | Frisingicoccus | | -0.162 |
| 59 | Streptomyces | -0.168 | Anaerococcus | | 0.162 |
| 60 | Lachnospiraceae\_UCG-003 | -0.166 | Holdemanella | | -0.158 |
| 61 | Tyzzerella | -0.166 | Sellimonas | | -0.154 |
| 62 | Coprobacter | -0.159 | Oscillospira | | -0.154 |
| 63 | Prevotellaceae\_NK3B31\_group | -0.158 | Streptomyces | | 0.151 |
| 64 | Parvimonas | -0.156 | Lachnospiraceae\_UCG-004 | | -0.15 |
| 65 | Campylobacter | -0.156 | Gallicola | | 0.148 |
| 66 | Megasphaera | -0.156 | Conexibacter | | 0.146 |
| 67 | UCG-005 | -0.156 | Lachnospiraceae\_UCG-003 | | -0.142 |
| 68 | Bifidobacterium | -0.154 | Eggerthella | | -0.139 |
| 69 | UBA1819 | -0.154 | Varibaculum | | 0.139 |
| 70 | Frisingicoccus | -0.152 | Victivallis | | -0.136 |
| 71 | DNF00809 | -0.146 | Fastidiosipila | | 0.136 |
| 72 | Facklamia | -0.144 | Flavonifractor | | -0.135 |
| 73 | Oscillospira | -0.142 | Faecalitalea | | -0.135 |
| 74 | Terrisporobacter | -0.139 | UC5-1-2E3 | | -0.134 |
| 75 | Stenotrophomonas | -0.139 | SH-PL14 | | 0.134 |
| 76 | Negativibacillus | -0.138 | alphaI\_cluster | | 0.134 |
| 77 | Romboutsia | -0.138 | LD29 | | -0.132 |
| 78 | Parasutterella | -0.136 | Helcobacillus | | 0.132 |
| 79 | Akkermansia | -0.135 | Romboutsia | | -0.13 |
| 80 | Sneathia | -0.133 | Mycoplasma | | 0.129 |
| 81 | Intestinibacter | -0.132 | Escherichia/Shigella | | 0.129 |
| 82 | Lawsonella | -0.132 | Finegoldia | | 0.129 |
| 83 | Rhodococcus | -0.128 | Sphingorhabdus | | -0.128 |
| 84 | DTU089 | -0.128 | Mitsuokella | | -0.127 |
| 85 | Murdochiella | -0.126 | Holdemania | | -0.127 |
| 86 | Moryella | -0.123 | Alloprevotella | | -0.125 |
| 87 | Lachnospiraceae\_UCG-010 | -0.122 | NK4A214\_group | | -0.125 |
| 88 | Porphyromonas | -0.121 | Campylobacter | | 0.125 |
| 89 | GCA-900066575 | -0.12 | Lactobacillus | | -0.124 |
| 90 | Defluviitaleaceae\_UCG-011 | -0.12 | Phocea | | -0.121 |
| 91 | Senegalimassilia | -0.119 | Succiniclasticum | | -0.121 |
| 92 | Ezakiella | -0.118 | Marmoricola | | -0.121 |
| 93 | Anaeroglobus | -0.116 | Turicibacter | | -0.12 |
| 94 | Helcococcus | -0.115 | Marvinbryantia | | -0.119 |
| 95 | Delftia | -0.113 | Negativibacillus | | -0.119 |
| 96 | Anaerosporobacter | -0.113 | Pseudomonas | | 0.118 |
| 97 | Eggerthella | -0.112 | Stenotrophomonas | | 0.117 |
| 98 | Acidibacter | -0.112 | Desulfovibrio | | -0.116 |
| 99 | Pseudomonas | -0.111 | Prevotellaceae\_UCG-001 | | -0.116 |
| 100 | Desulfovibrio | -0.111 | Anaerotruncus | | -0.114 |
| 101 | Ochrobactrum | -0.109 | Gordonibacter | | -0.114 |
| 102 | Duganella | -0.108 | Anaerosporobacter | | -0.114 |
| 103 | Mycobacterium | -0.106 | CAG-352 | | -0.112 |
| 104 | Negativicoccus | -0.106 | Helcococcus | | 0.111 |
| 105 | Acinetobacter | -0.104 | Prevotellaceae\_NK3B31\_group | | -0.107 |
| 106 | LD29 | -0.103 | Butyricimonas | | -0.106 |
| 107 | Actinobaculum | -0.102 | Eisenbergiella | | -0.104 |
| 108 | Pseudorhodobacter | -0.101 | Sneathia | | 0.103 |
| 109 | Pantoea | -0.101 | Merdibacter | | -0.101 |
| 110 | Rothia | -0.101 | Chryseobacterium | | 0.101 |
| 111 | Intestinimonas | -0.1 | Cutibacterium | | 0.1 |
| 112 | Catenibacterium | -0.1 | Pedobacter | | 0.096 |
| 113 | Sellimonas | -0.098 | Rhodoferax | | 0.096 |
| 114 | Sphingomonas | -0.097 | Pedomicrobium | | 0.095 |
| 115 | Succiniclasticum | -0.097 | Lachnospiraceae\_AC2044\_group | | -0.094 |
| 116 | Phocea | -0.097 | Ornithinimicrobium | | 0.094 |
| 117 | Marmoricola | -0.097 | Tuzzerella | | -0.093 |
| 118 | Actinotignum | -0.096 | Turicella | | -0.093 |
| 119 | Sphingorhabdus | -0.096 | Alkanindiges | | -0.092 |
| 120 | Propionimicrobium | -0.096 | Empedobacter | | 0.091 |
| 121 | Leifsonia | -0.096 | Thermicanus | | 0.091 |
| 122 | S5-A14a | -0.096 | Lachnospiraceae\_FCS020\_group | | -0.09 |
| 123 | Lactococcus | -0.096 | Variovorax | | 0.088 |
| 124 | UC5-1-2E3 | -0.094 | Macrococcus | | 0.088 |
| 125 | Microbacterium | -0.094 | Candidatus\_Soleaferrea | | -0.087 |
| 126 | Gallicola | -0.094 | Nesterenkonia | | -0.087 |
| 127 | Streptococcus | -0.094 | Acinetobacter | | 0.087 |
| 128 | Erysipelatoclostridium | -0.093 | Enhydrobacter | | 0.087 |
| 129 | Actinomyces | -0.092 | Pseudochrobactrum | | 0.086 |
| 130 | Oligella | -0.092 | Akkermansia | | -0.085 |
| 131 | Undibacterium | -0.091 | Bdellovibrio | | 0.085 |
| 132 | Treponema | -0.091 | Lawsonella | | 0.084 |
| 133 | Victivallis | -0.09 | Aerococcus | | 0.083 |
| 134 | Pseudochrobactrum | -0.089 | Delftia | | 0.083 |
| 135 | Sediminibacterium | -0.089 | Granulicatella | | 0.083 |
| 136 | Vibrionimonas | -0.088 | Mobiluncus | | 0.082 |
| 137 | Aggregatibacter | -0.087 | Leuconostoc | | -0.081 |
| 138 | Anaerotruncus | -0.086 | Anaeroplasma | | -0.081 |
| 139 | Gordonibacter | -0.086 | Granulicella | | -0.08 |
| 140 | Conexibacter | -0.085 | Moraxella | | 0.079 |
| 141 | Cutibacterium | -0.085 | Petrimonas | | 0.079 |
| 142 | Asteroleplasma | -0.085 | Propionimicrobium | | 0.078 |
| 143 | Petrimonas | -0.085 | Paludicola | | -0.077 |
| 144 | Rhizorhapis | -0.084 | Aeromonas | | 0.077 |
| 145 | Alloscardovia | -0.081 | Murdochiella | | 0.077 |
| 146 | F0332 | -0.081 | Aggregatibacter | | 0.077 |
| 147 | Ornithinimicrobium | -0.08 | Porphyromonas | | 0.076 |
| 148 | Alloprevotella | -0.08 | Rhodobacter | | 0.076 |
| 149 | Morganella | -0.079 | Fenollaria | | 0.076 |
| 150 | Abiotrophia | -0.079 | Lihuaxuella | | -0.074 |
| 151 | Bosea | 0.079 | Shewanella | | 0.073 |
| 152 | Capnocytophaga | -0.077 | Ignavigranum | | 0.073 |
| 153 | Lihuaxuella | -0.077 | F0332 | | 0.073 |
| 154 | Peptoanaerobacter | -0.077 | Capnocytophaga | | 0.072 |
| 155 | Dermabacter | -0.076 | UCG-009 | | -0.071 |
| 156 | Dermacoccus | -0.075 | Rikenellaceae\_RC9\_gut\_group | | -0.069 |
| 157 | Hungatella | -0.075 | Facklamia | | 0.069 |
| 158 | Butyricimonas | -0.075 | Rhodococcus | | 0.069 |
| 159 | Helcobacillus | -0.074 | Sphingobacterium | | -0.068 |
| 160 | Peredibacter | 0.074 | Christensenella | | -0.067 |
| 161 | Fusobacterium | -0.073 | Pseudorhodobacter | | -0.067 |
| 162 | Lachnospiraceae\_FCS020\_group | -0.073 | Pantoea | | -0.067 |
| 163 | Merdibacter | -0.073 | Pseudoglutamicibacter | | 0.067 |
| 164 | Aquabacterium | 0.073 | Actinotignum | | 0.067 |
| 165 | Legionella | -0.072 | Vibrionimonas | | 0.067 |
| 166 | Candidatus\_Soleaferrea | -0.071 | Sediminibacterium | | 0.067 |
| 167 | Nesterenkonia | -0.071 | Alloscardovia | | 0.065 |
| 168 | Bacillus | 0.071 | Libanicoccus | | -0.064 |
| 169 | Globicatella | -0.07 | Globicatella | | 0.064 |
| 170 | Lachnospiraceae\_AC2044\_group | -0.07 | FukuN57 | | 0.064 |
| 171 | Ignavigranum | -0.07 | Legionella | | 0.062 |
| 172 | Kocuria | -0.069 | Lachnospiraceae\_UCG-009 | | -0.061 |
| 173 | Howardella | -0.069 | Ralstonia | | 0.061 |
| 174 | Klebsiella | -0.068 | Janthinobacterium | | 0.061 |
| 175 | Methylobacterium-Methylorubrum | -0.067 | Parvimonas | | 0.06 |
| 176 | Faecalitalea | -0.066 | Brevibacterium | | 0.059 |
| 177 | Prevotellaceae\_UCG-001 | -0.066 | Diaphorobacter | | 0.059 |
| 178 | Brevundimonas | -0.066 | Angelakisella | | -0.058 |
| 179 | Brevibacterium | -0.066 | Megamonas | | -0.058 |
| 180 | Rhodoluna | -0.065 | Cellulosimicrobium | | -0.058 |
| 181 | Mageibacillus | -0.065 | Tepidiphilus | | 0.058 |
| 182 | Acetobacterium | -0.065 | Actinomyces | | 0.058 |
| 183 | UCG-009 | -0.065 | Streptococcus | | 0.058 |
| 184 | W5053 | -0.065 | Sphingobium | | -0.057 |
| 185 | Paludicola | -0.064 | Abiotrophia | | 0.057 |
| 186 | Escherichia/Shigella | -0.062 | Conchiformibius | | 0.056 |
| 187 | Achromobacter | -0.061 | Treponema | | -0.055 |
| 188 | Brucella | -0.061 | Ellin6055 | | -0.053 |
| 189 | Polynucleobacter | -0.061 | Klebsiella | | -0.052 |
| 190 | Clostridium\_sensu\_stricto\_10 | 0.061 | Aminobacter | | 0.051 |
| 191 | Turicibacter | -0.059 | Enterococcus | | 0.051 |
| 192 | Flavobacterium | -0.059 | Asteroleplasma | | 0.051 |
| 193 | Aquicella | 0.059 | Neisseria | | 0.05 |
| 194 | Conchiformibius | -0.058 | Erysipelatoclostridium | | -0.048 |
| 195 | Mitsuokella | -0.058 | Acidaminococcus | | 0.047 |
| 196 | Lachnoanaerobaculum | 0.058 | Coxiella | | 0.047 |
| 197 | Nosocomiicoccus | 0.058 | Duganella | | 0.047 |
| 198 | Variovorax | -0.057 | Nocardioides | | 0.047 |
| 199 | Geobacillus | 0.057 | Undibacterium | | -0.046 |
| 200 | Carnobacterium | 0.057 | Xylophilus | | -0.046 |
| 201 | Frigoribacterium | 0.057 | Acidibacter | | 0.046 |
| 202 | Brachybacterium | 0.057 | Peptoniphilus | | 0.046 |
| 203 | Pedomicrobium | -0.056 | Gordonia | | 0.045 |
| 204 | Chungangia | 0.056 | Pandoraea | | -0.044 |
| 205 | Sphaerotilus | 0.056 | Morganella | | -0.044 |
| 206 | Mogibacterium | -0.055 | Moheibacter | | 0.044 |
| 207 | Shuttleworthia | -0.055 | Haemophilus | | -0.042 |
| 208 | alphaI\_cluster | -0.055 | Olsenella | | -0.041 |
| 209 | SH-PL14 | -0.055 | Caenimonas | | 0.041 |
| 210 | Pseudoglutamicibacter | -0.055 | Methylobacterium-Methylorubrum | | -0.039 |
| 211 | Enhydrobacter | -0.054 | Catenibacterium | | -0.039 |
| 212 | Paucibacter | -0.054 | W5053 | | 0.038 |
| 213 | Lachnospiraceae\_NK4B4\_group | 0.054 | Coprobacillus | | -0.037 |
| 214 | Methylotenera | 0.054 | Terrisporobacter | | -0.037 |
| 215 | Tuzzerella | -0.053 | Polynucleobacter | | 0.037 |
| 216 | Ellin6055 | -0.051 | Brucella | | 0.037 |
| 217 | Sandaracinus | 0.051 | Clostridium\_sensu\_stricto\_10 | | -0.036 |
| 218 | Turicella | -0.05 | Chelatococcus | | -0.035 |
| 219 | Deinococcus | 0.05 | S5-A14a | | 0.035 |
| 220 | Rubellimicrobium | 0.05 | Anaeroglobus | | 0.034 |
| 221 | Lysobacter | 0.05 | Flavobacterium | | 0.034 |
| 222 | NK4A214\_group | -0.049 | Prevotella | | -0.033 |
| 223 | Pedobacter | -0.049 | Eikenella | | 0.033 |
| 224 | Conyzicola | 0.049 | Bifidobacterium | | 0.033 |
| 225 | Enterobacter | -0.048 | Sphingomonas | | 0.033 |
| 226 | Sphingobium | -0.048 | Fluviicola | | 0.032 |
| 227 | Tepidimonas | 0.048 | Paracoccus | | 0.032 |
| 228 | Mycoplasma | -0.047 | Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium | | -0.031 |
| 229 | Caenimonas | -0.047 | Photobacterium | | 0.031 |
| 230 | Blastomonas | 0.047 | Neochlamydia | | -0.03 |
| 231 | Serratia | 0.047 | Novosphingobium | | 0.03 |
| 232 | Luteimonas | 0.046 | Kocuria | | 0.03 |
| 233 | Eisenbergiella | -0.045 | Intestinimonas | | -0.029 |
| 234 | Nubsella | -0.045 | Hymenobacter | | -0.029 |
| 235 | Elizabethkingia | -0.045 | Clostridium\_sensu\_stricto\_1 | | -0.028 |
| 236 | Burkholderia-Caballeronia-Paraburkholderia | 0.045 | Anoxybacillus | | -0.028 |
| 237 | Aureimonas | 0.045 | Shuttleworthia | | 0.028 |
| 238 | Libanicoccus | -0.044 | Arcanobacterium | | 0.028 |
| 239 | Ralstonia | -0.044 | Brevundimonas | | 0.028 |
| 240 | Photobacterium | -0.044 | Agrococcus | | 0.027 |
| 241 | Pseudoxanthomonas | 0.044 | Mycobacterium | | -0.026 |
| 242 | Thermoanaerobacterium | 0.043 | Phyllobacterium | | 0.026 |
| 243 | Lysinibacillus | 0.042 | Roseomonas | | 0.026 |
| 244 | Hydrogenophilus | 0.042 | Actinobaculum | | 0.026 |
| 245 | Thermus | 0.042 | Pseudoxanthomonas | | 0.025 |
| 246 | Aerococcus | -0.041 | Howardella | | 0.025 |
| 247 | Pajaroellobacter | 0.041 | Lachnospiraceae\_UCG-010 | | -0.024 |
| 248 | Christensenella | -0.04 | Tepidimonas | | 0.024 |
| 249 | Actinobacillus | 0.04 | Fusobacterium | | 0.024 |
| 250 | Alcaligenes | 0.04 | Achromobacter | | 0.024 |
| 251 | SM1A02 | 0.04 | Chungangia | | -0.023 |
| 252 | Bdellovibrio | -0.039 | Peptostreptococcus | | 0.023 |
| 253 | Bradyrhizobium | 0.039 | Spirosoma | | 0.022 |
| 254 | Cyanobium\_PCC-6307 | 0.038 | Candidatus\_Amoebophilus | | 0.022 |
| 255 | Chelatococcus | 0.038 | Acetobacterium | | 0.022 |
| 256 | Veillonella | -0.037 | Veillonella | | 0.022 |
| 257 | Coxiella | -0.036 | Peptococcus | | 0.022 |
| 258 | Coprobacillus | 0.036 | Leifsonia | | 0.021 |
| 259 | Alkanindiges | -0.035 | Ezakiella | | 0.021 |
| 260 | Lachnospiraceae\_FE2018\_group | 0.035 | Bosea | | -0.019 |
| 261 | Neisseria | -0.034 | Trueperella | | 0.019 |
| 262 | Granulicatella | -0.034 | Massilia | | 0.019 |
| 263 | Rhodoferax | -0.034 | Peredibacter | | -0.018 |
| 264 | Novosphingobium | -0.033 | Sandaracinus | | -0.018 |
| 265 | Cloacibacterium | 0.032 | Dietzia | | -0.017 |
| 266 | Chryseobacterium | -0.031 | Lachnospiraceae\_NK4B4\_group | | -0.017 |
| 267 | Clostridium\_sensu\_stricto\_1 | -0.031 | Dermacoccus | | -0.017 |
| 268 | Arcanobacterium | -0.03 | Thermus | | 0.017 |
| 269 | Granulicella | -0.03 | Cloacibacterium | | 0.017 |
| 270 | Marvinbryantia | -0.03 | Rhizorhapis | | -0.016 |
| 271 | Trueperella | 0.029 | Aureimonas | | 0.015 |
| 272 | Empedobacter | -0.028 | Negativicoccus | | 0.014 |
| 273 | Pandoraea | -0.027 | Aquabacterium | | 0.013 |
| 274 | Tepidiphilus | -0.027 | Thiopseudomonas | | 0.013 |
| 275 | Nocardioides | -0.027 | Mageibacillus | | 0.013 |
| 276 | Roseomonas | -0.026 | Oligella | | 0.013 |
| 277 | Rickettsiella | 0.026 | Frigoribacterium | | 0.012 |
| 278 | Dietzia | 0.025 | Carnobacterium | | 0.012 |
| 279 | Xylophilus | 0.024 | Lachnospiraceae\_FE2018\_group | | 0.011 |
| 280 | Hyphomicrobium | -0.023 | Nosocomiicoccus | | 0.011 |
| 281 | Rikenellaceae\_RC9\_gut\_group | -0.023 | Burkholderia-Caballeronia-Paraburkholderia | | 0.011 |
| 282 | Agrococcus | 0.023 | Hungatella | | -0.011 |
| 283 | Phyllobacterium | 0.023 | Afipia | | 0.011 |
| 284 | Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium | 0.022 | Lactococcus | | 0.011 |
| 285 | Salinisphaera | 0.022 | Enterobacter | | 0.011 |
| 286 | Peptostreptococcus | -0.021 | Brachybacterium | | -0.01 |
| 287 | Sphingobacterium | -0.021 | Rubellimicrobium | | -0.01 |
| 288 | Ureaplasma | 0.021 | Lysobacter | | -0.01 |
| 289 | Enterococcus | -0.02 | Lachnoanaerobaculum | | -0.01 |
| 290 | Moheibacter | -0.02 | Aquicella | | -0.01 |
| 291 | Diaphorobacter | 0.02 | Serratia | | -0.01 |
| 292 | Afipia | 0.017 | Actinobacillus | | 0.01 |
| 293 | Shewanella | 0.017 | Gemella | | 0.01 |
| 294 | Gordonia | 0.017 | Methylotenera | | 0.009 |
| 295 | Rhodobacter | -0.016 | Pyramidobacter | | 0.009 |
| 296 | Fluviicola | -0.016 | Slackia | | 0.008 |
| 297 | Aliterella | 0.014 | Moryella | | 0.008 |
| 298 | Anoxybacillus | -0.013 | Geobacillus | | 0.008 |
| 299 | FukuN57 | -0.013 | Sphaerotilus | | 0.008 |
| 300 | Aminobacter | 0.013 | Rickettsiella | | 0.008 |
| 301 | Gemella | -0.011 | Rhodoluna | | 0.007 |
| 302 | Macrococcus | -0.011 | Conyzicola | | 0.006 |
| 303 | Paracoccus | -0.011 | Blastomonas | | 0.006 |
| 304 | Angelakisella | -0.011 | Lysinibacillus | | 0.006 |
| 305 | Megamonas | -0.011 | Hydrogenophilus | | 0.006 |
| 306 | Cellulosimicrobium | -0.011 | Deinococcus | | 0.006 |
| 307 | Massilia | -0.01 | Paucibacter | | 0.005 |
| 308 | Janibacter | -0.01 | Bradyrhizobium | | 0.005 |
| 309 | Moraxella | -0.01 | Candidatus\_Protochlamydia | | 0.005 |
| 310 | Thiopseudomonas | 0.01 | Agaricicola | | 0.005 |
| 311 | Spirosoma | -0.009 | Aliterella | | 0.004 |
| 312 | Candidatus\_Amoebophilus | -0.009 | Hyphomicrobium | | 0.004 |
| 313 | Olsenella | -0.008 | Cyanobium\_PCC-6307 | | 0.004 |
| 314 | Janthinobacterium | -0.008 | Thermoanaerobacterium | | 0.003 |
| 315 | Lachnospiraceae\_UCG-009 | 0.008 | Bacillus | | 0.003 |
| 316 | Hymenobacter | 0.008 | Alcaligenes | | 0.003 |
| 317 | Eikenella | 0.007 | SM1A02 | | 0.003 |
| 318 | Neochlamydia | -0.006 | Dialister | | 0.003 |
| 319 | Thermicanus | -0.006 | Pajaroellobacter | | 0.002 |
| 320 | Micrococcus | -0.006 | Janibacter | | 0.002 |
| 321 | Aeromonas | -0.005 | Elizabethkingia | | 0.002 |
| 322 | Anaeroplasma | 0.005 | Salinisphaera | | 0.002 |
| 323 | Aurantimicrobium | 0.004 | Aurantimicrobium | | 0.002 |
| 324 | Candidatus\_Protochlamydia | 0.002 | Peptoanaerobacter | | 0.001 |
| 325 | Agaricicola | 0.002 | Mogibacterium | | 0.001 |
| 326 | Leuconostoc | -0.001 | Micrococcus | | 0.001 |
| 327 | Acidaminococcus | 0.001 | Ureaplasma | | 0 |
| 328 | Pyramidobacter | 0.001 | Luteimonas | | 0 |
| 329 | Slackia | 0 | Microbacterium | | 0 |
| 330 | Haemophilus | 0 | Nubsella | | 0 |