| Sample | Description | OTU ID | %Amplicon | %Amplicon | %Amplicon | %Amplicon | %Amplicon | Phylum | Class | Order | Family | Genus | Species |
|--------|-------------|--------|------------|------------|------------|------------|------------|--------|-------|-------|--------|--------|--------|
| Sample_A02_2.bin_1 | A022.M001 | 40 | 4.69 | 171.34 | 53.85 | 249.75 | 99.28 | 0.30 | Enterobacteriaceae | Proteobacteria | Citrobacter koseri |
| Sample_A19_1.bin_1 | A191.M001 | 36 | 4.26 | 164.43 | 46.33 | 234.87 | 98.51 | 0.00 | Bacteroidales | Bacteroidetes | Bacteroides uniformis |
| Sample_A32_1.bin_1 | A321.M001 | 29 | 2.66 | 159.61 | 41.62 | 216.80 | 98.63 | 0.00 | Lachnospiraceae | Firmicutes | Eubacterium rectale |
| Sample_A24_1.bin_1 | A241.M001 | 96 | 2.87 | 39.84 | 50.62 | 211.49 | 98.42 | 0.12 | Bacteroidales | Bacteroidetes | Prevotella sp. CAG:520 |
| Sample_A24_2.bin_1 | A242.M001 | 43 | 1.99 | 61.96 | 59.96 | 199.93 | 93.95 | 1.17 | Clostridiales | Firmicutes | Clostridiales bacterium |
| Sample_B22_2.bin_1 | B222.M001 | 38 | 5.47 | 236.78 | 57.43 | 175.54 | 98.80 | 0.92 | Enterobacteriaceae | Proteobacteria | Klebsiella pneumoniae |
| Sample_B20_2.bin_1 | B202.M001 | 15 | 1.16 | 126.82 | 26.47 | 173.54 | 91.57 | 2.25 | Bacteroidales | Bacteroidetes | Bacteroides eggerthii |
| Sample_A17_3.bin_1 | A173.M001 | 44 | 3.61 | 124.46 | 44.42 | 170.00 | 96.34 | 4.00 | Bacteroidales | Bacteroidetes | Bacteroides eggerthii |
| Sample_A22_1.bin_1 | A221.M001 | 82 | 3.01 | 56.08 | 49.57 | 164.98 | 96.98 | 0.49 | Bacteroidales | Bacteroidetes | Prevotella sp. 885 |
| Sample_A09_2.bin_1 | A092.M001 | 52 | 2.54 | 58.74 | 54.35 | 158.79 | 97.09 | 0.00 | Prevotella | Bacteroidetes | Prevotella sp. |
| Sample_B16_1.bin_1 | B161.M001 | 114 | 2.46 | 36.62 | 44.79 | 154.07 | 93.09 | 0.00 | Bacteroidales | Bacteroidetes | Prevotella sp. CAG:5226 |
| Sample_A31_1.bin_1 | A311.M001 | 16 | 2.81 | 262.18 | 43.20 | 152.76 | 97.65 | 0.00 | Clostridiales | Firmicutes | Coprococcus eutactus CAG:665 |
| Sample_A07_3.bin_1 | A073.M001 | 31 | 3.05 | 125.40 | 44.53 | 151.70 | 97.46 | 4.11 | Clostridiales | Firmicutes | uncultured Blautia sp. |
| Sample_B16_3.bin_1 | B163.M001 | 39 | 3.28 | 110.47 | 46.07 | 149.11 | 91.09 | 0.00 | Bacteroidales | Bacteroidetes | Bacteroides stercoris |
| Sample_A07_1.bin_1 | A071.M001 | 12 | 1.75 | 240.43 | 31.08 | 138.54 | 100.00 | 0.00 | Euryarchaeota | Euryarchaeota | Methanobrevibacter smithii CAG:186 |
| Sample            | A053.M001  | 99  | 3.06 | 40.77 | 40.80 | 135.99 | 93.11 | 0.37 | Bacteroidales | Bacteroidetes | Bacteroides coprocola CAG:162 |
|-------------------|------------|-----|------|-------|-------|--------|-------|------|---------------|---------------|-------------------------------|
| Sample            | A063.M001  | 42  | 5.20 | 238.16| 57.97 | 134.73 | 98.71 | 0.46 | Enterobacteriaceae | Proteobacteria | Klebsiella pneumoniae          |
| Sample            | B142.M001  | 21  | 1.87 | 220.85| 43.82 | 134.00 | 97.31 | 0.00 | Clostridiales   | Firmicutes     | Anaerotruncus sp. CAG:528     |
| Sample            | A331.M001  | 103 | 3.16 | 43.50 | 43.19 | 133.89 | 96.41 | 0.63 | Clostridiales   | Firmicutes     | Clostridium sp. TM06-18        |
| Sample            | B022.M001  | 33  | 2.07 | 84.45 | 39.14 | 132.97 | 98.65 | 0.34 | Clostridiales   | Firmicutes     | Ruminococcaceae bacterium      |
| Sample            | A302.M001  | 57  | 2.71 | 80.73 | 46.78 | 132.70 | 97.98 | 0.67 | Clostridiales   | Firmicutes     | uncultured Ruminococcus sp.    |
| Sample            | A172.M001  | 79  | 3.36 | 72.91 | 51.19 | 131.62 | 98.64 | 0.34 | Prevotella      | Bacteroidetes  | Prevotella sp.                  |
| Sample            | B233.M001  | 27  | 2.74 | 137.81| 46.17 | 131.34 | 97.40 | 2.03 | Lachnospiraceae| Firmicutes     | Clostridium sp. CAG:510        |
| Sample            | A322.M001  | 73  | 3.02 | 53.56 | 44.58 | 126.30 | 94.77 | 0.00 | Bacteroidales   | Bacteroidetes  | Bacteroides plebeius           |
| Sample            | B211.M001  | 20  | 2.68 | 230.00| 42.96 | 126.21 | 91.94 | 2.68 | Clostridiales   | Firmicutes     | Coprococcus eutactus           |
| Sample            | A023.M001  | 47  | 2.74 | 95.76 | 35.26 | 122.87 | 90.26 | 3.58 | Clostridiales   | Firmicutes     | Lachnospiraceae bacterium      |
| Sample            | A291.M001  | 27  | 2.01 | 121.87| 41.80 | 114.00 | 98.69 | 0.26 | Lactobacillales| Firmicutes     | Lactobacillus agilis           |
| Sample            | A182.M002  | 86  | 2.82 | 52.64 | 48.27 | 112.61 | 96.66 | 0.12 | Bacteroidales   | Bacteroidetes  | Prevotella sp. CAG:592         |
| Sample            | B111.M002  | 29  | 2.58 | 151.27| 48.57 | 112.43 | 99.36 | 0.00 | Clostridiales   | Firmicutes     | Clostridium sp. AM28-20LB       |
| Sample            | B182.M002  | 10  | 1.20 | 402.08| 27.58 | 108.71 | 92.41 | 1.12 | Bacteria        | Firmicutes     | Clostridium sp. CAG:594        |
| Sample | Species          | Genus            | Family       | Order          | Class    | Division       | Percent | Percent | Percent | Percent | Percent |
|--------|------------------|------------------|--------------|----------------|----------|----------------|---------|---------|---------|---------|---------|
| A063.M002 | Clostridiales bacterium | Firmicutes | Clostridiales | Firmicutes | Clostridiales bacterium | 2.45 | 105.66 | 80.16 | 28.02 | 128.67 |
| A093.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.63 | 101.39 | 100.00 | 52.11 | 39.87 |
| A091.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 1.34 | 103.60 | 91.27 | 58.41 | 56.75 |
| A091.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.19 | 101.33 | 100.00 | 57.64 | 297.02 |
| A123.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 3.47 | 100.01 | 98.52 | 39.87 | 122.21 |
| A061.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.85 | 95.79 | 88.88 | 32.88 | 162.65 |
| A042.M002 | uncultured Ruminococcus sp. | Firmicutes | Clostridiales | Firmicutes | Clostridiales bacterium | 2.81 | 94.76 | 93.25 | 41.90 | 41.13 |
| A323.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.00 | 95.77 | 96.86 | 25.74 | 47.04 |
| B233.M002 | Bacteroidetes | Firmicutes | Clostridiales | Firmicutes | Clostridiales bacterium | 0.00 | 92.21 | 98.51 | 48.43 | 231.38 |
| B132.M002 | Bacteroidetes | Firmicutes | Clostridiales | Firmicutes | Clostridiales bacterium | 0.00 | 85.99 | 93.67 | 47.12 | 177.51 |
| A191.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.70 | 85.89 | 92.40 | 47.36 | 211.71 |
| A052.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.00 | 85.86 | 89.70 | 57.11 | 56.86 |
| A173.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.00 | 85.77 | 95.28 | 30.10 | 59.77 |
| A313.M002 | Firmicutes bacterium | Clostridiales | Firmicutes | Clostridiales bacterium | Firmicutes | 0.63 | 83.45 | 100.00 | 31.52 | 69.94 |
| Sample_Ref | Sample_ID | Read | HU | CT | Ph | H | Ph | Taxonomic Information |
|------------|-----------|------|----|----|----|----|----|-----------------------|
| A023.M002  | A023      | 41   | 2.16 | 86.57 | 59.88 | 82.82 | 98.38 | Clostridiales Firmicutes Ruminococcaceae Ruminococcus torques |
| B032.M002  | B032      | 71   | 3.00 | 57.58 | 43.30 | 82.19 | 91.31 | Clostridiales Firmicutes uncultured Blautia sp. |
| B203.M002  | B203      | 22   | 2.41 | 163.01 | 44.43 | 81.73 | 100.00 | Clostridiales Firmicutes Clostridium sp. CAG:632 |
| B122.M002  | B122      | 40   | 2.32 | 81.19 | 40.89 | 80.50 | 96.00 | Clostridiales Firmicutes Ruminococcus torques |
| A293.M002  | A293      | 82   | 3.42 | 68.52 | 59.26 | 80.47 | 98.65 | Clostridiales Firmicutes Ruminococcaceae bacterium |
| A072.M002  | A072      | 57   | 2.99 | 72.45 | 44.82 | 79.54 | 97.83 | Clostridiales Firmicutes Blautia sp. OM07-19 |
| A272.M002  | A272      | 17   | 1.75 | 157.00 | 49.91 | 79.24 | 94.63 | Clostridiales Firmicutes Ruminococcaceae bacterium |
| B201.M002  | B201      | 16   | 1.27 | 160.62 | 28.20 | 78.91 | 80.02 | Clostridiales Firmicutes Clostridium sp. CAG:452 |
| A013.M002  | A013      | 69   | 3.16 | 65.92 | 47.01 | 78.65 | 97.42 | Clostridiales Firmicutes uncultured Clostridium sp. |
| A021.M002  | A021      | 71   | 2.33 | 50.95 | 38.33 | 78.56 | 98.75 | Clostridiales Firmicutes Enterococcus faecium |
| A091.M002  | A091      | 33   | 2.50 | 135.91 | 49.97 | 77.74 | 98.30 | Bacteroidales Bacteroidetes Porphyromonadaceae bacterium |
| B222.M002  | B222      | 10   | 1.85 | 311.24 | 53.85 | 77.40 | 97.31 | Clostridiales Firmicutes Clostridiales bacterium |
| B212.M003  | B212      | 13   | 2.11 | 453.31 | 56.25 | 76.35 | 100.00 | Bifidobacteriaceae Actinobacteria Bifidobacterium pseudocatenulatum |
| B153.M003  | B153      | 36   | 5.90 | 224.78 | 55.01 | 75.64 | 98.80 | Enterobacteriaceae Proteobacteria Klebsiella oxytoca |
| B202.M003  | B202      | 91   | 1.99 | 30.36 | 60.86 | 74.18 | 85.96 | Clostridiales Firmicutes Faecalibacterium prausnitzii |
| Sample | Species | Genus | Family | Order | Class | Phylum | Relative Abundance | Reference | Scientific Name |
|--------|---------|-------|--------|-------|-------|--------|-------------------|-----------|-----------------|
| A182.M003 | Firmicutes | Firmicutes | Dialister sp. | CAG:357 |
| B142.M003 | Clostridiales | Firmicutes | Clostridiales bacterium |
| A073.M003 | Bacteroidetes | Bacteroidetes | Prevotella sp. | CAG:5226 |
| A323.M003 | Bacteroidetes | Bacteroidetes | Bacteroides dorei |
| A092.M003 | Lactobacillales | Firmicutes | Weissella confusa |
| A243.M003 | Bacteroidetes | Bacteroidetes | Alistipes onderdonkii |
| B061.M003 | Actinobacteria | Actinobacteria | Collinsella aerofaciens |
| B211.M003 | Enterobacteriaceae | Proteobacteria | Enterobacter sp. Z1 |
| A233.M003 | Clostridiales | Firmicutes | Ruminococcus sp. OM06-36AC |
| A313.M003 | Clostridiales | Firmicutes | Faecalibacterium prausnitzii |
| A171.M003 | Streptococcus | Firmicutes | Streptococcus parasanguinis |
| A292.M003 | Clostridiales | Firmicutes | Oscillibacter sp. |
| A071.M003 | Enterobacteriaceae | Proteobacteria | Citrobacter freundii |
| A322.M003 | Clostridiales | Firmicutes | Eubacterium sp. OM08-24 |
| A291.M003 | Clostridiales | Firmicutes | Eubacterium sp. CAG:156 |
| Sample A05_3.bin_3 | A052.M003 | 13 | 2.14 | 1112.88 | 40.54 | 64.34 | 99.32 | 0.67 | Clostridiales Firmicutes Ruminococcus bromii |
|-------------------|-----------|----|------|--------|-------|-------|-------|------|-----------------------------------------|
| Sample A01_3.bin_3 | A013.M003 | 72 | 2.98 | 54.72  | 41.72 | 64.01 | 96.13 | 0.00 | Lachnospiraceae Firmicutes Roseburia inulinivorans |
| Sample A23_2.bin_3 | A232.M003 | 27 | 2.24 | 172.91 | 59.95 | 61.83 | 100.00 | 0.81 | Actinobacteria Actinobacteria Collinsella aerofaciens |
| Sample A04_3.bin_3 | A043.M003 | 52 | 5.27 | 140.54 | 48.97 | 61.68 | 90.50 | 0.06 | Clostridiales Firmicutes Hungatella hathewayi |
| Sample B02_1.bin_3 | B021.M003 | 27 | 2.72 | 196.53 | 37.64 | 61.62 | 99.53 | 0.00 | Lactobacillales Firmicutes Enterococcus faecalis |
| Sample A31_2.bin_3 | A312.M003 | 65 | 2.18 | 50.43  | 59.28 | 61.23 | 93.62 | 0.67 | Clostridiales Firmicutes Oscillibacter sp. |
| Sample B24_1.bin_3 | B241.M003 | 42 | 1.91 | 60.11  | 61.58 | 60.56 | 89.26 | 1.13 | Clostridiales Firmicutes Oscillibacter sp. |
| Sample A18_3.bin_3 | A183.M003 | 19 | 2.96 | 226.39 | 58.18 | 59.51 | 97.95 | 0.00 | Bacteria Verrucomicrobia Akkermansia muciniphila |
| Sample A18_3.bin_4 | A183.M004 | 48 | 2.20 | 93.41  | 59.92 | 59.00 | 100.00 | 0.81 | Actinobacteria Actinobacteria Collinsella aerofaciens |
| Sample A06_1.bin_4 | A061.M004 | 32 | 1.63 | 63.01  | 60.44 | 58.89 | 86.93 | 0.00 | Clostridiales Firmicutes Firmicutes bacterium CAG:176 |
| Sample A21_2.bin_4 | A212.M004 | 19 | 2.73 | 305.61 | 55.32 | 57.52 | 97.95 | 0.00 | Bacteria Verrucomicrobia Akkermansia muciniphila |
| Sample A33_3.bin_4 | A333.M004 | 103 | 1.86 | 23.42  | 35.24 | 57.40 | 86.63 | 1.39 | Lactobacillales Firmicutes Lactococcus lactis |
| Sample A28_2.bin_4 | A282.M004 | 22 | 2.30 | 157.39 | 52.76 | 54.64 | 97.04 | 0.00 | Clostridiales Firmicutes Clostridium sp. CAG:413 |
| Sample B02_2.bin_4 | B022.M004 | 189 | 2.49 | 18.54  | 56.33 | 53.83 | 95.46 | 0.00 | Clostridiales Firmicutes Ruminococcaceae bacterium |
| Sample A36_1.bin_4 | A361.M004 | 14 | 2.29 | 184.58 | 41.92 | 53.69 | 96.64 | 0.00 | Clostridiales Firmicutes Butyrivibrio sp. CAG:318 |
| Sample_ID     | Sequence | Length | Mapped Percent | Total Percent | Profile Percent | Taxonomy                      |
|---------------|----------|--------|---------------|---------------|----------------|-------------------------------|
| Sample_B22_1.bin_4 | B221.M004 | 41     | 2.44          | 78.26         | 41.85          | Lachnospiraceae Firmicutes Dorea longicatena |
| Sample_A04_1.bin_4 | A041.M004 | 45     | 1.96          | 77.11         | 56.90          | Clostridiales Firmicutes Ruminococcaceae bacterium |
| Sample_B03_1.bin_4 | B031.M004 | 18     | 1.28          | 183.01        | 26.74          | Bacteria Firmicutes Firmicutes bacterium |
| Sample_A06_3.bin_4 | A063.M004 | 20     | 1.91          | 165.68        | 60.48          | Bifidobacteriaceae Actinobacteria Bifidobacterium animalis |
| Sample_B17_3.bin_4 | B173.M004 | 15     | 1.95          | 269.77        | 38.01          | Clostridiales Firmicutes Eubacterium sp. CAG:251 |
| Sample_B21_1.bin_4 | B211.M004 | 32     | 2.80          | 148.50        | 59.67          | Bacteroidetes Bacteroidetes Alistipes shahii |
| Sample_B13_2.bin_4 | B132.M004 | 40     | 2.57          | 94.29         | 41.98          | Lachnospiraceae Firmicutes Roseburia sp. OF03-24 |
| Sample_B12_1.bin_4 | B121.M004 | 35     | 2.23          | 107.05        | 59.77          | Actinobacteria Actinobacteria Collinsella aerofaciens |
| Sample_A23_2.bin_4 | A232.M004 | 18     | 2.66          | 225.22        | 45.08          | Clostridiales Firmicutes Clostridium sp. CAG:242 |
| Sample_B02_3.bin_4 | B023.M004 | 20     | 2.66          | 219.64        | 41.26          | Clostridiales Firmicutes Clostridium sp. AF15-41 |
| Sample_B16_3.bin_4 | B163.M004 | 28     | 2.34          | 159.00        | 50.31          | Clostridiales Firmicutes Ruminococcus sp. CAG:579 |
| Sample_A28_1.bin_4 | A281.M004 | 9      | 1.94          | 236.90        | 36.31          | Clostridiales Firmicutes Firmicutes bacterium CAG:341 |
| Sample_A18_1.bin_4 | A181.M004 | 38     | 5.28          | 308.61        | 50.31          | Clostridiales Firmicutes Hungatella hathewayi |
| Sample_A03_2.bin_4 | A032.M004 | 23     | 1.99          | 116.70        | 49.66          | Clostridiales Firmicutes Clostridiales bacterium |
| Sample_A27_2.bin_4 | A272.M004 | 92     | 2.18          | 43.71         | 51.19          | Firmicutes Firmicutes Dialister succinatophilus |
| Sample | Taxonomy | Relative Abundance |
|--------|----------|--------------------|
| A233.M005 | Clostridiales Firmicutes Lachnospiraceae bacterium AM25-39 | 0.00%
| A092.M005 | Clostridiales Firmicutes Faecalibacterium prausnitzii | 3.74%
| B113.M005 | Selenomonadales Firmicutes Phascolarctobacterium succinatutens | 0.90%
| B153.M005 | Bifidobacteriaceae Actinobacteria | 0.12%
| A361.M005 | Bacteria Cyanobacteria bacterium UBA10660 | 0.85%
| A272.M005 | Streptococcaceae Firmicutes Streptococcus anginosus | 3.16%
| B122.M005 | Lachnospiraceae Firmicutes Eisenbergiella tayi | 1.90%
| B222.M005 | Proteobacteria Proteobacteria | 0.11%
| A073.M005 | Clostridiales Firmicutes Ruminococcus sp. AF46-10NS | 0.00%
| B112.M005 | Clostridiales Firmicutes Coprococcus sp. OM04-5BH | 0.00%
| A231.M005 | Clostridiales Firmicutes Ruminococcus sp. CAG:83 | 0.67%
| A043.M005 | Bacteria Firmicutes Holdemanella biformis | 0.71%
| A023.M005 | Clostridiales Firmicutes Ruminococcus sp. CAG-563 | 0.00%
| A181.M005 | Lactobacillales Firmicutes Streptococcus gallolyticus | 1.69%
| A061.M005 | Clostridiales Firmicutes Ruminococcus sp. AF20-12LB | 0.34%
| Sample         | Code     | Prefix | Length | Cumulative Percent | Relative Abundance | Class       | Phylum     | Genus               | Species                        |
|---------------|----------|--------|--------|--------------------|-------------------|------------|-----------|---------------------|--------------------------------|
| Sample_A19_1 | A191.M005| 70     | 2.03   | 34.68              | 58.91             | Clostridiales| Firmicutes | Faecalibacterium    | praunitzii                     |
| Sample_B24_3 | B243.M005| 21     | 1.62   | 85.09              | 43.54             | Leuconostaceae| Firmicutes | Leuconostoc          | lactis                         |
| Sample_A22_1 | A221.M005| 25     | 1.01   | 72.44              | 26.13             | Bacteria    | Firmicutes | Clostridium          | sp. CAG:628                    |
| Sample_A30_2 | A302.M005| 45     | 2.21   | 86.44              | 53.07             | Clostridia  | Firmicutes | Clostridium          | sp. CAG:226                    |
| Sample_A09_1 | A091.M006| 49     | 2.65   | 73.30              | 56.15             | Firmicutes  | Firmicutes | Firmicutes bacterium | CAG:124                        |
| Sample_B17_2 | B172.M006| 42     | 4.01   | 133.01             | 52.30             | Enterobacteriaceae| Proteobacteria | Citrobacter portucalensis |                                |
| Sample_A31_2 | A312.M006| 11     | 3.29   | 494.09             | 43.65             | Bacteroidales| Bacteroidetes | Bacteroides          | sp. CAG:20                      |
| Sample_B20_2 | B202.M006| 81     | 2.24   | 54.95              | 59.95             | Actinobacteria| Actinobacteria | Collinsella          | aerofaciens                     |
| Sample_B13_1 | B131.M006| 17     | 2.20   | 214.97             | 45.47             | Clostridiales| Firmicutes | Firmicutes bacterium | CAG:145                        |
| Sample_B13_2 | B132.M006| 31     | 2.54   | 153.48             | 37.55             | Clostridiales| Firmicutes | Eubacterium          | sp.                            |
| Sample_A29_2 | A292.M006| 39     | 3.11   | 129.03             | 62.21             | Clostridiales| Firmicutes | Flavonifractor       | plautii                        |
| Sample_B12_2 | B122.M006| 27     | 2.24   | 147.51             | 59.86             | Actinobacteria| Actinobacteria | Collinsella          | aerofaciens                     |
| Sample_A36_3 | A363.M006| 11     | 1.60   | 295.31             | 48.64             | Clostridia  | Firmicutes | Subdoligranulum      | sp. CAG:314                    |
| Sample_B05_2 | B052.M006| 70     | 2.84   | 48.18              | 41.69             | Clostridiales| Firmicutes | Blautia             | obeum                          |
| Sample_A33_3 | A333.M006| 17     | 2.59   | 226.38             | 35.91             | Clostridiales| Firmicutes | Eubacterium          | sp. CAG:76                     |
| Sample   | 500        | 500        | 500        | 500        | 500        | 500        | 500        |
|----------|------------|------------|------------|------------|------------|------------|------------|
| A093.M06 | 2.77       | 66.00      | 46.87      | 37.46      | 92.75      | 1.87       | Lachnospiraceae Firmicutes Lachnospiraceae bacterium |
| A012.M06 | 2.55       | 136.35     | 45.06      | 37.24      | 98.99      | 0.00       | Clostridiales Firmicutes Eubacterium siraeum |
| B223.M06 | 2.84       | 127.03     | 48.29      | 37.24      | 97.67      | 0.63       | Clostridiales Firmicutes Fuscatenibacter saccharivorans |
| A213.M06 | 2.71       | 52.82      | 46.32      | 37.15      | 90.29      | 0.06       | Bacteroidales Bacteroidetes Bacteroides coprophilus CAG:333 |
| B201.M06 | 4.69       | 337.29     | 56.05      | 36.89      | 99.37      | 0.04       | Enterobacteriaceae Proteobacteria Enterobacter bugandensis |
| B112.M06 | 2.81       | 148.12     | 51.72      | 36.68      | 92.61      | 1.34       | Clostridiales Firmicutes Ruminococcaceae bacterium |
| B213.M06 | 1.27       | 50.88      | 34.63      | 36.41      | 99.37      | 0.63       | Lactobacillales Firmicutes Lactobacillus sanfranciscensis |
| A331.M06 | 2.52       | 109.83     | 41.50      | 36.10      | 98.42      | 0.00       | Lachnospiraceae Firmicutes Dorea longicatena |
| B132.M07 | 1.67       | 58.54      | 53.62      | 36.09      | 96.62      | 0.19       | Bacteria Elusimicrobia Elusimicrobium sp. An273 |
| A303.M07 | 3.15       | 82.43      | 44.77      | 35.90      | 93.80      | 0.00       | Bacteroidales Bacteroidetes Bacteroides plebeius |
| B122.M07 | 1.86       | 246.11     | 44.59      | 35.81      | 97.98      | 0.34       | Clostridiales Firmicutes Eubacterium sp. CAG:180 |
| A181.M07 | 2.71       | 225.13     | 44.17      | 35.67      | 98.65      | 0.00       | Clostridiales Firmicutes Lachnospiraceae bacterium |
| A173.M07 | 2.81       | 105.06     | 52.81      | 35.26      | 98.73      | 0.00       | Clostridiales Firmicutes Clostridium sp. CAG:58 |
| A023.M07 | 3.35       | 80.16      | 53.84      | 34.95      | 91.14      | 0.00       | Bacteroidales Bacteroidetes Bacteroides sp. CAG:462 |
| A273.M07 | 2.10       | 42.46      | 53.89      | 34.89      | 86.24      | 0.67       | Clostridiales Firmicutes Ruminococcus sp. CAG:330 |
| Sample  | ID       | Species                  | Genus, Family, Order    |
|---------|----------|--------------------------|-------------------------|
| Sample_B05_2.bin_ | B052.M007 | 47 | 1.33 | 44.25 | 26.91 | 34.33 | 93.82 | 0.00 | Bacteria, Firmicutes, Clostridium sp. CAG:710 |
| Sample_B15_3.bin_ | B153.M007 | 61 | 2.35 | 54.83 | 44.79 | 34.01 | 98.18 | 0.63 | Clostridiales, Firmicutes, uncultured Ruminococcaceae bacterium |
| Sample_B11_2.bin_ | B112.M007 | 22 | 2.12 | 136.47 | 37.49 | 33.28 | 99.32 | 0.00 | Clostridiales, Firmicutes, Butyrivibrio sp. |
| Sample_B14_3.bin_ | B143.M007 | 6 | 1.94 | 358.82 | 30.48 | 32.72 | 88.88 | 0.85 | Bacteria, Firmicutes, Clostridium sp. CAG:768 |
| Sample_A32_2.bin_ | A322.M007 | 32 | 2.08 | 84.05 | 47.56 | 32.70 | 97.98 | 0.00 | Clostridiales, Firmicutes, Anaerotignum faecicola |
| Sample_B16_3.bin_ | B163.M007 | 46 | 2.24 | 62.57 | 54.15 | 32.58 | 100.00 | 0.00 | Selenomonadales, Firmicutes, Megasphaera sp. NM10 |
| Sample_A06_2.bin_ | A062.M007 | 75 | 2.47 | 63.68 | 46.40 | 32.22 | 94.63 | 1.34 | Clostridiales, Firmicutes, Ruminococcales bacterium |
| Sample_A04_2.bin_ | A042.M007 | 52 | 3.24 | 83.90 | 30.94 | 31.69 | 97.16 | 0.00 | Bacteria, Firmicutes, Coprobacillus cateniformis |
| Sample_A24_3.bin_ | A243.M007 | 77 | 2.95 | 73.93 | 29.25 | 31.44 | 100.00 | 2.25 | Bacteria, Fusobacteria, Fusobacterium varium |
| Sample_A03_1.bin_ | A031.M007 | 42 | 3.54 | 119.02 | 37.92 | 31.36 | 92.61 | 2.01 | Clostridiales, Firmicutes, Lachnospiraceae bacterium |
| Sample_B24_1.bin_ | B241.M007 | 30 | 2.77 | 144.32 | 43.05 | 31.34 | 99.41 | 0.00 | Lachnospiraceae, Firmicutes, Ruminococcus gnavus |
| Sample_A27_1.bin_ | A271.M007 | 59 | 2.42 | 51.33 | 43.33 | 31.13 | 87.34 | 0.42 | Clostridiales, Firmicutes, Ruminococcus sp. AF41-9 |
| Sample_A03_2.bin_ | A032.M007 | 44 | 2.02 | 62.79 | 55.52 | 31.07 | 81.69 | 0.38 | Bacteroidales, Bacteroidetes, Muribaculaceae bacterium Isolate-013 (NCI) |
| Sample_B16_2.bin_ | B162.M007 | 78 | 2.12 | 39.85 | 34.19 | 30.77 | 93.66 | 0.37 | Bacteria, Firmicutes, Eubacterium sp. AM28-29 |
| Sample_A24_1.bin_ | A241.M007 | 79 | 2.67 | 49.09 | 47.92 | 30.10 | 95.28 | 0.13 | Bacteroidales, Bacteroidetes, Porphyromonadaceae bacterium |
| Sample       | Sample ID   | Genome   | MC    | MT    | CO    | DG    | DG%  | Detection                      |
|--------------|-------------|----------|-------|-------|-------|-------|------|--------------------------------|
| Sample_B02_2.bin_8 | B022.M008 | 46       | 6.31  | 163.97 | 43.54 | 30.02 | 98.46 | 0.77 Bacteroidales Bacteroidetes Parabacteroides goldsteinii |
| Sample_A18_2.bin_8 | A182.M008 | 27       | 2.71  | 120.47 | 43.76 | 29.87 | 94.92 | 0.48 Lachnospiraceae Firmicutes Roseburia faecis |
| Sample_B21_1.bin_8 | B211.M008 | 71       | 2.16  | 64.61  | 48.50 | 29.77 | 95.96 | 0.81 Clostridia Firmicutes Clostridiales bacterium |
| Sample_A33_1.bin_8 | A331.M008 | 49       | 2.54  | 94.95  | 41.36 | 29.74 | 98.83 | 0.00 Lachnospiraceae Firmicutes uncultured Ruminococcus sp. |
| Sample_B16_3.bin_8 | B163.M008 | 91       | 3.00  | 50.10  | 58.22 | 29.62 | 100.00 | 1.01 Clostridia Firmicutes Clostridiales bacterium |
| Sample_A36_2.bin_8 | A362.M008 | 37       | 2.68  | 105.98 | 44.09 | 29.34 | 95.65 | 1.93 Lachnospiraceae Firmicutes Lachnospiraceae bacterium |
| Sample_B17_1.bin_8 | B171.M008 | 57       | 1.98  | 43.66  | 43.28 | 29.24 | 87.15 | 0.00 Lachnospiraceae Firmicutes Ruminococcus lactaris |
| Sample_A28_2.bin_8 | A282.M008 | 32       | 1.17  | 54.71  | 26.72 | 28.99 | 90.16 | 1.69 Bacteria Firmicutes Firmicutes bacterium CAG:321 |
| Sample_A30_2.bin_8 | A302.M008 | 20       | 3.87  | 336.81 | 43.46 | 28.54 | 82.25 | 0.00 Bacteroidales Bacteroidetes Bacteroides fragilis |
| Sample_A29_2.bin_8 | A292.M008 | 44       | 2.97  | 103.40 | 45.22 | 28.45 | 86.94 | 0.95 Clostridiales Firmicutes uncultured Blautia sp. |
| Sample_B15_2.bin_8 | B152.M008 | 23       | 2.18  | 151.87 | 36.17 | 28.34 | 96.42 | 0.00 Lactobacillales Firmicutes Lactobacillus crispatus |
| Sample_A28_3.bin_8 | A283.M008 | 21       | 2.20  | 156.67 | 37.11 | 28.33 | 99.32 | 0.34 Clostridiales Firmicutes uncultured Ruminococcus sp. |
| Sample_A21_1.bin_8 | A211.M008 | 21       | 2.96  | 297.89 | 43.77 | 28.05 | 99.32 | 0.00 Clostridiales Firmicutes Coprococcus sp. BIOML-A1 |
| Sample_B14_3.bin_8 | B143.M008 | 64       | 3.05  | 65.57  | 29.01 | 27.96 | 99.05 | 0.00 Bacteria Firmicutes uncultured Clostridium sp. |
| Sample_A06_1.bin_8 | A061.M008 | 32       | 2.50  | 113.71 | 33.18 | 27.67 | 99.32 | 0.00 Clostridiales Firmicutes uncultured Eubacterium sp. |
| Sample Name        | Accession | Count | Length (kb) | G+C (%)  | GC3 (%) | GC2 (%) | GC1 (%) | Metabolites                              |
|-------------------|-----------|-------|-------------|----------|---------|---------|---------|------------------------------------------|
| Sample_A02_2.bin_9| A022.M008 | 28    | 1.85        | 88.39    | 32.58   | 27.41   | 99.47   | Lactobacillus salivarius                |
| Sample_B18_1.bin_9| B181.M009 | 41    | 2.76        | 83.65    | 49.09   | 27.24   | 97.46   | Lachnoclostridium sp.                  |
| Sample_A36_3.bin_9| A363.M009 | 74    | 2.41        | 47.93    | 61.75   | 27.19   | 97.37   | Sutterella megalosphaeroides           |
| Sample_B05_3.bin_9| B053.M009 | 27    | 2.12        | 180.56   | 35.17   | 27.19   | 87.17   | Candidatus Gastranaerophilales bacterium HUM_10 |
| Sample_B15_2.bin_9| B152.M009 | 98    | 3.20        | 54.90    | 56.12   | 26.96   | 98.38   | Clostridiales bacterium                 |
| Sample_A03_1.bin_9| A031.M009 | 79    | 2.22        | 36.64    | 38.55   | 26.93   | 89.93   | uncultured Eubacterium sp.             |
| Sample_A19_1.bin_9| A191.M009 | 21    | 2.34        | 158.59   | 33.04   | 26.81   | 98.12   | Eubacterium sp. CAG:274                |
| Sample_A12_2.bin_9| A122.M009 | 32    | 2.20        | 173.60   | 46.08   | 26.73   | 97.98   | Ruminococcus sp.                       |
| Sample_A09_2.bin_9| A092.M009 | 25    | 2.52        | 138.36   | 51.47   | 26.68   | 95.30   | Ruminococcus sp. OM06-36AC             |
| Sample_B23_3.bin_9| B233.M009 | 33    | 2.06        | 84.56    | 58.84   | 26.31   | 97.98   | Oscillibacter sp.                      |
| Sample_A30_1.bin_9| A301.M009 | 48    | 1.75        | 66.81    | 38.91   | 26.04   | 98.58   | Streptococcus thermophilus             |
| Sample_B02_1.bin_9| B021.M009 | 29    | 5.51        | 259.88   | 49.47   | 25.94   | 94.90   | Enterocloster bolteae                 |
| Sample_A06_3.bin_9| A063.M009 | 31    | 1.90        | 83.47    | 56.93   | 25.87   | 86.57   | Clostridiales bacterium                |
| Sample_A04_3.bin_9| A043.M009 | 29    | 2.57        | 156.09   | 36.34   | 25.81   | 98.65   | Eubacterium sp. CAG:86                |
| Sample_B16_2.bin_9| B162.M009 | 11    | 1.71        | 189.57   | 47.12   | 25.63   | 86.57   | Ruminococcus sp. CAG:403              |
| Sample_A29_3.bin_10 | A293.M009 | 19   | 1.72 | 164.09 | 45.16 | 25.61 | 92.17 | 0.67 | Clostridiales Firmicutes | Eubacterium sp. CAG:841 |
| Sample_A21_2.bin_10 | A212.M010 | 39   | 2.65 | 97.88  | 42.37 | 25.51 | 91.27 | 0.00 | Clostridiales Firmicutes | Roseburia sp. CAG:309   |
| Sample_B15_3.bin_10 | B153.M010 | 40   | 2.39 | 100.34 | 34.28 | 25.43 | 99.32 | 0.00 | Clostridiales Firmicutes | Eubacterium ventriosum  |
| Sample_A18_3.bin_10 | A183.M010 | 29   | 2.05 | 98.27  | 57.81 | 25.40 | 96.64 | 0.00 | Clostridiales Firmicutes | Oscillibacter sp. 57_20  |
| Sample_B03_3.bin_10 | B033.M010 | 16   | 1.98 | 227.64 | 45.28 | 25.37 | 99.40 | 1.20 | Selenomonadales Firmicutes | Phascolarctobacterium sp. CAG:266 |
| Sample_A01_2.bin_10 | A012.M010 | 25   | 2.23 | 160.82 | 33.27 | 25.33 | 99.32 | 0.00 | Clostridiales Firmicutes | Eubacterium sp. AF36-5BH |
| Sample_A03_2.bin_10 | A032.M010 | 48   | 1.86 | 48.17  | 59.64 | 25.31 | 81.50 | 0.17 | Clostridiales Firmicutes | Subdoligranulum sp. 60_17 |
| Sample_A09_1.bin_10 | A091.M010 | 34   | 2.10 | 122.40 | 48.47 | 25.25 | 81.71 | 0.54 | Rhodospirales Proteobacteria | Alphaproteobacteria bacterium |
| Sample_A23_3.bin_10 | A233.M010 | 45   | 2.24 | 83.24  | 60.72 | 25.16 | 94.55 | 0.00 | Clostridiales Firmicutes | Subdoligranulum sp. 60_17 |
| Sample_B21_2.bin_10 | B212.M010 | 62   | 2.37 | 55.24  | 57.40 | 24.91 | 96.87 | 0.00 | Proteobacteria Proteobacteria | Mesosutterella multiformis |
| Sample_A07_2.bin_10 | A072.M010 | 101  | 2.25 | 39.41  | 44.15 | 24.90 | 99.38 | 1.05 | Selenomonadales Firmicutes | Phascolarctobacterium faecium |
| Sample_A23_2.bin_10 | A232.M010 | 45   | 3.28 | 127.17 | 58.21 | 24.74 | 97.95 | 0.00 | Clostridiales Firmicutes | Ruthenibacterium lactatiformans |
| Sample_A18_2.bin_10 | A182.M010 | 32   | 1.95 | 115.82 | 59.54 | 24.69 | 100.00 | 0.81 | Actinobacteria Actinobacteria | Collinsella sp. WCA1-178-WT-3 (M2) |
| Sample_A33_1.bin_10 | A331.M010 | 114  | 4.70 | 65.02  | 55.76 | 24.65 | 98.09 | 4.63 | Enterobacteriaceae Proteobacteria | Enterobacter cloacae |
| Sample_B02_3.bin_10 | B023.M010 | 27   | 2.50 | 99.14  | 41.20 | 24.55 | 98.06 | 1.22 | Lachnospiraceae Firmicutes | Roseburia sp. AF15-21 |
| Sample           | Bacteria Family | Bacteria Species         | Bacteria Genus     | Fungus Genus | Fungi Type | Maturity | 16S rRNA | 97% OTU | 99% OTU |
|------------------|-----------------|--------------------------|-------------------|--------------|------------|----------|---------|---------|---------|
| Sample_B02_1.bin | Proteobacteria  | Proteobacteria Sutterella | S. megalosphaeroides |               |            |          |         |         |         |
| Sample_A03_1.bin | Bacteria        | Tenericutes               | Mycoplasma sp. CAG:611 |               |            |          |         |         |         |
| Sample_A27_2.bin | Lachnospiraceae | Lachnospiraceae bacterium |               |              |            |          |         |         |         |
| Sample_A31_2.bin | Clostridiales   | Ruminococcaceae bacterium |               |              |            |          |         |         |         |
| Sample_A19_2.bin | Proteobacteria  | Proteobacteria Sutterella | S. sp. AM11-39    |               |            |          |         |         |         |
| Sample_A18_2.bin | Lachnospiraceae | Lachnospiraceae bacterium |               |              |            |          |         |         |         |
| Sample_A36_3.bin | Clostridiales   | Clostridium sp. CAG:299  |               |              |            |          |         |         |         |
| Sample_A16_3.bin | Clostridiales   | Clostridiales bacterium   |               |              |            |          |         |         |         |
| Sample_B16_3.bin | Proteobacteria  | Proteobacteria Sutterella | wadsworthensis    |               |            |          |         |         |         |
| Sample_A31_2.bin | Clostridiales   | un cultured Lachnospira  | sp.               |              |            |          |         |         |         |
| Sample_A01_3.bin | Bacteria        | Synergistes Pyramidobacter | piscolens         |               |            |          |         |         |         |
| Sample_B15_2.bin | Lactobacillales | Lactobacillus reuteri     |               |              |            |          |         |         |         |
| Sample_B11_3.bin | Lachnospiraceae | Roseburia sp. CAG:197    |               |              |            |          |         |         |         |
| Sample_A29_1.bin | Clostridiales   | Clostridiales bacterium   |               |              |            |          |         |         |         |
| Sample  | #    | Stat1  | Stat2  | Stat3  | Stat4  | Stat5  | Stat6  | Class  | Phylum  | Genus                |
|---------|------|--------|--------|--------|--------|--------|--------|--------|---------|----------------------|
| Sample_A22_1.bin_11 | A221.M011 | 49   | 2.50   | 72.17  | 42.27  | 23.22  | 98.65  | 0.00   | Clostridiales  | Firmicutes  | Clostridium sp. OM05-6BH |
| Sample_A03_2.bin_11 | A032.M011 | 36   | 2.21   | 128.55 | 54.47  | 23.16  | 98.12  | 0.63   | Proteobacteria  | Proteobacteria | Sutterella sp. AM11-39 |
| Sample_A30_1.bin_12 | A301.M012 | 27   | 1.22   | 108.21 | 26.13  | 23.03  | 90.66  | 1.33   | Bacteria  | Firmicutes  | Firmicutes bacterium CAG:321 |
| Sample_B21_2.bin_12 | B212.M012 | 28   | 2.60   | 132.69 | 40.67  | 22.93  | 98.65  | 0.00   | Clostridiales  | Firmicutes  | Lachnospiraceae bacterium |
| Sample_A23_2.bin_12 | A232.M012 | 14   | 2.04   | 214.26 | 40.69  | 22.87  | 99.32  | 0.00   | Clostridiales  | Firmicutes  | Ruminococcus bromii |
| Sample_A27_2.bin_12 | A272.M012 | 13   | 2.05   | 181.00 | 59.58  | 22.83  | 99.54  | 0.00   | Bifidobacteriaceae | Actinobacteria | Bifidobacterium adolescentis |
| Sample_B05_2.bin_12 | B052.M012 | 19   | 2.68   | 185.02 | 55.01  | 22.83  | 100.00 | 0.00   | Bacteroidetes  | Bacteroidetes | Alistipes sp. AF17-16 |
| Sample_A02_3.bin_12 | A023.M012 | 22   | 2.46   | 149.02 | 42.32  | 22.72  | 95.30  | 0.00   | Clostridiales  | Firmicutes  | Bacteroides pectinophilus |
| Sample_B17_3.bin_12 | B173.M012 | 54   | 2.23   | 62.99  | 60.93  | 22.58  | 89.26  | 1.34   | Clostridiales  | Firmicutes  | uncultured Flavonifractor sp. |
| Sample_A23_3.bin_12 | A233.M012 | 23   | 1.99   | 150.20 | 39.38  | 22.50  | 98.97  | 0.00   | Pasteurellaceae | Proteobacteria | Haemophilus parainfluenzae |
| Sample_B20_3.bin_12 | B203.M012 | 15   | 1.94   | 175.13 | 36.69  | 22.45  | 98.12  | 0.00   | Lactobacillales  | Firmicutes  | Streptococcus mutans |
| Sample_B15_1.bin_12 | B151.M012 | 42   | 2.49   | 120.13 | 57.48  | 22.44  | 95.30  | 0.00   | Clostridiales  | Firmicutes  | Ruminococcaceae bacterium |
| Sample_B05_3.bin_12 | B053.M012 | 41   | 2.57   | 85.57  | 38.58  | 22.44  | 91.54  | 0.00   | Lachnospiraceae  | Firmicutes  | Eubacterium rectale |
| Sample_A31_2.bin_12 | A312.M012 | 64   | 2.12   | 61.92  | 33.74  | 22.35  | 98.65  | 0.34   | Clostridiales  | Firmicutes  | Eubacterium sp. CAG:581 |
| Sample_A29_1.bin_12 | A291.M012 | 59   | 2.51   | 86.61  | 54.89  | 22.22  | 98.65  | 0.67   | Clostridiales  | Firmicutes  | uncultured Butyricicoccus sp. |
| Sample   | Strain            | OTU   | 16S rDNA | 23S rDNA | 16s/23s  | 16s/23s  | RDP      | RDP      | RDP      | Genus            | Family          | phylum           | 16S rDNA | 23S rDNA | 16s/23s  | 16s/23s  | RDP      | RDP      | RDP      | Genus            | Family          | phylum           |
|----------|-------------------|-------|----------|----------|----------|----------|----------|----------|----------|----------------|-----------------|----------------|----------|----------|----------|----------|----------|----------|----------|----------------|-----------------|----------------|
| B182.M012| Parabacteroides  | 69    | 4.82     | 106.19   | 45.08    | 22.19    | 99.42    | 0.00     | Bacteroides| Parabacteroides| Parabacteroides| Parabacteroides| 22.19    | 45.08    | 22.19    | 99.42    | 0.00     | Bacteroides| Parabacteroides| Parabacteroides| Parabacteroides |
| A092.M013| Collinsella      | 35    | 2.20     | 103.86   | 59.90    | 22.19    | 100.00   | 0.81     | Actinobacteria| Collinsella   | Collinsella    | 22.19    | 59.90    | 22.19    | 100.00   | 0.81    | Actinobacteria| Collinsella | Collinsella    | Collinsella |
| B143.M013| Clostridiales     | 52    | 2.19     | 63.16    | 60.34    | 22.11    | 88.30    | 0.27     | Firmicutes| Clostridiales | Clostridiales | Firmicutes | 22.11    | 60.34    | 22.11    | 88.30    | 0.27    | Firmicutes| Clostridiales | Clostridiales | Firmicutes |
| A282.M013| Ruminococcaceae  | 74    | 1.96     | 43.70    | 48.22    | 22.09    | 94.63    | 0.02     | Firmicutes| Ruminococcaceae| Ruminococcaceae| Firmicutes | 22.09    | 48.22    | 22.09    | 94.63    | 0.02    | Firmicutes| Ruminococcaceae| Ruminococcaceae| Firmicutes |
| A242.M013| Prevotella        | 37    | 2.97     | 122.70   | 49.41    | 22.08    | 95.17    | 0.37     | Bacteroides| Prevotella | Prevotella | 22.08    | 49.41    | 22.08    | 95.17    | 0.37    | Bacteroides| Prevotella | Prevotella | Prevotella |
| A233.M013| Clostridiales     | 29    | 2.12     | 94.55    | 61.25    | 22.02    | 96.30    | 0.67     | Firmicutes| Clostridiales | Clostridiales | Firmicutes | 22.02    | 61.25    | 22.02    | 96.30    | 0.67    | Firmicutes| Clostridiales | Clostridiales | Firmicutes |
| B171.M013| Anaerostipes     | 52    | 2.67     | 66.70    | 36.92    | 21.99    | 98.65    | 1.34     | Firmicutes| Anaerostipes| Anaerostipes | Firmicutes | 21.99    | 36.92    | 21.99    | 98.65    | 1.34    | Firmicutes| Anaerostipes | Anaerostipes | Firmicutes |
| B181.M013| Clostridiales     | 53    | 1.74     | 40.74    | 57.44    | 21.96    | 84.91    | 0.00     | Firmicutes| Clostridiales | Clostridiales | Firmicutes | 21.96    | 57.44    | 21.96    | 84.91    | 0.00    | Firmicutes| Clostridiales | Clostridiales | Firmicutes |
| A182.M013| Melissococcus    | 38    | 1.92     | 75.76    | 33.47    | 21.93    | 97.09    | 0.00     | Firmicutes| Melissococcus | Melissococcus | Firmicutes | 21.93    | 33.47    | 21.93    | 97.09    | 0.00    | Firmicutes| Melissococcus | Melissococcus | Firmicutes |
| A272.M013| Eggerthella       | 10    | 1.76     | 186.44   | 53.98    | 21.86    | 100.00   | 0.12     | Actinobacteria| Eggerthella | Eggerthella | 21.86    | 53.98    | 21.86    | 100.00   | 0.12    | Actinobacteria| Eggerthella | Eggerthella |
| B221.M013| Ruminococcaceae  | 46    | 2.52     | 90.72    | 45.86    | 21.72    | 95.30    | 0.67     | Firmicutes| Ruminococcaceae| Ruminococcaceae| Firmicutes | 21.72    | 45.86    | 21.72    | 95.30    | 0.67    | Firmicutes| Ruminococcaceae| Ruminococcaceae| Firmicutes |
| B222.M013| Dialister         | 10    | 2.01     | 229.73   | 38.57    | 21.69    | 98.20    | 0.00     | Firmicutes| Dialister | Dialister | 21.69    | 38.57    | 21.69    | 98.20    | 0.00    | Firmicutes| Dialister | Dialister | Dialister |
| A192.M014| Veillonella       | 91    | 2.43     | 43.12    | 52.33    | 21.63    | 100.00   | 0.00     | Firmicutes| Veillonella| Veillonella | 21.63    | 52.33    | 21.63    | 100.00   | 0.00    | Firmicutes| Veillonella | Veillonella | Veillonella |
| B213.M014| Alistipes         | 12    | 2.42     | 289.44   | 58.52    | 21.63    | 98.39    | 0.00     | Bacteroides| Alistipes | Alistipes | 21.63    | 58.52    | 21.63    | 98.39    | 0.00    | Bacteroides| Alistipes | Alistipes | Alistipes |
| A021.M014| Ruminococcaceae  | 21    | 2.30     | 174.23   | 56.30    | 21.53    | 94.63    | 0.67     | Firmicutes| Ruminococcaceae| Ruminococcaceae| Firmicutes | 21.53    | 56.30    | 21.53    | 94.63    | 0.67    | Firmicutes| Ruminococcaceae| Ruminococcaceae| Firmicutes |
| Sample         | accession | count | reads | reads% | contig1 | contig2 | contig3 | contig4 | contig5 | contig6 | contig7 | contig8 | contig9 | contig10 | bacteria     |
|---------------|-----------|-------|-------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|----------------|
| Sample_B23_3.bin_14 | B233.M014 | 35    | 3.90  | 142.43 | 45.50   | 21.18   | 99.61   | 0.00    | Bacteroidales | Bacteroidetes | Parabacteroides merdae |
| Sample_B20_3.bin_14 | B203.M014 | 30    | 2.16  | 159.43 | 59.73   | 20.93   | 100.00  | 0.81    | Actinobacteria | Actinobacteria | Collinsella aerofaciens |
| Sample_A06_3.bin_14 | A063.M014 | 38    | 2.64  | 90.51  | 38.52   | 20.92   | 97.77   | 0.00    | Clostridiales | Firmicutes | Firmicutes bacterium AM10-47 |
| Sample_A22_1.bin_14 | A221.M014 | 56    | 2.80  | 65.01  | 46.75   | 20.89   | 96.13   | 1.93    | Lachnospiraceae | Firmicutes | uncultured Clostridium sp. |
| Sample_A02_3.bin_14 | A023.M014 | 26    | 2.57  | 111.00 | 45.16   | 20.85   | 88.25   | 0.00    | Clostridiales | Firmicutes | Clostridium sp. OM07-9AC |
| Sample_A28_3.bin_14 | A283.M014 | 62    | 2.74  | 66.24  | 38.24   | 20.67   | 97.98   | 1.01    | Clostridiales | Firmicutes | uncultured Clostridium sp. |
| Sample_A23_3.bin_14 | A233.M014 | 42    | 2.73  | 87.50  | 57.37   | 20.66   | 97.76   | 2.68    | Clostridiales | Firmicutes | Firmicutes bacterium CAG:137 |
| Sample_A24_1.bin_14 | A241.M014 | 27    | 1.64  | 100.58 | 34.70   | 20.64   | 91.77   | 1.08    | Bacteria | Firmicutes | Faecalitalea cylindroides |
| Sample_A30_2.bin_14 | A302.M014 | 51    | 3.17  | 82.69  | 42.93   | 20.52   | 93.71   | 0.12    | Lachnospiraceae | Firmicutes | Roseburia intestinalis |
| Sample_A36_1.bin_14 | A361.M014 | 28    | 3.14  | 177.69 | 57.85   | 20.48   | 97.95   | 1.36    | Bacteria | Verrucomicrobina | Akkermansia muciniphila |
| Sample_B02_2.bin_15 | B022.M015 | 182   | 1.96  | 14.46  | 53.62   | 20.37   | 86.12   | 0.00    | Clostridiales | Firmicutes | Ruminococcaceae bacterium |
| Sample_A33_2.bin_15 | A332.M015 | 9     | 2.68  | 360.40 | 55.03   | 20.25   | 100.00  | 0.00    | Bacteroidetes | Bacteroidetes | Alistipes indistinctus |
| Sample_B22_2.bin_15 | B222.M015 | 53    | 1.13  | 28.47  | 24.37   | 20.11   | 84.83   | 4.09    | Bacteria | Firmicutes | Firmicutes bacterium |
| Sample_A23_3.bin_15 | A233.M015 | 26    | 2.54  | 130.81 | 38.89   | 20.11   | 87.24   | 0.00    | Clostridiales | Firmicutes | Clostridium sp. CAG:230 |
| Sample_A32_2.bin_15 | A322.M015 | 29    | 2.50  | 146.63 | 58.56   | 20.05   | 96.33   | 1.38    | Delta proteobacteria | Proteobacteria | Desulfovibrio sp. |
| Sample Name   | Description      | Abundance | Proportion | Concentration | RDA Score | Result          |
|--------------|------------------|-----------|------------|---------------|------------|----------------|
| Sample_A07_3.bin_15 | A073.M015        | 81        | 3.01       | 55.94         | 44.17      | Clostridiales Firmicutes Clostridium sp. TM06-18 |
| Sample_A22_3.bin_15 | A223.M015        | 79        | 3.90       | 73.44         | 43.44      | Bacteria Bacteroidetes Odoribacter splanchnicus |
| Sample_A05_1.bin_15 | A051.M015        | 32        | 1.73       | 95.51         | 60.00      | Clostridiales Firmicutes Clostridia bacterium |
| Sample_A22_2.bin_15 | A222.M015        | 19        | 2.09       | 170.35        | 33.54      | Clostridiales Firmicutes Eubacterium sp. CAG:274 |
| Sample_B22_3.bin_15 | B223.M015        | 38        | 2.10       | 80.48         | 57.68      | Clostridiales Firmicutes Faecalibacterium prausnitzii |
| Sample_B06_1.bin_15 | B061.M015        | 45        | 2.89       | 84.95         | 37.02      | Clostridiales Firmicutes Eubacterium sp. CAG:252 |
| Sample_A27_2.bin_15 | A272.M015        | 56        | 2.25       | 76.94         | 61.10      | Clostridiales Firmicutes Clostridiales bacterium |
| Sample_B22_1.bin_15 | B221.M015        | 61        | 2.56       | 64.00         | 58.38      | Clostridiales Firmicutes Ruminococcaceae bacterium |
| Sample_A01_1.bin_15 | A011.M015        | 64        | 2.91       | 71.70         | 46.14      | Clostridiales Firmicutes Lachnospiraceae bacterium AM48-27BH |
| Sample_A17_1.bin_15 | A171.M015        | 20        | 1.73       | 95.77         | 61.33      | Clostridiales Firmicutes Oscillibacter sp. CAG:155 |
| Sample_A01_2.bin_15 | A012.M015        | 57        | 1.90       | 47.24         | 62.16      | Proteobacteria Proteobacteria Sutterella sp. AM11-39 |
| Sample_B18_1.bin_15 | B181.M015        | 65        | 2.14       | 42.79         | 58.86      | Clostridiales Firmicutes Subdoligranulum variabile |
| Sample_A18_1.bin_16 | A181.M016        | 31        | 2.58       | 105.96        | 43.76      | Clostridiales Firmicutes Coprococcus catus |
| Sample_B02_2.bin_16 | B022.M016        | 56        | 2.27       | 64.58         | 56.97      | Clostridiales Firmicutes Firmicutes bacterium CAG:110 |
| Sample_A33_3.bin_16 | A333.M016        | 48        | 2.60       | 80.59         | 46.13      | Clostridiales Firmicutes Blautia sp. KGMB01111 |

| Sample File          | ID        | Aact | Bact | Cact | Dact | Eact | Fact | Gact | Hact | Iact | Jact | Kact | Lact | Mact | Nact | Oact | Pact | Qact | Ract | Sact | Tact | Uact | Vact | Wact | Xact | Yact | Zact | label                                      |
|----------------------|-----------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-------------------------------------------|
| A311.M016            | 52        | 2.30 | 56.53| 44.98| 18.67| 87.34| 1.27 | Clostridiales | Firmicutes | uncultured Blautia sp. |
| A013.M016            | 48        | 2.59 | 82.87| 37.73| 18.64| 95.97| 1.34 | Clostridiales | Firmicutes | uncultured Eubacterium sp. |
| A023.M016            | 24        | 2.48 | 149.26| 42.91| 18.56| 99.31| 0.00 | Clostridiales | Firmicutes | uncultured Ruminococcus sp. |
| A032.M016            | 37        | 2.10 | 76.20| 36.70| 18.51| 89.93| 1.51 | Clostridiales | Firmicutes | Anaerostipes hadrus |
| A043.M016            | 42        | 2.78 | 90.69| 46.18| 18.47| 97.98| 1.65 | Clostridiales | Firmicutes | Lachnospiraceae bacterium |
| A222.M016            | 26        | 1.99 | 94.77| 49.04| 18.39| 99.26| 0.18 | Bacteria | Bacteroidetes | Flavobacteriales bacterium |
| A061.M016            | 33        | 2.48 | 95.12| 42.68| 18.27| 94.30| 0.02 | Clostridiales | Firmicutes | uncultured Blautia sp. |
| A012.M016            | 26        | 2.76 | 223.84| 41.83| 18.17| 98.65| 0.00 | Clostridiales | Firmicutes | Eubacterium sp. CAG:38 |
| B213.M017            | 27        | 2.08 | 90.80| 41.75| 18.13| 91.57| 1.11 | Lachnospiraceae | Firmicutes | Lachnospiraceae bacterium |
| A313.M017            | 49        | 2.48 | 60.73| 59.26| 17.98| 97.27| 0.00 | Clostridiales | Firmicutes | Subdoligranulum sp. 60_17 |
| A273.M017            | 35        | 2.06 | 99.33| 61.28| 17.97| 91.61| 0.67 | Clostridiales | Firmicutes | Firmicutes bacterium CAG:176_63_11 |
| A012.M017            | 56        | 2.53 | 64.40| 29.13| 17.93| 98.87| 1.12 | Bacteria | Fusobacteria | Fusobacterium mortiferum |
| A311.M017            | 36        | 1.74 | 67.38| 61.42| 17.86| 95.80| 0.67 | Clostridiales | Firmicutes | Firmicutes bacterium CAG:129 |
| A092.M017            | 101       | 3.07 | 54.14| 52.33| 17.84| 97.31| 0.00 | Clostridiales | Firmicutes | Eubacterium sp. CAG:115 |
| B162.M017            | 47        | 3.43 | 105.94| 71.62| 17.81| 99.48| 1.38 | Actinomycetales | Actinobacteria | Aeromicrobium sp. Leaf289 |
| Sample    | ID            | Organism                                      |
|-----------|---------------|----------------------------------------------|
| Sample_A31_2.bin_17 | A312.M017 | 67   2.89  51.79  48.88  17.72  99.36  0.00 Clostridiales Firmicutes uncultured Clostridium sp. |
| Sample_A29_1.bin_17 | A291.M017 | 29   2.22  115.97  40.62  17.69  91.13  0.00 Clostridiales Firmicutes Tyzzerella nexilis |
| Sample_A24_1.bin_17 | A241.M017 | 188  5.59  44.16  59.72  17.67  93.91  4.05 Bacteria Lentisphaerae Victivallis vadensis |
| Sample_A02_3.bin_18 | A023.M018 | 20   1.99  142.24  38.39  17.64  95.97  0.00 Clostridiales Firmicutes Anaeromassilibacillus sp. An250 |
| Sample_A18_2.bin_18 | A182.M018 | 58   2.40  52.94  56.76  17.64  99.10  0.67 Clostridiales Firmicutes Clostridiales bacterium |
| Sample_A31_3.bin_18 | A313.M018 | 29   1.09  55.14  26.74  17.60  86.51  0.00 Bacteria Firmicutes Acholeplasma sp. CAG:878 |
| Sample_B02_2.bin_18 | B022.M018 | 119  4.35  48.05  47.92  17.53  82.73  1.27 Clostridiales Firmicutes uncultured Clostridium sp. |
| Sample_A03_2.bin_18 | A032.M018 | 39   2.09  81.30  58.29  17.41  94.40  0.00 Clostridiales Firmicutes Clostridiales bacterium |
| Sample_A29_1.bin_18 | A291.M018 | 37   2.15  97.09  60.05  17.39  89.93  0.00 Clostridiales Firmicutes Clostridiales bacterium |
| Sample_A06_3.bin_18 | A063.M018 | 108  3.27  44.11  38.53  17.29  97.35  0.00 Bacteroidales Bacteroidetes Coprobacter fastidiousus |
| Sample_A22_1.bin_18 | A221.M018 | 161  4.20  41.11  59.95  17.07  100.00 0.00 Deltaproteobacteria Proteobacteria Bilophila wadsworthia |
| Sample_B22_2.bin_18 | B222.M018 | 91   2.17  36.67  60.02  16.93  98.09  2.42 Actinobacteria Actinobacteria Collinsella aerofaciens |
| Sample_A27_1.bin_18 | A271.M018 | 36   2.11  108.24  51.92  16.71  98.65  0.67 Clostridiales Firmicutes Clostridium sp. CAG:169 |
| Sample_B21_2.bin_18 | B212.M018 | 78   2.11  44.88  60.06  16.57  96.77  0.81 Actinobacteria Actinobacteria Collinsella aerofaciens |
| Sample_B16_3.bin_19 | B163.M019  | 142  1.89  17.45  33.89  16.57  99.05  0.00 Bacteria Firmicutes Catenibacterium sp. AM22-15 |
| Sample   | Sample Name | M | Base | Cover | Seq. | Phyla     | Class      | Order       | Family      | Genus         | Species          |
|----------|-------------|---|------|-------|------|-----------|------------|-------------|-------------|---------------|-----------------|
| Sample_B21_3.bin_19 | B213.M019 51 | 5.13 | 167.20 | 42.61 | 16.50 | 98.37 | 0.11 | Bacteria | Bacteroidetes | Odoribacter      | sp. AF21-41      |
| Sample_A19_2.bin_19 | A192.M019 30 | 2.35 | 141.43 | 46.37 | 16.49 | 100.00 | 0.48 | Bacteroidetes | Bacteroidetes | Alistipes        | indistinctus     |
| Sample_A03_2.bin_19 | A032.M019 50 | 2.08 | 96.88 | 60.10 | 16.46 | 99.19 | 2.42 | Actinobacteria | Actinobacteria | Collinsella      | sp. AM34-10      |
| Sample_A36_3.bin_19 | A363.M019 27 | 2.41 | 119.30 | 42.22 | 16.44 | 87.81 | 0.63 | Clostridiales | Firmicutes    | Blautia          | obeum            |
| Sample_A27_2.bin_19 | A272.M019 5  | 1.21 | 621.57 | 27.73 | 16.37 | 93.25 | 1.28 | Bacteria     | Firmicutes    | Clostridium      | sp. CAG:417      |
| Sample_B15_3.bin_19 | B153.M019 44 | 2.86 | 99.70 | 37.34 | 16.33 | 97.98 | 0.00 | Clostridiales | Firmicutes    | Lachnospira      | eligens          |
| Sample_A04_3.bin_19 | A043.M019 55 | 3.00 | 76.49 | 41.08 | 16.30 | 97.42 | 0.00 | Clostridiales | Firmicutes    | Eubacterium      | sp.             |
| Sample_A02_2.bin_19 | A022.M019 26 | 1.90 | 125.91 | 47.90 | 16.24 | 94.63 | 0.00 | Clostridiales | Firmicutes    | Ruminococcaceae  | bacterium        |
| Sample_A18_2.bin_19 | A182.M019 68 | 2.71 | 51.44 | 58.54 | 16.14 | 90.72 | 1.08 | Clostridia    | Firmicutes    | Clostridiales    | bacterium        |
| Sample_A07_2.bin_19 | A072.M019 64 | 1.98 | 60.49 | 39.48 | 15.93 | 98.50 | 0.88 | Pasteurellaceae | Proteobacteria | Haemophilus       | parainfluenzae   |
| Sample_A01_2.bin_19 | A012.M019 50 | 2.25 | 57.24 | 58.90 | 15.88 | 90.41 | 1.34 | Clostridiales | Firmicutes    | Firmicutes       | bacterium CAG:170 |
| Sample_A23_2.bin_20 | A232.M020 12 | 1.93 | 196.86 | 45.41 | 15.86 | 88.70 | 0.12 | Actinobacteria | Actinobacteria | Cryptobacterium   | sp. CAG:338      |
| Sample_B16_1.bin_20 | B161.M020 109 | 2.25 | 26.65 | 48.40 | 15.81 | 80.23 | 0.00 | Bacteroidetes | Bacteroidetes | Prevotella        | sp. CAG:891      |
| Sample_B16_2.bin_20 | B162.M020 43 | 1.98 | 78.90 | 38.98 | 15.74 | 100.00 | 0.00 | Selenomonadales | Firmicutes    | Veillonella       | atypica          |
| Sample_B21_3.bin_20 | B213.M020 80 | 2.26 | 46.54 | 60.02 | 15.65 | 100.00 | 0.81 | Actinobacteria | Actinobacteria | Collinsella       | aerofaciens      |
| Sample_Name | Sample_ID | OTU | Relative_Abundance | Taxonomic_Class | Genus_Species | Comments |
|-------------|-----------|-----|--------------------|-----------------|---------------|----------|
| Sample_A18_3.bin_20 | A183.M020 169 | 2.44 | 26.23 | 49.92 | 15.61 | 85.13 | 1.90 | Clostridiales Firmicutes | Clostridium sp. AM33-3 |
| Sample_A07_2.bin_20 | A072.M020 75 | 2.64 | 46.25 | 26.79 | 15.57 | 93.99 | 0.00 | Clostridiales Firmicutes | uncultured Clostridium sp. |
| Sample_A18_2.bin_20 | A182.M020 84 | 2.60 | 55.76 | 63.75 | 15.53 | 98.12 | 0.89 | Deltaproteobacteria | Desulfovibrio piger |
| Sample_A33_3.bin_20 | A333.M020 94 | 2.55 | 50.05 | 64.79 | 15.41 | 99.31 | 2.04 | Clostridiales Firmicutes | Fournierella massiliensis |
| Sample_B17_1.bin_21 | B171.M021 37 | 2.21 | 74.56 | 38.13 | 15.38 | 86.17 | 0.58 | Lachnospiraceae Firmicutes | Ruminococcus sp. B05 |
| Sample_A07_3.bin_21 | A073.M021 348 | 2.58 | 11.16 | 27.42 | 15.17 | 84.48 | 0.00 | Bacteria Firmicutes | Romboutsia ilealis |
| Sample_A32_2.bin_21 | A322.M021 95 | 3.00 | 45.04 | 46.08 | 15.13 | 97.04 | 2.01 | Bacteroidales Bacteroidetes Porphyromonadaceae bacterium | |
| Sample_A31_2.bin_21 | A312.M021 41 | 2.90 | 91.31 | 28.21 | 15.08 | 98.38 | 0.00 | Clostridiales Firmicutes | Clostridium perfringens |
| Sample_B16_1.bin_21 | B161.M021 99 | 4.25 | 60.63 | 42.38 | 14.95 | 95.69 | 0.32 | Bacteria Bacteroidetes | Butyricimonas virosa |
| Sample_A05_3.bin_21 | A053.M021 53 | 1.82 | 68.88 | 46.76 | 14.91 | 95.69 | 0.00 | Bacteria Proteobacteria | Azospirillum sp. |
| Sample_A07_2.bin_22 | A072.M022 88 | 3.60 | 66.35 | 44.28 | 14.89 | 88.50 | 1.42 | Bacteria Firmicutes | Clostridium innocuum |
| Sample_B22_3.bin_22 | B223.M022 72 | 1.98 | 40.16 | 57.28 | 14.68 | 87.46 | 0.00 | Clostridiales Firmicutes | Clostridiales bacterium |
| Sample_A27_1.bin_22 | A271.M022 54 | 1.76 | 59.01 | 41.18 | 14.57 | 93.61 | 0.00 | Clostridiales Firmicutes | Mogibacterium diversum |
| Sample_A04_3.bin_22 | A043.M022 84 | 2.88 | 54.80 | 35.77 | 14.54 | 99.32 | 0.67 | Clostridiales Firmicutes | Eubacterium sp. |
| Sample_A31_2.bin_22 | A312.M022 221 | 3.44 | 28.32 | 64.42 | 14.54 | 100.00 | 0.81 | Actinobacteria Actinobacteria | Eggerthella lenta |
| Sample         | Designation | Reads | 1% Identity | 97% Identity | 99% Identity | OTU Identity | Identity Match | Taxonomy                                   |
|----------------|-------------|-------|-------------|--------------|--------------|--------------|---------------|--------------------------------------------|
| Sample_B17_3.bin_22 | B173.M022   | 34    | 2.28        | 96.71        | 45.40        | 14.49        | 96.61         | 0.74 Lachnospiraceae Firmicutes Roseburia sp AM16-25 |
| Sample_A04_1.bin_22 | A041.M022   | 58    | 2.89        | 70.25        | 49.71        | 14.44        | 98.53         | 0.24 Lachnospiraceae Firmicutes Roseburia hominis |
| Sample_A29_1.bin_22 | A291.M022   | 31    | 2.56        | 133.88       | 60.00        | 14.41        | 95.92         | 0.00 Bacteroidetes Bacteroidetes Alistipes communis |
| Sample_A31_1.bin_23 | A311.M023   | 235   | 2.49        | 15.28        | 50.03        | 14.37        | 86.39         | 4.84 Clostridiales Firmicutes uncultured Clostridium sp. |
| Sample_A22_2.bin_23 | A222.M023   | 146   | 2.56        | 39.19        | 48.65        | 14.30        | 100.00        | 0.11 Proteobacteria Bacteroidetes Proteobacteria bacterium CAG:139 |
| Sample_A27_2.bin_23 | A272.M023   | 70    | 1.27        | 28.40        | 24.96        | 14.25        | 91.57         | 1.69 Bacteria Firmicutes Clostridium sp CAG:433 |
| Sample_A33_2.bin_23 | A332.M023   | 30    | 2.09        | 116.86       | 44.20        | 14.25        | 92.61         | 0.00 Clostridiales Firmicutes Frisingicoccus caecimuris |
| Sample_A27_1.bin_23 | A271.M023   | 50    | 3.43        | 89.36        | 42.21        | 14.21        | 81.59         | 0.56 Bacteroidetes Bacteroidetes Bacteroides sp CAG:462 |
| Sample_A03_2.bin_23 | A032.M023   | 121   | 1.97        | 25.81        | 57.13        | 14.19        | 95.62         | 0.00 Proteobacteria Proteobacteria Sutterella sp CAG:397 |
| Sample_B15_1.bin_23 | B151.M023   | 76    | 2.05        | 33.83        | 49.28        | 14.00        | 86.20         | 1.34 Lachnospiraceae Firmicutes uncultured Clostridium sp. |
| Sample_A24_2.bin_23 | A242.M023   | 49    | 2.15        | 68.91        | 49.67        | 13.99        | 93.95         | 0.00 Clostridiales Firmicutes Ruminococcus sp OM06-36AC |
| Sample_A27_2.bin_24 | A272.M024   | 52    | 2.32        | 58.69        | 62.01        | 13.67        | 95.30         | 2.68 Clostridiales Firmicutes Lawsonibacter asaccharolyticus |
| Sample_A27_1.bin_24 | A271.M024   | 53    | 2.28        | 62.74        | 57.62        | 13.62        | 91.05         | 0.67 Clostridiales Firmicutes Firmicutes bacterium CAG:137 |
| Sample_B17_1.bin_24 | B171.M024   | 48    | 2.58        | 90.54        | 63.44        | 13.38        | 99.19         | 0.00 Actinobacteria Actinobacteria Asaccharobacter celatus |
| Sample_B15_2.bin_24 | B152.M024   | 62    | 2.33        | 55.09        | 46.92        | 13.26        | 93.04         | 3.29 Selenomonadales Firmicutes Phascolarctobacterium faecium |
| Sample | Metadata | Abundance | Proportion of | Genus | Family | Class | Order | Phylum | Species | Other Information |
|--------|----------|-----------|---------------|-------|--------|-------|-------|--------|---------|-------------------|
| Sample_B24_3.bin_24 | B243.M024 | 109 | 5.43 | 67.98 | 56.33 | 13.20 | 94.70 | Enterobacteriaceae | Proteobacteria | Klebsiella oxytoca |
| Sample_A18_2.bin_24 | A182.M024 | 38 | 1.70 | 58.40 | 48.64 | 12.92 | 89.14 | Clostridiales | Firmicutes | Eubacterium sp. CAG:841 |
| Sample_A32_2.bin_24 | A322.M024 | 226 | 2.51 | 18.05 | 34.48 | 12.85 | 85.02 | Bacillales | Firmicutes | Turicibacter sanguinis |
| Sample_B02_2.bin_24 | B022.M024 | 57 | 2.65 | 80.46 | 54.98 | 12.71 | 98.38 | Clostridiales | Firmicutes | Clostridiales bacterium |
| Sample_B16_1.bin_25 | B161.M025 | 64 | 2.09 | 69.05 | 49.83 | 12.71 | 94.35 | Clostridiales | Firmicutes | Clostridiales bacterium |
| Sample_A05_2.bin_25 | A052.M025 | 125 | 2.41 | 37.88 | 62.41 | 12.55 | 98.13 | Proteobacteriaceae | Proteobacteria | Sutterella wadsworthensis |
| Sample_A32_1.bin_25 | A321.M025 | 67 | 3.39 | 65.46 | 45.38 | 12.51 | 87.50 | Bacteroidales | Bacteroidetes | Parabacteroides johnsonii |
| Sample_B21_3.bin_25 | B213.M025 | 52 | 2.18 | 68.37 | 44.60 | 12.38 | 97.09 | Clostridiales | Firmicutes | Ruminococcus sp. CAG:488 |
| Sample_B14_1.bin_25 | B141.M025 | 75 | 2.58 | 46.01 | 44.48 | 12.36 | 87.60 | Lachnospiraceae | Firmicutes | Lachnospiraceae bacterium |
| Sample_B12_2.bin_25 | B122.M025 | 64 | 1.64 | 42.07 | 52.67 | 12.36 | 87.84 | Clostridiales | Firmicutes | Firmicutes bacterium CAG:555 |
| Sample_A23_2.bin_25 | A232.M025 | 57 | 1.84 | 46.17 | 49.49 | 12.25 | 95.96 | Clostridiales | Firmicutes | Clostridiales bacterium |
| Sample_A04_3.bin_26 | A043.M026 | 41 | 2.22 | 58.73 | 62.16 | 12.21 | 91.27 | Clostridiales | Firmicutes | uncultured Oscillibacter sp. |
| Sample_A19_1.bin_26 | A191.M026 | 255 | 3.11 | 16.98 | 56.04 | 11.95 | 97.96 | Bacteria | Synergistetes | Cloacibacillus porcorum |
| Sample_A03_2.bin_26 | A032.M026 | 103 | 2.12 | 34.71 | 62.95 | 11.91 | 99.02 | Bifidobacteriaceae | Actinobacteria | Bifidobacterium bifidum |
| Sample_B15_1.bin_26 | B151.M026 | 255 | 2.10 | 11.23 | 58.88 | 11.90 | 86.05 | Clostridiales | Firmicutes | Faecalibacterium prausnitzii |
| Sample      | Accession | M    | 1.65 | 49.75 | 43.13 | 11.86 | 91.72 | 0.00 |
|------------|-----------|------|------|-------|-------|-------|-------|------|
| B17 M026   | 57        | 1.65 | 49.75| 43.13 | 11.86 | 91.72 | 0.00  |      |
| A29 M026   | 87        | 1.84 | 34.32| 52.68 | 11.85 | 97.95 | 0.00  |      |
| B21 M026   | 79        | 1.64 | 34.59| 40.21 | 11.82 | 80.60 | 0.58  |      |
| A31 M026   | 150       | 2.05 | 19.35| 56.59 | 11.78 | 91.39 | 0.67  |      |
| B16 M026   | 81        | 2.32 | 39.07| 45.39 | 11.65 | 86.20 | 2.51  |      |
| A31 M026   | 68        | 1.95 | 33.88| 57.20 | 11.38 | 94.73 | 0.67  |      |
| A04 M026   | 129       | 2.72 | 31.65| 53.83 | 11.37 | 97.03 | 1.01  |      |
| A01 M026   | 164       | 2.05 | 22.23| 58.93 | 11.35 | 90.82 | 2.06  |      |
| A29 M027   | 78        | 1.51 | 31.41| 46.70 | 11.25 | 93.43 | 0.00  |      |
| B16 M027   | 79        | 1.94 | 38.66| 37.26 | 11.23 | 95.46 | 0.00  |      |
| A23 M027   | 77        | 1.84 | 50.64| 60.12 | 11.23 | 84.22 | 0.67  |      |
| A33 M027   | 187       | 1.79 | 12.74| 53.62 | 11.18 | 96.15 | 3.29  |      |
| B17 M027   | 136       | 3.34 | 31.34| 56.29 | 11.05 | 80.44 | 1.58  |      |
| A28 M027   | 85        | 2.20 | 38.08| 62.55 | 10.99 | 97.98 | 0.81  |      |
| A27 M027   | 214       | 2.13 | 14.27| 59.92 | 10.90 | 95.34 | 1.61  |      |

**Sample**

**B17 M026**

**Accession**

**57**

**1.65**

**49.75**

**43.13**

**11.86**

**91.72**

**0.00**

**Clostridiales**

**Firmicutes**

**Ruminococcaceae bacterium**

**Sample**

**A29 M026**

**87**

**1.84**

**34.32**

**52.68**

**11.85**

**97.95**

**0.00**

**Lactobacillales**

**Firmicutes**

**Lactobacillus fermentum**

**Sample**

**B21 M026**

**79**

**1.64**

**34.59**

**40.21**

**11.82**

**80.60**

**0.58**

**Streptococcus**

**Firmicutes**

**Streptococcus salivarius**

**Sample**

**A31 M026**

**150**

**2.05**

**19.35**

**56.59**

**11.78**

**91.39**

**0.67**

**Clostridiales**

**Firmicutes**

**Ruminococcaceae bacterium**

**Sample**

**B16 M026**

**81**

**2.32**

**39.07**

**45.39**

**11.65**

**86.20**

**2.51**

**Lachnospiraceae**

**Firmicutes**

**uncultured Clostridium sp.**

**Sample**

**A04 M026**

**68**

**1.95**

**33.88**

**57.20**

**11.38**

**94.73**

**0.67**

**Clostridiales**

**Firmicutes**

**Clostridiales bacterium**

**Sample**

**A04 M027**

**129**

**2.72**

**31.65**

**53.83**

**11.37**

**97.03**

**1.01**

**Clostridiales**

**Firmicutes**

**Ruminococcaceae bacterium**

**Sample**

**A01 M026**

**164**

**2.05**

**22.23**

**58.93**

**11.35**

**90.82**

**2.06**

**Clostridiales**

**Firmicutes**

**Butyricicoccus sp. OM04-18BH**

**Sample**

**A29 M027**

**78**

**1.51**

**31.41**

**46.70**

**11.25**

**93.43**

**0.00**

**Firmicutes**

**Firmicutes**

**Veillonellaceae bacterium**

**Sample**

**B16 M027**

**79**

**1.94**

**38.66**

**37.26**

**11.23**

**95.46**

**0.00**

**Clostridiales**

**Firmicutes**

**Ruminococcus sp. CAG:624**

**Sample**

**A23 M027**

**77**

**1.84**

**50.64**

**60.12**

**11.23**

**84.22**

**0.67**

**Clostridiales**

**Firmicutes**

**Eteptia gabavorous**

**Sample**

**A33 M027**

**187**

**1.79**

**12.74**

**53.62**

**11.18**

**96.15**

**3.29**

**Clostridia**

**Firmicutes**

**Clostridia bacterium**

**Sample**

**B17 M027**

**136**

**3.34**

**31.34**

**56.29**

**11.05**

**80.44**

**1.58**

**Enterobacteriaceae**

**Proteobacteria**

**Leclercia adecarboxylata**

**Sample**

**A28 M027**

**85**

**2.20**

**38.08**

**62.55**

**10.99**

**97.98**

**0.81**

**Actinobacteria**

**Actinobacteria**

**Olsenella sp. AF21-51**

**Sample**

**A27 M027**

**214**

**2.13**

**14.27**

**59.92**

**10.90**

**95.34**

**1.61**

**Actinobacteria**

**Actinobacteria**

**Collinsella aerofaciens**
| Sample    | A03_2.bin  |    |    |    |    |    |    | Bacteria    | Bacteroides     | Butyricimonas faecalis |
|-----------|------------|----|----|----|----|----|----|-------------|----------------|---------------------|
| A07_2.bin | A072.M027  | 119| 1.74| 29.36| 58.14| 10.84| 90.21| Clostridiales | Firmicutes | Oscillibacter sp. 57_20 |
| A31_3.bin | A313.M027  | 361| 2.16| 7.10 | 51.22| 10.84| 89.82| Clostridiales | Firmicutes | Clostridium leptum |
| B21_3.bin | B213.M027  | 99 | 2.36| 45.87| 58.73| 10.81| 99.20| Bifidobacteriaceae | Firmicutes | Bifidobacterium sp. MSTE12 |
| B15_1.bin | B151.M027  | 209| 2.27| 17.00| 55.26| 10.81| 88.91| Clostridiales | Firmicutes | Clostridiales bacterium |
| A12_3.bin | A123.M027  | 164| 2.94| 23.93| 46.27| 10.80| 90.31| Prevotella     | Bacteroidetes | Prevotella CAG:732 |
| A27_2.bin | A272.M027  | 58 | 2.01| 51.54| 44.05| 10.66| 86.39| Clostridiales | Firmicutes | Clostridium sp. CAG:167 |
| A22_2.bin | A222.M027  | 100| 2.42| 33.21| 55.81| 10.63| 91.61| Clostridiales | Firmicutes | Clostridiales bacterium |
| A27_3.bin | A273.M028  | 458| 2.81| 8.03 | 43.55| 10.56| 88.19| Lactobacillales | Firmicutes | Enterococcus casseliflavus |
| B16_2.bin | B162.M028  | 68 | 2.10| 43.67| 46.39| 10.55| 82.24| Lachnospiraceae | Firmicutes | Sellimonas intestinalis |
| A33_2.bin | A332.M028  | 200| 2.43| 18.11| 50.22| 10.30| 85.44| Clostridiales | Firmicutes | Clostridium sp. AF27-2AA |
| B21_3.bin | B213.M028  | 142| 2.06| 19.40| 56.71| 10.23| 86.62| Clostridiales | Firmicutes | Clostridiales bacterium |
| A03_2.bin | A032.M028  | 571| 4.51| 10.95| 52.21| 10.16| 94.79| Enterobacteriaceae | Proteobacteria | uncultured Citrobacter sp. |
| B11_2.bin | B112.M028  | 180| 2.19| 20.84| 51.81| 10.14| 94.12| Clostridiales | Firmicutes | Butyricoccus porcorum |
| A27_2.bin | A272.M029  | 423| 4.71| 14.79| 51.03| 10.08| 91.94| Clostridiales | Firmicutes | Enterocloster aldensis |
| Sample | ID | Reads | Mean CV | Mean FF | Mean PD | Mean V1 | Mean V2 | Genus     | Class     | Order     | Family     | Species                |
|--------|----|-------|----------|---------|----------|---------|---------|-----------|-----------|-----------|------------|------------------------|
| Sample_B17_1.bin_29 | B171.M029 | 572 | 3.71 | 8.23 | 60.05 | 9.90 | 82.54 | 3.09 | Actinobacteria | Actinobacteria | Eggerthella lenta |
| Sample_A09_2.bin_29 | A092.M029 | 244 | 2.29 | 14.07 | 51.58 | 9.69 | 88.09 | 4.11 | Clostridales | Firmicutes | uncultured Clostridium sp. |
| Sample_B15_1.bin_30 | B151.M030 | 368 | 2.83 | 10.29 | 46.02 | 9.69 | 84.57 | 3.76 | Lachnospiraceae | Firmicutes | Lachnospiraceae bacterium |
| Sample_B16_1.bin_30 | B161.M030 | 142 | 1.65 | 17.03 | 60.66 | 9.61 | 80.66 | 0.34 | Clostridales | Firmicutes | Evtepia gabavorous |
| Sample_A27_2.bin_30 | A272.M030 | 182 | 2.32 | 19.81 | 44.74 | 9.54 | 96.64 | 0.00 | Clostridales | Firmicutes | Ruminococcaceae bacterium |
| Sample_A19_2.bin_30 | A192.M030 | 338 | 1.79 | 6.60 | 57.11 | 9.53 | 82.36 | 2.07 | Clostridiales | Firmicutes | Clostridium sp. CAG:242 |
| Sample_B02_2.bin_30 | B022.M030 | 168 | 1.90 | 20.26 | 57.63 | 9.53 | 86.18 | 2.37 | Clostridales | Firmicutes | Oscillibacter sp. |
| Sample_A03_2.bin_31 | A032.M031 | 97 | 1.95 | 27.87 | 43.07 | 9.52 | 85.11 | 0.00 | Clostridales | Firmicutes | Clostridiales bacterium |
| Sample_B24_1.bin_31 | B241.M031 | 177 | 1.70 | 12.30 | 49.23 | 9.50 | 96.23 | 0.00 | Bacteria | Proteobacteria | Azospirillum sp. CAG:239 |
| Sample_A32_1.bin_31 | A321.M031 | 278 | 2.02 | 9.02 | 64.65 | 9.35 | 86.45 | 2.01 | Clostridales | Firmicutes | Oscillibacter sp. PC13 |
| Sample_A23_3.bin_31 | A233.M031 | 284 | 2.06 | 8.52 | 56.25 | 9.26 | 87.70 | 0.89 | Clostridales | Firmicutes | Ruminococcaceae bacterium AM28-23LB |
| Sample_A12_3.bin_32 | A123.M032 | 173 | 1.93 | 14.37 | 58.66 | 9.02 | 85.79 | 1.74 | Clostridales | Firmicutes | Ruminococcaceae bacterium |
| Sample_B24_1.bin_32 | B241.M032 | 332 | 2.15 | 8.71 | 63.58 | 9.02 | 90.47 | 0.75 | Proteobacteria | Proteobacteria | Sutterella megalosphaeroides |
| Sample_A19_1.bin_33 | A191.M033 | 494 | 3.97 | 11.89 | 65.19 | 8.99 | 93.06 | 3.51 | Actinobacteria | Actinobacteria | Eggerthella sinensis |
| Sample_A31_2.bin_33 | A312.M033 | 303 | 2.23 | 9.20 | 63.03 | 8.80 | 88.44 | 2.51 | Clostridales | Firmicutes | Clostridiales bacterium |
| Sample      | ID     | Count | GC   | GSN   | Segment | Taxonomy                                      |
|------------|--------|-------|------|-------|---------|-----------------------------------------------|
| A271.M034  | 353    | 2.14  | 7.51 | 50.60 | 8.61    | 83.73  | 0.71  | Clostridiales Firmicutes Firmicutes bacterium CAG:238 |
| A272.M035  | 363    | 2.25  | 7.76 | 52.37 | 8.48    | 80.62  | 3.76  | Lachnospiraceae Firmicutes Lachnoclostridium sp. An118 |
| A271.M037  | 243    | 1.74  | 8.96 | 33.27 | 8.00    | 86.72  | 0.06  | Clostridiales Firmicutes Ruminococcus sp. |
| A031.M038  | 260    | 1.70  | 8.14 | 53.69 | 7.92    | 80.80  | 1.01  | Clostridiales Firmicutes Ruminococcaceae bacterium |
| A312.M038  | 234    | 1.56  | 8.10 | 51.56 | 7.89    | 81.77  | 1.34  | Clostridiales Firmicutes Clostridiales bacterium |
| A271.M049  | 216    | 1.48  | 8.68 | 57.83 | 7.87    | 80.11  | 0.00  | Clostridiales Firmicutes Clostridia bacterium |
| A271.M056  | 325    | 1.59  | 5.48 | 39.63 | 7.23    | 82.53  | 1.78  | Pasteurellaceae Proteobacteria Haemophilus parainfluenzae |