|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **IDa** | **Taxonomyb** | | **Bin size**  **(Mb)** | **Completeness**  **(%)c** | **Contamination**  **(%)c** | **GC**  **(%)** | **% Communityd** | | |
| **(Median)** | **(Mean)** | |
| k01 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales*; f\_*S24-7* | | 4.46 | 95.5 | 0.9 | 51.3 | 7.78 | 6.69 | |
| k02 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Lachnospiraceae* | | 3.34 | 98.7 | 0.8 | 52.8 | 4.16 | 4.34 | |
| k03 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Lachnospiraceae* | | 1.61 | 81.5 | 6.2 | 55.8 | 4.16 | 3.87 | |
| k04 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Oscillospiraceae* | | 2.36 | 86.6 | 9.8 | 60.6 | 3.75 | 3.63 | |
| k05 | k\_*Bacteria*; p\_*Proteobacteria*; c\_*Betaproteobacteria*; o\_*Rhodocyclales*; f\_*Rhodocyclaceae* | | 2.83 | 67.0 | 6.5 | 56.5 | 2.30 | 2.31 | |
| k06 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Oscillospiraceae* | | 1.98 | 67.2 | 0.7 | 58.4 | 2.12 | 2.65 | |
| k07 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Ruminococcaceae*; g\_*Ruminococcus* | | 2.08 | 68.5 | 4.9 | 47.0 | 1.52 | 1.21 | |
| k08 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales*; f\_*Rikenellaceae*; g\_*Alistipes* | | 3.51 | 91.5 | 0.0 | 58.8 | 1.27 | 1.06 | |
| k09 | k\_*Bacteria*; p\_*Synergistetes*; c\_*Synergistia*; o\_*Synergistales*; f\_*Synergistaceae* | | 3.44 | 99.4 | 3.4 | 55.3 | 1.26 | 1.60 | |
| k10 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales*; f\_*S24-7* | | 2.75 | 98.8 | 1.1 | 51.2 | 1.23 | 0.94 | |
| k11 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Ruminococcaceae*; g\_*Ruminococcus* | | 2.00 | 94.3 | 0.0 | 45.1 | 1.02 | 1.90 | |
| k12 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Oscillospiraceae* | | 1.90 | 78.6 | 0.0 | 45.8 | 0.27 | 0.32 | |
| k13 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Lachnospiraceae* | | 3.30 | 90.5 | 10.1 | 49.5 | 0.25 | 0.28 | |
| k14 | k\_*Bacteria*; p\_*Proteobacteria*; c\_*Deltaproteobacteria*; o\_*Desulfovibrionales*; f\_*Desulfovibrionaceae*; g\_*Desulfovibrio* | | 2.68 | 53.5 | 7.5 | 60.6 | 0.21 | 0.22 | |
| k15 | k\_*Bacteria*; p\_*Cyanobacteria*; c\_*4C0d-2*; o\_*YS2* | | 1.74 | 69.4 | 0.0 | 34.7 | 0.00 | 0.19 | |
|  |  | |  |  | Total: | | 31.19 | | 31.30 |
|  | | | | | | | | | |
| w01 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Christensenellales*; f\_*Christensenellaceae* | 2.85 | | 98.4 | 0.0 | 52.2 | 7.10 | 7.16 | |
| w02 | k\_*Bacteria*; p\_*Tenericutes*; c\_*Mollicutes*; o\_*RF39* | 1.57 | | 93.3 | 9.4 | 25.8 | 4.20 | 5.49 | |
| w03 | k\_*Bacteria*; p\_*Spirochaetes*; c\_*Spirochaetes*; o\_*Spirochaetales*; f\_*Spirochaetaceae*; g\_*Sphaerochaeta* | 2.36 | | 90.2 | 2.2 | 48.1 | 3.41 | 2.84 | |
| w04 | k\_*Archaea*; p\_*Euryarchaeota*; c\_*Methanomicrobia*; o\_*Methanomicrobiales*; f\_*Methanocorpusculaceae* | | 1.97 | 91.6 | 2.3 | 52.8 | 1.81 | 2.08 | |
| w05 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Lachnospirales* | 1.04 | | 62.4 | 1.8 | 28.9 | 1.48 | 1.58 | |
| w06 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales*; f\_*BS11* | 2.59 | | 97.6 | 0.3 | 38.0 | 1.37 | 3.64 | |
| w07 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Christensenellales*; f\_*Christensenellaceae* | 2.21 | | 96.7 | 0.8 | 46.2 | 1.26 | 1.44 | |
| w08 | k\_*Bacteria*; p\_*Verrucomicrobia*; c\_*Verrucomicrobiae*; o\_*Verrucomicrobiales*; f\_*Verrucomicrobiaceae*; g\_*Akkermansia* | 2.44 | | 88.6 | 0.7 | 55.3 | 1.25 | 1.01 | |
| w09 | k\_*Bacteria*; p\_*Proteobacteria*; c\_*Gammaproteobacteria*; o\_*Aeromonadales*; f\_*Succinivibrionaceae*; g\_*Succinivibrio* | 2.31 | | 93.1 | 0.3 | 36.8 | 1.15 | 1.20 | |
| w10 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Christensenellales*; f\_*Christensenellaceae* | 1.02 | | 68.3 | 1.5 | 46.7 | 0.79 | 0.84 | |
| w11 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Ruminococcaceae*; g\_*Ruminococcus* | 3.71 | | 98.7 | 0.0 | 54.8 | 0.71 | 1.20 | |
| w12 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales*; f\_*BS11* | 2.96 | | 98.4 | 2.4 | 37.5 | 0.66 | 0.91 | |
| w13 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales*; f\_*Bacteroidaceae*; g\_*Bacteroides* | 5.83 | | 95.4 | 3.6 | 42.4 | 0.55 | 0.64 | |
| w14 | k\_*Bacteria*; p\_*Tenericutes*; c\_*Mollicutes* | 1.69 | | 92.1 | 0.0 | 28.5 | 0.54 | 0.49 | |
| w15 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Ruminococcaceae*; g\_*Ruminococcus* | 2.08 | | 93.3 | 1.0 | 44.7 | 0.52 | 0.44 | |
| w16 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 1.64 | | 96.5 | 0.9 | 39.3 | 0.44 | 0.51 | |
| w17 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 2.62 | | 86.9 | 0.8 | 59.1 | 0.35 | 0.40 | |
| w18 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 1.61 | | 66.5 | 0.7 | 27.3 | 0.43 | 0.34 | |
| w19 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales* | 3.62 | | 94.5 | 1.9 | 51.0 | 1.06 | 0.29 | |
| w20 | k\_*Bacteria*; p\_*Spirochaetes*; c\_*Spirochaetia*; o\_*Spirochaetales*; f\_*Spirochaetaceae*; g\_*Treponema* | 2.50 | | 96.1 | 0.7 | 31.8 | 0.32 | 0.27 | |
| w21 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales* | 2.37 | | 93.5 | 5.0 | 48.9 | 0.25 | 0.19 | |
| w22 | k\_*Bacteria*; p\_*Lentisphaerae*; c\_*Lentisphaeria*; o\_*Victivallales* | 2.20 | | 88.8 | 1.3 | 57.8 | 0.24 | 0.18 | |
| w23 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 2.89 | | 65.4 | 9.4 | 61.6 | 0.21 | 0.17 | |
| w24 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Clostridiaceae*; g\_*Clostridium* | 1.98 | | 73.0 | 1.5 | 27.4 | 0.12 | 0.14 | |
| w25 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 2.56 | | 60.7 | 8.0 | 52.5 | 0.16 | 0.13 | |
| w26 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Lachnospiraceae* | 2.79 | | 91.7 | 0.6 | 39.0 | 0.35 | 0.11 | |
| w27 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 2.00 | | 71.9 | 1.7 | 62.5 | 0.27 | 0.11 | |
| w28 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Ruminococcaceae* | 1.60 | | 64.1 | 1.9 | 42.7 | 0.13 | 0.11 | |
| w29 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Lachnospiraceae* | 2.94 | | 95.9 | 0.2 | 35.0 | 0.26 | 0.10 | |
| w30 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 3.19 | | 82.6 | 5.9 | 54.3 | 0.30 | 0.07 | |
| w31 | k\_*Bacteria*; p\_*Tenericutes*; c\_*Mollicutes*; o\_*RF39* | 0.85 | | 70.9 | 0.0 | 24.0 | 0.13 | 0.07 | |
| w32 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales*; f\_*Lachnospiraceae* | 3.71 | | 69.7 | 5.2 | 38.4 | 0.11 | 0.07 | |
| w33 | k\_*Bacteria*; p\_*Bacteroidetes*; c\_*Bacteroidia*; o\_*Bacteroidales* | 3.72 | | 88.6 | 9.4 | 49.1 | 0.14 | 0.06 | |
| w34 | k\_*Bacteria*; p\_*Proteobacteria*; c\_*Deltaproteobacteria*; o\_*Desulfovibrionales*; f\_*Desulfovibrionaceae* | 2.79 | | 61.6 | 2.5 | 59.0 | 0.12 | 0.02 | |
| w35 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 1.61 | | 60.0 | 1.4 | 49.1 | 0.10 | 0.02 | |
| w36 | k\_*Archaea*; p\_*Thermoplasmata* | 3.30 | | 65.2 | 6.0 | 56.2 | 0.07 | 0.01 | |
| w37 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 1.61 | | 62.8 | 2.3 | 27.9 | 0.14 | 0.00 | |
| w38 | k\_*Bacteria*; p\_*Firmicutes*; c\_*Clostridia*; o\_*Clostridiales* | 1.60 | | 63.8 | 2.1 | 30.8 | 0.11 | 0.00 | |
|  |  |  | |  | Total: | | 36.86 | 30.10 | |

a Named for host (**k**oala or **w**ombat) and rank based on median abundance.

b Assigned based on alignment of kingdom-specific (bacterial or archaeal) concatenated marker genes alongside RefSeq reference genomes.

c Calculated based on lineage-specific single-copy marker genes.

d Calculated based on average read coverage of population genome contigs across time-points.