**S8 Table. Top 10 indicator taxa for each utility**. Indicator value was calculated using package {indicspecies} in R.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Utility** | **Taxonomy** | **Indicator value** | **P** | **Avg. RAa** |
| **A** | k\_\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Bacillales;f\_\_Staphylococcaceae;g\_\_Staphylococcus | 0.863 | 0.0002 | 9.23E-03 |
| k\_\_Bacteria;p\_\_Planctomycetes;c\_\_Phycisphaerae;o\_\_Phycisphaerales;f\_\_;g\_\_ | 0.844 | 0.0002 | 3.53E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_;g\_\_  | 0.812 | 0.0002 | 3.08E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Novosphingobium | 0.804 | 0.0002 | 5.93E-03 |
| k\_\_Bacteria;p\_\_Firmicutes;c\_\_Bacilli;o\_\_Bacillales;f\_\_Alicyclobacillaceae;g\_\_Alicyclobacillus | 0.769 | 0.0002 | 8.43E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Xanthomonadales;f\_\_Xanthomonadaceae;g\_\_ | 0.746 | 0.0002 | 3.06E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Pseudomonadales;f\_\_Pseudomonadaceae;g\_\_Pseudomonas | 0.711 | 0.0006 | 1.54E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Rhizobiaceae;g\_\_Agrobacterium | 0.704 | 0.0004 | 5.89E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Acidovorax | 0.675 | 0.0002 | 6.39E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Hyphomonadaceae;g\_\_ | 0.653 | 0.0002 | 1.64E-02 |
| **B** | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Hydrogenophaga | 0.787 | 0.0002 | 3.33E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacterales;f\_\_Caulobacteraceae;g\_\_Mycoplana | 0.636 | 0.0006 | 2.86E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Caulobacterales;f\_\_Caulobacteraceae;g\_\_Caulobacter | 0.585 | 0.0096 | 3.41E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Erythrobacteraceae;g\_\_Erythrobacter | 0.528 | 0.0002 | 6.02E-05 |
| k\_\_Bacteria;p\_\_Cyanobacteria;c\_\_4C0d-2;o\_\_MLE1-12;f\_\_;g\_\_ | 0.528 | 0.0016 | 1.12E-01 |
| k\_\_Bacteria;p\_\_Firmicutes;c\_\_Erysipelotrichi;o\_\_Erysipelotrichales;f\_\_Erysipelotrichaceae;g\_\_PSB-M-3 | 0.34 | 0.0002 | 3.55E-05 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Pseudomonadales;Other;Other | 0.313 | 0.0002 | 8.87E-06 |
| k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_OPB54;f\_\_;g\_\_ | 0.265 | 0.005 | 3.36E-05 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_Alteromonadaceae;g\_\_Cellvibrio | 0.262 | 0.0038 | 6.97E-06 |
| k\_\_Bacteria;p\_\_Gemmatimonadetes;c\_\_Gemmatimonadetes;o\_\_Ellin5290;f\_\_;g\_\_ | 0.236 | 0.0078 | 2.53E-05 |
| **C** | k\_\_Bacteria;p\_\_Verrucomicrobia;c\_\_[Methylacidiphilae];o\_\_Methylacidiphilales;f\_\_LD19;g\_\_ | 0.991 | 0.0002 | 8.44E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Methylococcales;f\_\_Methylococcaceae;g\_\_Methylocaldum | 0.991 | 0.0002 | 5.08E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Legionellales;f\_\_Legionellaceae;g\_\_ | 0.981 | 0.0002 | 6.53E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Hyphomicrobiaceae;g\_\_ | 0.971 | 0.0002 | 2.92E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Methylophilales;f\_\_Methylophilaceae;g\_\_ | 0.952 | 0.0002 | 2.74E-02 |
| k\_\_Bacteria;p\_\_TM6;c\_\_;o\_\_;f\_\_;g\_\_ | 0.939 | 0.0002 | 1.47E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Hyphomicrobiaceae;g\_\_Hyphomicrobium | 0.91 | 0.0002 | 9.36E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Oxalobacteraceae;Other | 0.907 | 0.0002 | 8.82E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Methylophilales;f\_\_Methylophilaceae;Other | 0.903 | 0.0002 | 5.61E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Hyphomicrobiaceae;Other | 0.870 | 0.0002 | 2.82E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodospirillales;f\_\_Acetobacteraceae;g\_\_ | 0.857 | 0.0002 | 4.10E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Limnobacter | 0.852 | 0.0002 | 5.94E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Legionellales;f\_\_Legionellaceae;Other | 0.843 | 0.0002 | 2.92E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_;f\_\_;g\_\_ | 0.839 | 0.0002 | 1.85E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Burkholderiaceae;g\_\_Burkholderia | 0.834 | 0.0002 | 2.52E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Oxalobacteraceae;g\_\_Ralstonia | 0.833 | 0.0002 | 1.18E-01 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Legionellales;f\_\_Legionellaceae;g\_\_Legionella | 0.828 | 0.0002 | 3.05E-04 |
| k\_\_Bacteria;p\_\_Chlamydiae;c\_\_Chlamydiia;o\_\_Chlamydiales;f\_\_;g\_\_ | 0.824 | 0.0002 | 5.08E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Blastomonas | 0.811 | 0.0002 | 4.43E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;Other;Other | 0.809 | 0.0002 | 3.95E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_;g\_\_ | 0.796 | 0.0002 | 4.81E-04 |
| D | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Xanthomonadales;f\_\_Sinobacteraceae;g\_\_Nevskia | 0.929 | 0.0002 | 1.36E-01 |
| k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_Cytophagia;o\_\_Cytophagales;f\_\_Cytophagaceae;g\_\_ | 0.889 | 0.0002 | 1.43E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Polaromonas | 0.885 | 0.0002 | 3.47E-04 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Sphingobium | 0.799 | 0.0002 | 1.40E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Comamonadaceae;g\_\_Methylibium | 0.744 | 0.0002 | 1.65E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodospirillales;f\_\_Acetobacteraceae;g\_\_Roseococcus | 0.713 | 0.0002 | 1.29E-03 |
| k\_\_Bacteria;p\_\_Acidobacteria;c\_\_Solibacteres;o\_\_Solibacterales;f\_\_[Bryobacteraceae];g\_\_ | 0.713 | 0.0002 | 1.27E-03 |
| k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_[Saprospirae];o\_\_[Saprospirales];f\_\_Chitinophagaceae;g\_\_ | 0.694 | 0.0002 | 1.33E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhodobacterales;f\_\_Rhodobacteraceae;g\_\_ | 0.675 | 0.0076 | 7.78E-04 |
| k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_Flavobacteriia;o\_\_Flavobacteriales;f\_\_Cryomorphaceae;g\_\_Fluviicola | 0.670 | 0.0002 | 8.45E-04 |
| E | k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Nitrosomonadales;f\_\_Nitrosomonadaceae;g\_\_ | 0.998 | 0.0002 | 1.27E-02 |
| k\_\_Bacteria;p\_\_Planctomycetes;c\_\_Planctomycetia;o\_\_Planctomycetales;f\_\_Planctomycetaceae;g\_\_Planctomyces | 0.976 | 0.0002 | 8.90E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Rhizobiaceae;g\_\_ | 0.969 | 0.0002 | 3.88E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Rhizobiaceae;Other | 0.942 | 0.0002 | 2.82E-03 |
| k\_\_Bacteria;p\_\_Planctomycetes;c\_\_Planctomycetia;o\_\_Pirellulales;f\_\_Pirellulaceae;g\_\_Pirellula | 0.891 | 0.0002 | 4.61E-04 |
| k\_\_Bacteria;p\_\_Bacteroidetes;c\_\_Sphingobacteriia;o\_\_Sphingobacteriales;f\_\_;g\_\_ | 0.830 | 0.0002 | 7.99E-03 |
| k\_\_Bacteria;p\_\_Nitrospirae;c\_\_Nitrospira;o\_\_Nitrospirales;f\_\_Nitrospiraceae;g\_\_Nitrospira | 0.796 | 0.0002 | 1.74E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Rhizobiales;f\_\_Methylobacteriaceae;g\_\_Methylobacterium | 0.776 | 0.0002 | 6.78E-02 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Rhodocyclales;f\_\_Rhodocyclaceae;g\_\_ | 0.773 | 0.0002 | 1.53E-03 |
| k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Alphaproteobacteria;o\_\_Sphingomonadales;f\_\_Sphingomonadaceae;g\_\_Sphingopyxis | 0.748 | 0.0002 | 5.74E-02 |

a Average RA is calculated based on average number of RA within same utility samples using taxonomy table at genus level (rarefied table). Rank is within each utility’s samples and omitted “0” ones.