# Table S1

## Core Reservoir Microbiome (present in soils)

| Family | Genus | DNA.min | DNA.max | RNA.min | RNA.max | Soil.max |
| --- | --- | --- | --- | --- | --- | --- |
| Spartobacteria\_unclassified | Spartobacteria\_unclassified | 0 | 0.000105 | 0 | 2.83e-05 | 0 |
| Caulobacteraceae | Phenylobacterium | 0 | 0.00107 | 0 | 1.12e-05 | 4.83e-06 |
| Moraxellaceae | Acinetobacter | 0 | 0.00186 | 1.55e-05 | 0.862 | 1.93e-05 |
| Micrococcaceae | Micrococcus | 6.84e-05 | 0.0215 | 1.56e-05 | 0.734 | 2.41e-05 |
| Pseudomonadaceae | Pseudomonas | 4.21e-05 | 0.0328 | 3.12e-05 | 0.495 | 0.000232 |
| Clostridiales\_Incertae\_Sedis\_XI | Finegoldia | 0 | 0.00102 | 0 | 0.446 | 6.27e-06 |
| Xanthomonadaceae | Stenotrophomonas | 0 | 0.000679 | 0 | 0.388 | 9.66e-06 |
| Burkholderiaceae | Burkholderia | 0 | 0.0129 | 0 | 0.385 | 0.00311 |
| Planococcaceae | Planococcaceae\_unclassified | 0 | 0.000497 | 0 | 0.323 | 6.27e-06 |
| Pseudomonadaceae | Pseudomonas | 0 | 0.0232 | 5.23e-06 | 0.288 | 0.00227 |
| Comamonadaceae | Comamonadaceae\_unclassified | 0.00616 | 0.0186 | 8.5e-06 | 0.28 | 0.00268 |
| Bacteroidetes\_unclassified | Bacteroidetes\_unclassified | 0.00101 | 0.0326 | 0 | 0.279 | 6.27e-06 |
| Opitutae\_unclassified | Opitutae\_unclassified | 0.00421 | 0.0332 | 5.23e-06 | 0.277 | 9.68e-06 |
| Pseudomonadaceae | Pseudomonas | 0 | 0.0412 | 3.1e-05 | 0.271 | 0.00046 |
| Rhizobiales\_unclassified | Rhizobiales\_unclassified | 0.00136 | 0.0398 | 5.16e-06 | 0.209 | 0.000136 |
| Acetobacteraceae | Roseomonas | 0.00021 | 0.015 | 0 | 0.19 | 9.66e-06 |
| Spartobacteria\_unclassified | Spartobacteria\_unclassified | 0.0016 | 0.06 | 2.69e-05 | 0.161 | 2.42e-05 |
| Alcaligenaceae | Alcaligenaceae\_unclassified | 0.000777 | 0.0399 | 0 | 0.15 | 4.83e-06 |
| Actinomycetales\_unclassified | Actinomycetales\_unclassified | 0.00327 | 0.127 | 0 | 0.142 | 1.45e-05 |
| Comamonadaceae | Comamonadaceae\_unclassified | 9.55e-06 | 0.00397 | 0 | 0.137 | 1.25e-05 |
| Saprospiraceae | Saprospiraceae\_unclassified | 0.000158 | 0.00806 | 0 | 0.107 | 1.45e-05 |
| Microbacteriaceae | Microbacteriaceae\_unclassified | 0.00233 | 0.0271 | 0 | 0.0978 | 9.68e-06 |
| Betaproteobacteria\_unclassified | Betaproteobacteria\_unclassified | 0.000108 | 0.0731 | 5.23e-06 | 0.0908 | 6.27e-06 |
| Comamonadaceae | Comamonadaceae\_unclassified | 0.00465 | 0.026 | 5.1e-05 | 0.0906 | 0.00348 |
| Chitinophagaceae | Sediminibacterium | 0.00155 | 0.0369 | 0 | 0.0789 | 0.000295 |
| Actinomycetales\_unclassified | Actinomycetales\_unclassified | 0.000716 | 0.0288 | 0 | 0.0707 | 9.68e-06 |
| Verrucomicrobia\_unclassified | Verrucomicrobia\_unclassified | 0.000573 | 0.0317 | 0 | 0.0676 | 9.66e-06 |
| Sphingomonadaceae | Sphingomonas | 7.52e-05 | 0.118 | 0 | 0.0672 | 0.000853 |
| Methylococcaceae | Methylococcaceae\_unclassified | 0.000373 | 0.0179 | 0 | 0.0649 | 1.25e-05 |
| Cyclobacteriaceae | Algoriphagus | 0.000735 | 0.0293 | 0 | 0.0594 | 4.84e-06 |
| Actinomycetales\_unclassified | Actinomycetales\_unclassified | 0.00103 | 0.0141 | 0 | 0.055 | 9.68e-06 |
| Actinomycetales\_unclassified | Actinomycetales\_unclassified | 0.00108 | 0.0512 | 0 | 0.0524 | 6.27e-06 |
| Comamonadaceae | Comamonas | 0.000143 | 0.0142 | 0 | 0.0494 | 8.78e-05 |
| Proteobacteria\_unclassified | Proteobacteria\_unclassified | 0.00297 | 0.134 | 4.25e-05 | 0.0481 | 1.94e-05 |
| Bacteroidetes\_unclassified | Bacteroidetes\_unclassified | 0.000367 | 0.00679 | 0 | 0.0448 | 4.84e-06 |
| Oxalobacteraceae | Duganella | 4.56e-05 | 0.0269 | 5.23e-06 | 0.0391 | 0.000364 |
| Burkholderiales\_unclassified | Burkholderiales\_unclassified | 0 | 0.00126 | 0 | 0.0376 | 4.83e-06 |
| Microbacteriaceae | Microbacteriaceae\_unclassified | 0.000115 | 0.0268 | 0 | 0.03 | 4.83e-06 |
| Acidobacteria\_Gp4\_unclassified | Acidobacteria\_Gp4\_unclassified | 1.91e-05 | 0.00619 | 0 | 0.016 | 0 |
| Actinobacteria\_unclassified | Actinobacteria\_unclassified | 0.000363 | 0.0675 | 0 | 0.0127 | 1.45e-05 |
| Cytophagaceae | Cytophagaceae\_unclassified | 0.000697 | 0.0844 | 0 | 0.0126 | 1.45e-05 |
| Oxalobacteraceae | Janthinobacterium | 0.000957 | 0.0141 | 0 | 0.0115 | 0 |
| Flavobacteriaceae | Flavobacterium | 5.63e-06 | 0.00306 | 0 | 0.00533 | 0.000232 |
| Micrococcaceae | Arthrobacter | 0 | 0.0435 | 0 | 0.00456 | 0.000343 |
| Sphingobacteriaceae | Pedobacter | 0 | 0.0344 | 0 | 0.0042 | 0.000194 |
| Oxalobacteraceae | Oxalobacteraceae\_unclassified | 0.00103 | 0.0214 | 0 | 0.00368 | 0.000864 |
| Flavobacteriaceae | Flavobacterium | 0 | 0.0154 | 0 | 0.00224 | 0.000157 |
| Neisseriaceae | Neisseriaceae\_unclassified | 0 | 0.00132 | 0 | 0.0016 | 0 |
| Bacillales\_unclassified | Bacillales\_unclassified | 0 | 0.0022 | 0 | 0.000658 | 0.0023 |
| Bradyrhizobiaceae | Bradyrhizobium | 7.74e-06 | 0.000906 | 0 | 0.00024 | 0.000232 |
| Enterobacteriaceae | Yersinia | 0 | 2.32e-05 | 0 | 0.000202 | 0.000126 |
| Solirubrobacterales\_unclassified | Solirubrobacterales\_unclassified | 0 | 0.000241 | 0 | 0.000178 | 0.00154 |
| Sphingobacteriaceae | Sphingobacteriaceae\_unclassified | 0 | 0.000247 | 0 | 0.000127 | 0 |
| Bacillaceae\_1 | Bacillus | 0 | 2.87e-05 | 0 | 0 | 1.45e-05 |
| Solirubrobacteraceae | Solirubrobacter | 0 | 0.000245 | 0 | 0 | 0.000634 |

## Core Reservoir Microbiome (absent from soils)

| Family | Genus | DNA.min | DNA.max | RNA.min | RNA.max |
| --- | --- | --- | --- | --- | --- |
| Comamonadaceae | Comamonadaceae\_unclassified | 0 | 0.000364 | 0 | 7.07e-05 |
| Rubrobacteraceae | Rubrobacter | 0 | 1.68e-05 | 0 | 7.07e-05 |
| Dermabacteraceae | Brachybacterium | 0 | 6.48e-05 | 0 | 5.16e-06 |
| Opitutae\_unclassified | Opitutae\_unclassified | 0 | 0.00123 | 0 | 0.187 |
| Bacteria\_unclassified | Bacteria\_unclassified | 0 | 0.000755 | 0 | 0.123 |
| Actinomycetales\_unclassified | Actinomycetales\_unclassified | 0.00153 | 0.0222 | 0 | 0.0986 |
| Burkholderiaceae | Polynucleobacter | 0.000697 | 0.0207 | 0 | 0.0865 |
| Actinomycetales\_unclassified | Actinomycetales\_unclassified | 0.00348 | 0.0602 | 0 | 0.0227 |
| Bacteroidetes\_unclassified | Bacteroidetes\_unclassified | 1.91e-05 | 0.0189 | 0 | 0.0188 |
| Actinobacteria\_unclassified | Actinobacteria\_unclassified | 0 | 0.000249 | 0 | 0.000141 |
| Bacteria\_unclassified | Bacteria\_unclassified | 0 | 0.000459 | 0 | 0 |
| Dietziaceae | Dietzia | 0 | 5.04e-05 | 0 | 0 |