# Table S1

## Core Reservoir Microbiome (present in soils)

| Family | Genus | DNA.min | DNA.max | RNA.min | RNA.max | Soil.max |
| --- | --- | --- | --- | --- | --- | --- |
| Moraxellaceae | Acinetobacter | 0 | 0.00213 | 1.89e-05 | 0.867 | 1.96e-05 |
| Micrococcaceae | Micrococcus | 0 | 0.0199 | 2.13e-05 | 0.73 | 3.92e-05 |
| Pseudomonadaceae | Pseudomonas | 4.63e-05 | 0.0372 | 3.41e-05 | 0.726 | 0.000251 |
| Clostridiales\_Incertae\_Sedis\_XI | Finegoldia | 0 | 0.00122 | 0 | 0.479 | 6.6e-06 |
| Burkholderiaceae | Burkholderia | 0 | 0.0155 | 0 | 0.401 | 0.00389 |
| Xanthomonadaceae | Stenotrophomonas | 0 | 0.000767 | 0 | 0.383 | 1.47e-05 |
| unclassified | unclassified | 0.00614 | 0.063 | 1.31e-05 | 0.355 | 1.96e-05 |
| unclassified | unclassified | 0 | 0.000597 | 0 | 0.33 | 6.6e-06 |
| Comamonadaceae | unclassified | 0.00202 | 0.0184 | 0 | 0.282 | 0.00256 |
| Pseudomonadaceae | Pseudomonas | 0 | 0.0505 | 1.14e-05 | 0.266 | 0.00258 |
| Pseudomonadaceae | Pseudomonas | 0 | 0.000881 | 2.36e-05 | 0.266 | 7.92e-05 |
| unclassified | unclassified | 0.00149 | 0.0442 | 7.03e-06 | 0.257 | 9.12e-05 |
| unclassified | unclassified | 0.000509 | 0.0197 | 0 | 0.224 | 1.32e-05 |
| Acidobacteria\_Gp4\_family\_incertae\_sedis | Gp4 | 0 | 0.0016 | 0 | 0.189 | 0.000245 |
| Rhodobacteraceae | Rhodobacter | 9.26e-06 | 0.00475 | 0 | 0.171 | 1.32e-05 |
| unclassified | unclassified | 0.00337 | 0.143 | 0 | 0.142 | 1.47e-05 |
| Saprospiraceae | unclassified | 0.000188 | 0.00858 | 0 | 0.132 | 1.52e-05 |
| Bradyrhizobiaceae | Bradyrhizobium | 0 | 0.0107 | 0 | 0.129 | 0.0541 |
| Microbacteriaceae | unclassified | 0.0027 | 0.0315 | 0 | 0.106 | 1.32e-05 |
| unclassified | unclassified | 0.000389 | 0.0151 | 0 | 0.106 | 6.6e-06 |
| unclassified | unclassified | 0.00173 | 0.0838 | 1.42e-05 | 0.0994 | 1.01e-05 |
| Comamonadaceae | unclassified | 0.00491 | 0.0223 | 3.25e-05 | 0.097 | 0.00451 |
| unclassified | unclassified | 0.000275 | 0.0163 | 0 | 0.0959 | 6.6e-06 |
| Chitinophagaceae | Sediminibacterium | 0.00164 | 0.0411 | 0 | 0.0903 | 0.000317 |
| unclassified | unclassified | 0.00208 | 0.0569 | 1.31e-05 | 0.0845 | 2.53e-05 |
| unclassified | unclassified | 0.00246 | 0.0226 | 0 | 0.0832 | 5.07e-06 |
| Sphingomonadaceae | Sphingomonas | 8.12e-05 | 0.118 | 1.06e-05 | 0.0696 | 0.000937 |
| unclassified | unclassified | 0.00037 | 0.0162 | 0 | 0.0694 | 1.32e-05 |
| Cyclobacteriaceae | Algoriphagus | 0.000778 | 0.0338 | 0 | 0.0622 | 5.07e-06 |
| Comamonadaceae | Comamonas | 0.000176 | 0.0089 | 0 | 0.0559 | 0.000243 |
| unclassified | unclassified | 0.000565 | 0.0084 | 0 | 0.0509 | 1.01e-05 |
| unclassified | unclassified | 0.00341 | 0.147 | 4.25e-05 | 0.0478 | 3.04e-05 |
| Microbacteriaceae | unclassified | 0.000111 | 0.0307 | 0 | 0.0326 | 4.9e-06 |
| Flavobacteriaceae | Flavobacterium | 0.000268 | 0.0466 | 1.06e-05 | 0.0317 | 0.003 |
| unclassified | unclassified | 0.00346 | 0.0665 | 0 | 0.0251 | 6.6e-06 |
| Flavobacteriaceae | Flavobacterium | 2.78e-05 | 0.0208 | 0 | 0.023 | 6.6e-06 |
| unclassified | unclassified | 0.00038 | 0.0783 | 0 | 0.0164 | 1.47e-05 |
| Comamonadaceae | unclassified | 0.000167 | 0.0116 | 0 | 0.0159 | 1.32e-05 |
| Cytophagaceae | unclassified | 0.000722 | 0.0927 | 0 | 0.0133 | 1.52e-05 |
| Comamonadaceae | unclassified | 0.000204 | 0.0162 | 0 | 0.011 | 0.00029 |
| Micrococcaceae | Arthrobacter | 0 | 0.0516 | 0 | 0.00617 | 0.000372 |
| Planococcaceae | Lysinibacillus | 0 | 0.0644 | 0 | 0.00423 | 0.00517 |
| Pseudomonadaceae | Pseudomonas | 0 | 0.0244 | 5.31e-06 | 0.0029 | 0.000137 |
| Oxalobacteraceae | Janthinobacterium | 0 | 0.0184 | 0 | 0.0029 | 0.00031 |
| Bacillaceae\_1 | Bacillus | 0 | 0.0303 | 0 | 0.00262 | 1.01e-05 |
| Sphingobacteriaceae | Mucilaginibacter | 0 | 0.0182 | 0 | 0.00192 | 0.00189 |
| Oxalobacteraceae | Duganella | 0 | 0.0171 | 0 | 0.00158 | 0.000383 |
| Solirubrobacteraceae | Solirubrobacter | 0 | 0.00276 | 0 | 0.000857 | 0.00201 |
| Sphingomonadaceae | unclassified | 0 | 0.000696 | 0 | 0.000591 | 0.00312 |
| Enterobacteriaceae | Yersinia | 0 | 0.00796 | 0 | 0.000586 | 1.98e-05 |
| unclassified | unclassified | 0 | 0.00136 | 0 | 0.000583 | 9.9e-05 |
| Spartobacteria\_family\_incertae\_sedis | Spartobacteria\_genera\_incertae\_sedis | 0 | 0.00727 | 0 | 0.000408 | 0.0379 |
| Acidobacteria\_Gp6\_family\_incertae\_sedis | Gp6 | 0 | 0.0144 | 0 | 0.00029 | 0.0387 |
| unclassified | unclassified | 0 | 0.00125 | 0 | 9.08e-05 | 0.0107 |
| unclassified | unclassified | 0 | 0.00188 | 0 | 7.95e-05 | 0.00199 |
| unclassified | unclassified | 0 | 0.000102 | 0 | 5.23e-05 | 0.00095 |
| Acidobacteria\_Gp1\_family\_incertae\_sedis | Gp1 | 0 | 0.000141 | 0 | 1.29e-05 | 0.00222 |

## Core Reservoir Microbiome (absent from soils)

| Family | Genus | DNA.min | DNA.max | RNA.min | RNA.max |
| --- | --- | --- | --- | --- | --- |
| Burkholderiaceae | Polynucleobacter | 0.000713 | 0.0286 | 0 | 0.179 |
| unclassified | unclassified | 0.000251 | 0.0173 | 0 | 0.177 |
| unclassified | unclassified | 8.33e-05 | 0.00462 | 0 | 0.14 |
| unclassified | unclassified | 0.0018 | 0.0255 | 0 | 0.112 |
| unclassified | unclassified | 0.000267 | 0.00552 | 0 | 0.0309 |
| Chitinophagaceae | unclassified | 0.000343 | 0.012 | 0 | 0.0239 |
| unclassified | unclassified | 0.000298 | 0.019 | 0 | 0.0204 |
| unclassified | unclassified | 9.26e-06 | 0.0164 | 0 | 0.00191 |
| Rubrobacteraceae | Rubrobacter | 0 | 0.00671 | 0 | 0.00149 |
| Micrococcaceae | unclassified | 0 | 0.00529 | 0 | 0.00059 |