

| Sample | Sequencing technology | Cohort | Number of reads (M) | Sequencing depth (Gbp) | Number of species |
|----------------|---------------------------|-----------------------|---------------------|------------------------|-------------------|
| SAMEA110452918 | NovaSeq 6000, 2x150 bp | Federici et al., 2022 | 258.36 | 38.72 | 229 |
| SAMEA110452924 | NovaSeq 6000, 2x150 bp | Federici et al., 2022 | 189.18 | 28.44 | 357 |
| SAMN00040286 | Genome Analyzer II, 2x100 | HMP1 | 149.76 | 14.98 | 403 |
| SAMN00036649 | Genome Analyzer II, 2x100 | HMP1 | 149.16 | 14.90 | 394 |
| SAMN00037108 | Genome Analyzer II, 2x100 | HMP1 | 146.07 | 14.60 | 139 |
| SAMN00146983 | HiSeq 2000, 2x100 | HMP2 | 131.49 | 13.50 | 221 |
| SAMN00099612 | HiSeq 2000, 2x100 | HMP2 | 116.72 | 11.67 | 197 |
| SAMN00143093 | HiSeq 2000, 2x100 | HMP2 | 112.29 | 11.23 | 186 |

Note:
(M) - Million
(Gbp) - Giga base pairs