Table S2: Sequence assembly statistics for three different metagenomes and two different assembly algorithms.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Cahuil | | Combined Santa Pola | | Combined Chula Vista | |
| Assembler | Newbler | Velvet | Newbler | Velvet | Newbler | Velvet |
| N50 value | 881\* | 205 | 996\* | 106 | 882\* | 102 |
| Average contig length (100 bp cutoff) | 687 | 239 | 709 | 200 | 315 | 152 |
| Number of contigs (100 bp cutoff) | 8,167 | 140,071 | 156,214 | 1,639,903 | 18,519 | 75,046 |