Supplementary Table 1. Summary of metagenome sequence reads mapped to “*Ca.* Desulforudis audaxviator”, “*Ca.* D. audaxviator”-related scaffolds from IMG-M, and genomic bin A32 from metagenome U1362A.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Metagenome | Recruitment method | Target for fragment recruitment | | | Subtotalb | Totalc |
| “*Ca.* D. audaxviator” | “*Ca.* D. audaxviator”-related scaffolds | 1362A\_maxbin32 |
| U1362A | bbmap | 524916 (696450)a | 1102222 (1240214) | 778190 (877474) | 1782646 | 1785284 |
| Bowtie2 | 40273 (61946) | 857214 (896816) | 585010 (594926) | 1010798 |
| U1362B | bbmap | 262753 (365430) | 192421 (270268) | 140984 (203622) | 575918 | 576460 |
| Bowtie2 | 22140 (36418) | 63280 (76286) | 29640 (35486) | 117954 |

aNumbers in parentheses equal the number of reads identified when mate pairs of solo mapped reads are included

bTotal number of unique reads, including all mate pairs, found via mapping with three references combined

cTotal number of unique reads, including all mate pairs, found via mapping with three references combined and using the two mapping methods.