**Supplemental material for**

**The First Complete Genome Sequence of Species *Shewanella decolorationis*, from a Bioremediation Competent Strain Ni1-3**

Yicheng Wang,\*,[[1]](#footnote-1) Xunchao Cai,\*,†,1 and Yanping Mao\*,§

\*College of Chemistry and Environmental Engineering, Shenzhen University, Shenzhen, Guangdong, 518071, P. R. China

†Department of Gastroenterology and Hepatology, Shenzhen University General Hospital, Shenzhen, Guangdong, 518071, P. R. China

§Corresponding author: College of Chemistry and Environmental Engineering, Shenzhen University, Shenzhen, Guangdong, P. R. China; Tel: +86-755-26558094; E-mail address: maoy@szu.edu.cn (Y. Mao)



**Figure S1** The chromosome collinearity analysis of *S. decolorationis* Ni1-3 and *S. decolorationis* LDS1.

**Table S1** The quality control of Nanopore MinION sequencing

|  |  |
| --- | --- |
| Summary | Value |
| Number of reads | 74,257 |
| Mean read length (bp) | 13,775.8 |
| Mean read quality | 9.8 |
| Median read length (bp) | 9,578 |
| Median read quality | 10.0 |
| Read length N50 (bp) | 24,505 |
| STDEV read length (bp) | 13,019.8 |
| Total bases | 1,022,946,925 |
| Estimated coverage (times ×) | 210 |
| Percentage of reads above quality cutoffs |  |
| >Q7 (%) | 99.9 |
| >Q10 (%) | 49.0 |
| >Q12 (%) | 0.2 |
| >Q15 (%) | 0 |

**Table S2** The quality control of Illumina NovaSeq sequencing

|  |  |
| --- | --- |
| Summary | Value |
| Number of raw reads | 9,083,075 |
| Number of clean reads | 9,067,958 |
| Number of clean bases (GB) | 2.72 |
| GC content (%) | 47.23 |
| Estimated coverage (times ×) | 280 |
| Percentage of clean reads above quality cutoffs |  |
| >Q20 (%) | 96.96 |
| >Q30 (%) | 91.63 |

**Table S3** Summary of Unicycler hybrid assembly

|  |  |  |
| --- | --- | --- |
| Assembly information | Chromosome | Plasmid |
| Assembly size (bp) | 5,001,960 | 286,397 |
| Number of contigs | 1 | 1 |
| GC content (%) | 47.2 | 45.1 |
| N's | 0 | 0 |
| Coverage (times ×) | 1.00 | 1.52 |

**Table S4** The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) identified in *S. decolorationis* Ni1-3 genome

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| CRISPR | Start | End | Repeat | Number of spacer | Average spacer length | Percentage of genome (%) |
| 1 | 1570111 | 1576922 | GTTCACTGCCTTACAGGCAGCTTAGAAA | 113 | 32 | 0.136 |
| 2 | 2470876 | 2473574 | GTCTAAGTCCCTTTAAATGGCGGGGCGTCTTTCAGAG | 38 | 33 | 0.054 |
| 3 | 2482416 | 2482578 | TTAATCCCCTTAAATGGCGGGGC | 2 | 47 | 0.003 |
| 4 | 2483313 | 2484260 | GTCTTAATCCCCTTAAATGGCGGGGCATCTTTCAGAG | 13 | 33 | 0.019 |
| 5 | 2484874 | 2485611 | GTCTTAATCCCCTTAAATGGCGGGGCGTCTTTCAGAG | 10 | 33 | 0.015 |
| Total | | | | 176 |  | 0.227 |

1. **1Yicheng Wang and Xunchao Cai contributed equally to this work.** [↑](#footnote-ref-1)