**Supplemental material for**

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

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**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)