Table S2. General statistics of whole metagenome sequencing reads quality control and assembly for IMG/MER submission.

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| --- | --- | --- | --- |
| Sample | Raw data | After quality processing | After assembly |
| Number of reads | Mean reads length (bp) ± SD | Number of sequences | Mean sequence length (bp) | Low-quality sequences discarded | Number of sequences | Mean sequence length (bp) ± SD |
| SCD0 | R1 | 7,123,094 | 99.8 ± 5.6 | 6,314,501 | 85.2 ± 5.3 | 808,593 (11%) | 73,571 | 374 ± 303 |
| R2 | 7,123,094 | 99.8 ± 5.6 | 5,576,029 | 85.2 ± 5.7 | 1,547,065 (21%) |
| SCDE | R1 | 7,830,432 | 99.8 ± 5.5 | 6,581,133 | 81.2 ± 5.5 | 1,249,299 (15%) | 86,670 | 489 ± 703 |
| R2 | 7,830,432 | 99.8 ± 5.4 | 5,570,859 | 83.2 ± 5.3 | 2,259,573 (28%) |