Table S1. General statistics of whole metagenome sequencing reads quality control performed by EBI Metagenomics.

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| --- | --- | --- | --- | --- | --- |
| Sample | Raw data  (nº of sequences) | After quality processing | | | |
| Number of sequences | Mean sequence length (bp) ± SD | Average GC% | Low-quality sequences discarded |
| SCD0 | 14,246,188 | 10,620,194 | 103.1 ± 11.7 | 43.30 | 3,625,994 (25%) |
| SCDE | 15,660,864 | 10,980,517 | 102.6 ± 10.6 | 53.29 | 4,680,347 (30%) |