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

|  |  |  |
| --- | --- | --- |
| 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%) |