

Supplementary Table S1: Overview of the results of metagenomes before and after assembling and quality filtering

Metagenomes Statistics	Metagenomes		
	KS1	KS2	KS3
Upload	25,950	107,337	39,343
Post QC^a	23,313	85,019	33,516
Size (nt)^b	5,936,028	24,454,837	8,966,141
Mean seqs. Length (nt)^b	254 ± 99	287 ± 76	267 ± 75
Mean GC %^b	56 ± 7	57 ± 6	58 ± 6
Classified ORG^{b,c}	55.94	86.17	83.95
Classified FCN^{b,c}	0.82	1.58	1.79
Number of contigs	542	2,329	1,065
Aligned reads in contigs	16,879 (0.65%)	74,804 (69.7%)	27,286 (69.4%)
Singleton	7,597 (29.3%)	29,107 (27.1%)	10,401 (26.4%)
Short (< nt)	591 (2.3%)	1,517 (1.4%)	632 (1.6%)
Largest contig size (nt)	687	818	693
Assembled Sequences used in the phylogenetic reconstruction	9 (1.6%)	167 (7.2%)	56 (5.2%)

^a - QC – MG-RAST 3 quality control.

^b - Values obtained considering the post QC.

^c – Percentages obtained with post QC data and using $1e^{-5}$.

ORG – Organism; FCN – Function; Seqs. – Sequences.