

Table S2A: Metagenomic sequencing efforts and representation of raw reads in the assemblies and MAGs

Sample	Produced data (Gbp)	Mio. raw read pairs (2x150 bp)	Mio. Error-corrected Read pairs	Nonpareil % of diversity covered	Nonpareil diversity index	Mapping to assembly (with > 95% identity)	Mapping to Final MAGs (with > 95% identity)
B20	28	92	84	74%	20.7	54%	36%
F08	32	107	96	67%	21.7	40%	24%
G19	28	94	85	65%	21.6	43%	31%
C15-24h	16	55	52	56%	21.8	34%	26%
F12-24h	20	68	66	58%	21.9	34%	24%

Table S2B: Initial metagenome assembly metrics

	Initial assembly (contigs > 1000 bp)
Total size (Gbp)	1.14
Number of contigs	431,850
Largest contig (bp)	167,554
Contig length N50	3140
Contig length L50	89605
GC content	69%
Mapping B20 (>95% id)	54%
Mapping F08 (>95% id)	40%
Mapping G19 (>95% id)	43%
Mapping C15 (>95% id)	34%
Mapping F12 (>95% id)	34%