

Table S1. Summary of the results obtained by binning of the first raw assembly using MyCC. Clustering has been performed taken into consideration the coverage and the genomic signature of the contigs.

	Total Length	N50	Number of contigs	Number of reads	Percentage of total reads	Average Coverage
Cluster 1	213,66	10,332	33	2,401,822	5.46%	2,810.33
Cluster 2	180,548,803	26,802	14,789	38,092,766	86.6%	52.7
Cluster 3	1,480,805	9,209	316	481,203	1.09%	81.2