

Table S2. Metagenome read and assembly data including sample source, pre- and post-quality filtered reads, genome equivalent and average size values, and assembly statistics for both single and co-assemblies.

Sample ID	Month	Depth (m)	# Raw Reads	# Filtered Reads	Kraken2	MicrobeCensus (reads pre-assembly)		SPAdes Assembly			Co-assembly		
					% reads taxonomically classified	Estimated genome equivalents	Estimated average genome size (bp)	# contigs > 1Kbp	N50	longest contig (bp)	# contigs > 1Kbp	N50	longest contig (bp)
BH0560M	May	60	3,240,148	2,202,966	17	663.76	2,511,984	9,869	2,247	405,204	10,696	12,222	625,129
BH05106M	May	106	3,729,927	1,483,928	11	402.55	3,340,433	7,425	1,733	108,892	11,167	12,834	453,391
BH0960M	September	60	13,150,727	13,134,788	18	2,395.80	2,476,305	31,896	3,527	421,576	10,696	12,222	625,129
BH0995M	September	95	11,894,511	9,488,634	9	1,265.38	4,453,747	40,713	2,673	598,144	11,167	12,834	453,391