

Table S1. Summary statistics of the Baikal 1600 m long-read sequencing and metagenomic assembly.

Read Type (Processing)	1600 m deep PacBio Sequel II	
	Raw Reads	CCS Reads 5
Sequencing statistics (Reads > 1 Kb):		
#Sequences (Millions)	6.61	0.31
Nucleotides sequenced (Gb)	90.83	4.46
Largest read size (bp)	435,307	29,377
Average length read size (bp)	13,744	14,334
Predicted proteins (Reads > 1 Kb):		
Proteins (Millions)	96.0	6.6
Average Protein Size (aa)	135.4	183.4
Proteins / Mb Sequenced	1,057.0	1,482.4
Assembly statistics (Contigs > 1 Kb):		
#Sequences	-	2,913
#Nucleotides assembled (Mb)	-	192.2
Largest contig size (bp)	-	2,256,336
Average length contig size (bp)	-	65,968