

Table S4. Genomic parameters of the resulting bins from the Baikal 1600 m CCS sequences. The four *Ca. Baikalibacteria* bins are highlighted in yellow.

Read Binning	Total Size (Mb)	#Reads grouped	Total Deep Baikal 16S rRNA	16S rRNA reads matching CPR (% total CPR)	Dereplicated Deep Baikal 16S rRNA (97%)	Size after scaffolding (Mb)	Largest Sequence Size and average (Kb)	Completeness (%)	Contamination (%)	GC content ($\pm$ SD)
RBin01	8.77	606	4	1.23	3	--	--	96.0	629.0	38.7 ($\pm$ 2.4)
RBin02	12.27	838	5	1.54	4	--	--	94.0	851.8	51.4 ($\pm$ 2.2)
RBin03	7.98	554	6	1.85	2	--	--	100.0	820.0	45.1 ($\pm$ 5.2)
RBin04	22.35	1528	36	11.11	16	19.62	173 / 16.4	97.0	1792.9	48.3 ($\pm$2.5)
RBin05	11.75	814	6	1.85	1	--	--	100.0	1137.5	35.4 ($\pm$ 1.5)
RBin06	20.98	1575	0	0.00	0	--	--	94.0	930.0	64.1 ($\pm$ 3.1)
RBin07	7.71	528	8	2.47	3	--	--	96.2	828.9	39.9 ($\pm$ 1.4)
RBin08	11.15	766	19	5.86	9	10.73	53 / 14.7	92.9	732.1	38.6 ($\pm$1.4)
RBin09	5.38	362	22	6.79	4	4.72	360 / 16.5	96.2	414.4	43.9 ($\pm$2.1)
RBin10	24.49	1658	17	5.25	10	21.31	88 / 16.1	48.9	801.3	44.0 ($\pm$2.0)
RBin11	3.22	218	0	0.00	0	--	--	89.4	296.2	40.1 ($\pm$ 1.4)
RBin12	3.80	258	2	0.62	2	--	--	93.2	236.9	56.8 ($\pm$ 1.9)
RBin13	1.43	98	4	1.23	1	--	--	65.4	50.0	51.3 ($\pm$ 1.6)
RBin14	0.53	38	5	1.54	1	--	--	20.2	11.5	31.4 ($\pm$ 1.0)