Supplementary Table S1. Genome estimation of *Chionobathyscus dewitti* using K-mer anaysis.

K-mer	Genome size (bp)	Heterozygosity (%)	Error (%)	Duplication (%)
17	862,611,855	0.397	0.266	0.787
19	881,696,158	0.421	0.317	0.738
25	925,384,674	0.412	0.313	0.724

Supplementary Table S2. Completeness of *Chionobathyscus dewitti* genome assembly estimated by using BUSCO (Benchmarking Universal Single-Copy Orthologs).

Eukaryote odb10	No.	%
Complete BUSCOs (C)	112	43.9
Complete and single-copy BUSCOs (S)	110	43.1
Complete and duplicated BUSCOs (D)	2	0.8
Fragmented BUSCOs (F)	115	45.1
Missing BUSCOs (M)	28	11.0
Total BUSCO groups searched	255	