Supplementary Table S5 Average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) of *Polaribacter* spp. Hel1_33_49 and Hel1_85 compared to the currently available *Polaribacter* genomes (*P. franzmannii* 301^T was excluded due to its fragmented status). ANI was calculated using JSpecies (Richter & Rosselló-Móra, 2009) and dDDH was calculated using the Genome-to-Genome Distance Calculator (GGDC, Auch *et al.*, 2010).

	P. sp. Hel1_33_49	*P.* sp. Hel1_85	*P. irgensii* 23-P^T	*P.* sp. MED152
ANIb (ANI with blast)				
Polaribacter sp. Hel1_33_49	–	80.0	69.8	77.1
Polaribacter sp. Hel1_85	80.1	–	69.1	77.7
dDDH				
Polaribacter sp. Hel1_33_49	–	23.9	15.9	21.2
Polaribacter sp. Hel1_85	23.9	–	15.4	20.5

Auch AF, von Jan M, Klenk H-P, Göker M. (2010). Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. *Stand Genomic Sci* **2:** 117-134.

Richter M, Rosselló-Móra R. (2009). Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci USA* **106:** 19126-19131.