Supplementary Table S4 Selected features of the currently available *Polaribacter* genomes (due to its fragmented status no gene numbers are provided for *P. franzmannii*). Significantly elevated numbers are highlighted.

	P. sp. Hel1_33_49	*P.* sp. Hel1_85	*P. irgensii* 23-P^{T}	*P.* sp. MED152	*P. franzmannii* 301^{T}
size (Mbp)	3.01	3.91	2.76	2.96	6.91
contigs / scaffolds	2 / 2	4 / 4	7 / 2	1 / 1	69 / 56
G+C [%]	30.4	29.2	34.5	30.6	32.5
protein-coding genes	2,620	3,433	2,557	2,635	-
rRNA operons	3	4	3	2	-
ABC transporter genes	30**	39**	24**	24**	-
TBDR	26* / 16**	40* / 24**	23**	16**	-
TBDR + SusD-like protein pairs	5**	11**	8**	8**	-
CBMs	18* / 12#	23* / 17#	6#	10#	-
CEs	6* / 5#	13* / 7#	7#	6#	-
GHs	56* / 45#	60* / 57#	17#	31#	-
GTs	43* / 42#	49* / 49#	24#	36#	-
PLs	0* / 0#	16* / 10#	0#	8#	-
∑CAZymes	123* / 104#	161* / 140#	54#	91#	-
peptidases	168##	161##	162##	167##	-
sulfatases	12**	33**	2**	3**	-
histine kinases	24**	37**	17**	26**	-
response regulators	22**	41**	19**	30**	-

TBDR = TonB-dependent receptor; CBM = carbohydrate-binding module; CE = carbohydrate esterase; GH = glycoside hydrolase; GT = glycosyltransferase; PL = polysaccharide lyase.*manual annotations; **annotations based on HMMer 3 hits better than E-10 against the Pfam database (search profiles:, ABC_tran, ABC2_membrane, HATPase, His_kinase, Response_reg, Sulfatase , SusD, SusD-like, TonB_dep_Rec) #automated annotations based on combined Pfam, CAZy and DBCan searches; ##predictions based MEROPS database searches.