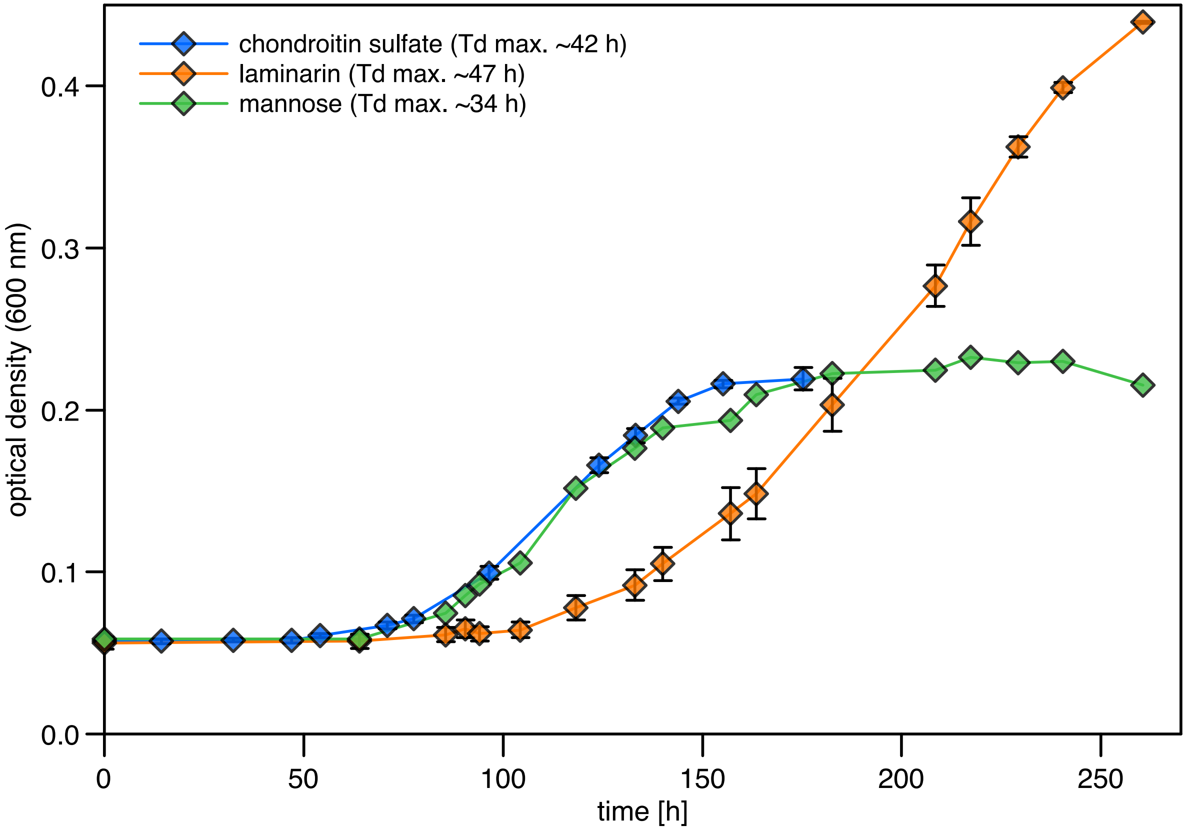
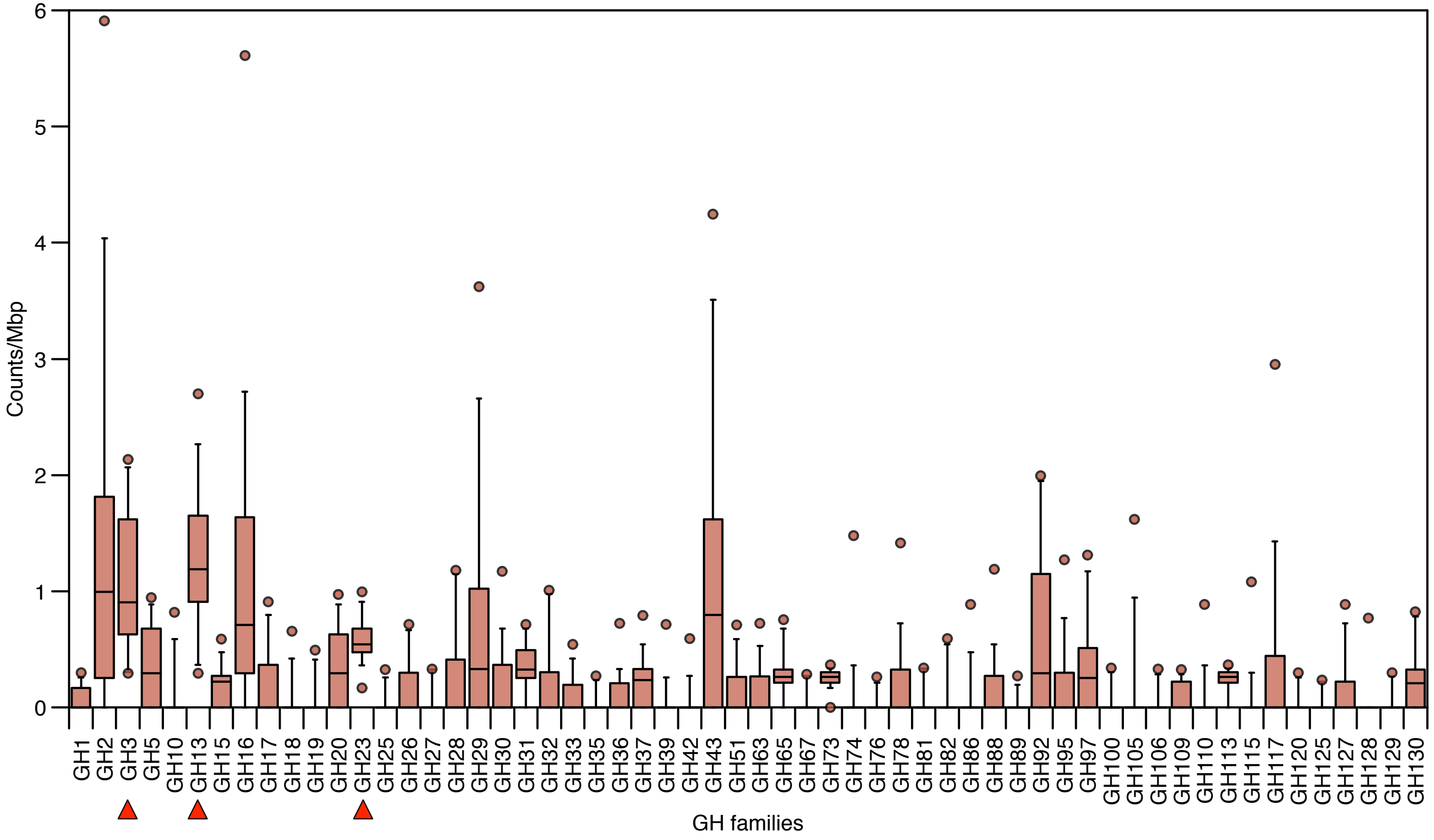
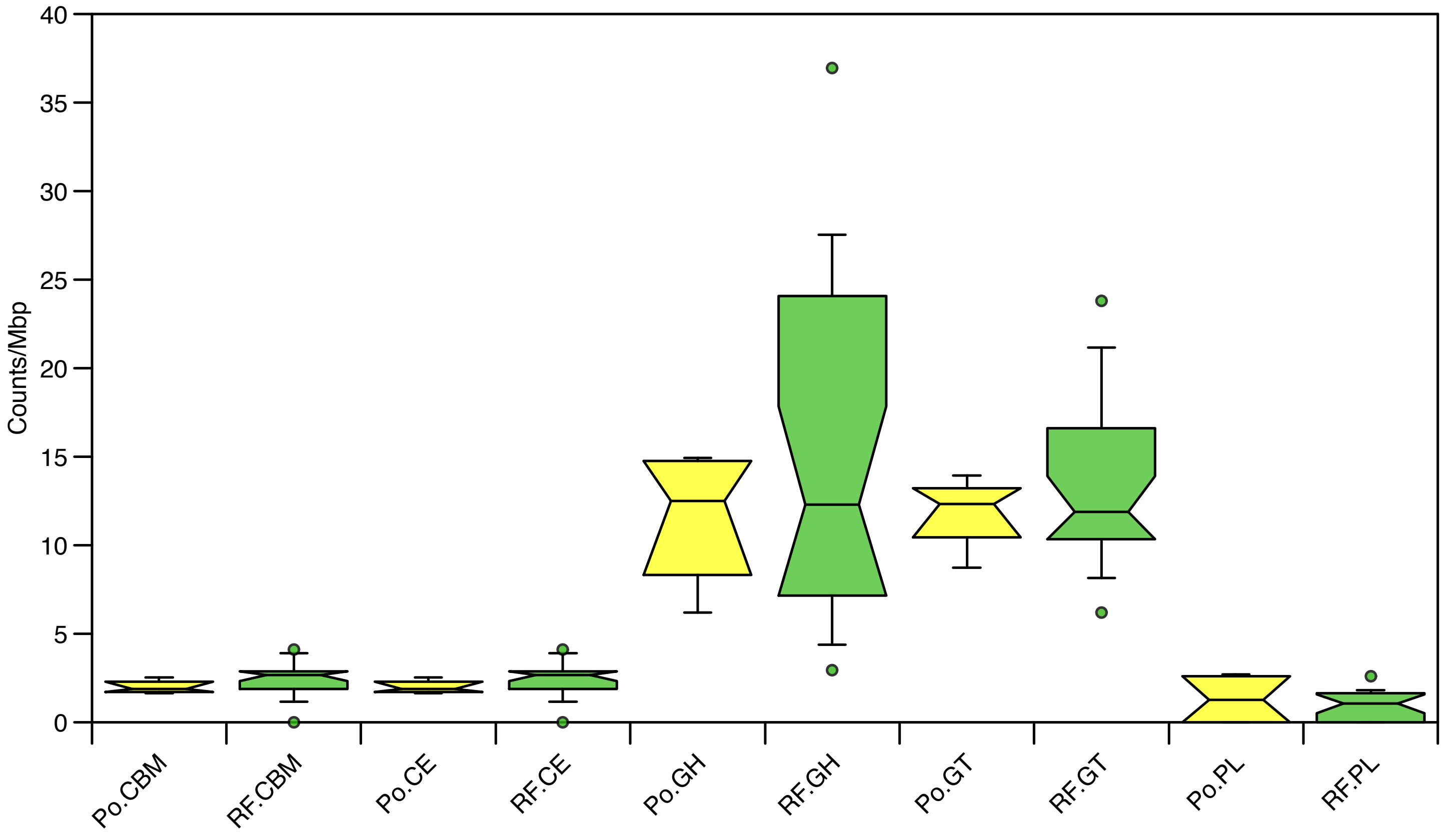


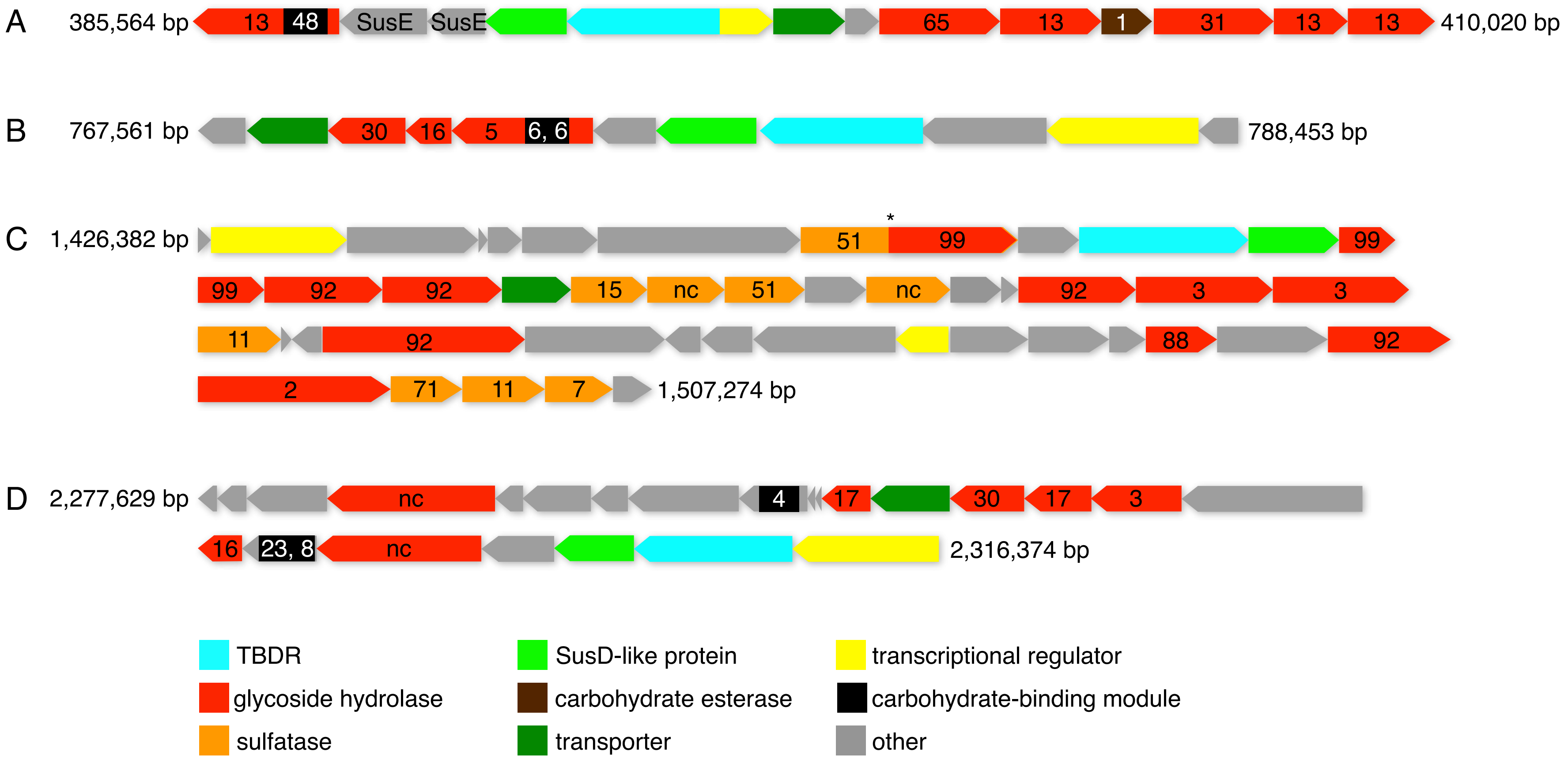
Supplementary Figure S1 Growth curves of *Polaribacter* sp. Hel1_33_49. The strain was grown at 12 °C in modified HaHa_100 medium with 0.1 g L^{-1} peptone, 0.1 g L^{-1} casamino acids, 200 μM NH_4Cl, and 16 μM KH_2PO_4. Laminarin (L9634, Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) or chondroitin 4-sulfate (27042, Sigma-Aldrich) were used as carbon source, and D-mannose served as control (concentrations: 2.0 g L^{-1}). Experiments with laminarin and chondroitin sulfate were carried out in triplicates. Maximum doubling times (Td) were estimated from semi-logarithmic plots of the data.



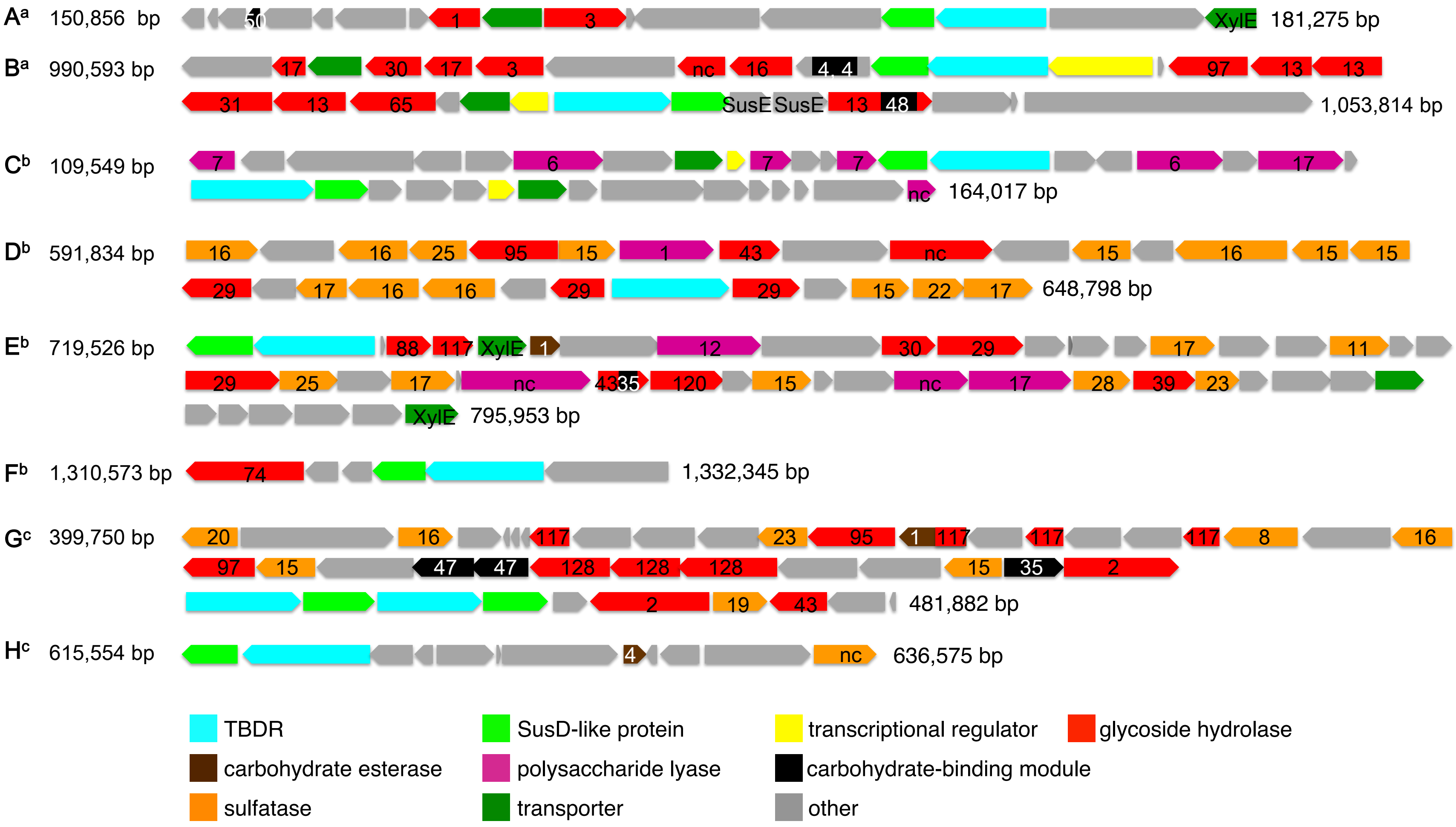
Supplementary Figure S2 Variation of abundant GH families in 27 marine *Flavobacteriaceae* genomes (Supplementary Table S3). Data are shown as box and whisker plots with boxes representing inner quartiles Q2 and Q3 and whiskers extending to 5% and 95% percentiles. Circles represent data outside these boundaries. Only those 58 GH families are shown that are represented by at least three copies in the entire dataset. Only families GH3, GH13 and GH23 were universally present in all analyzed genomes (red triangles).



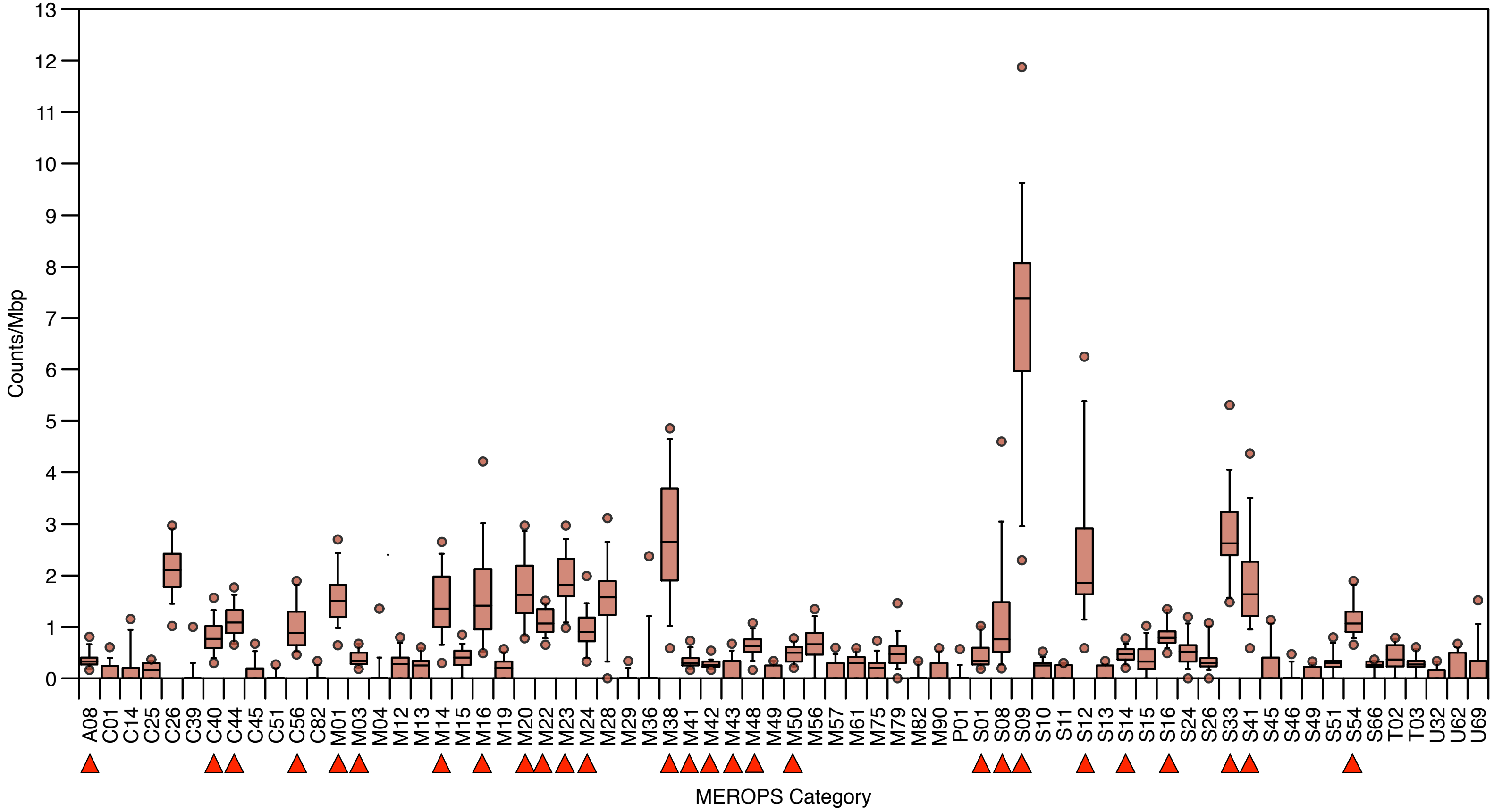
Supplementary Figure S3 Comparison of CAZyme categories (CBM, CE, GH, GT, PL) between *Polaribacter* species (Po) and other marine reference *Flavobacteriaceae* (RF) with sequenced genomes (Supplementary Table S3). Data are shown as notched box and whisker plots with boxes representing quartiles Q2 and Q3 and whiskers and extending to 5% and 95% percentiles. Circles represent data outside these boundaries. CBM = carbohydrate-binding module; CE = carbohydrate esterase; GH = glycoside hydrolase; GT = glycosyltransferase; PL = polysaccharide lyase.



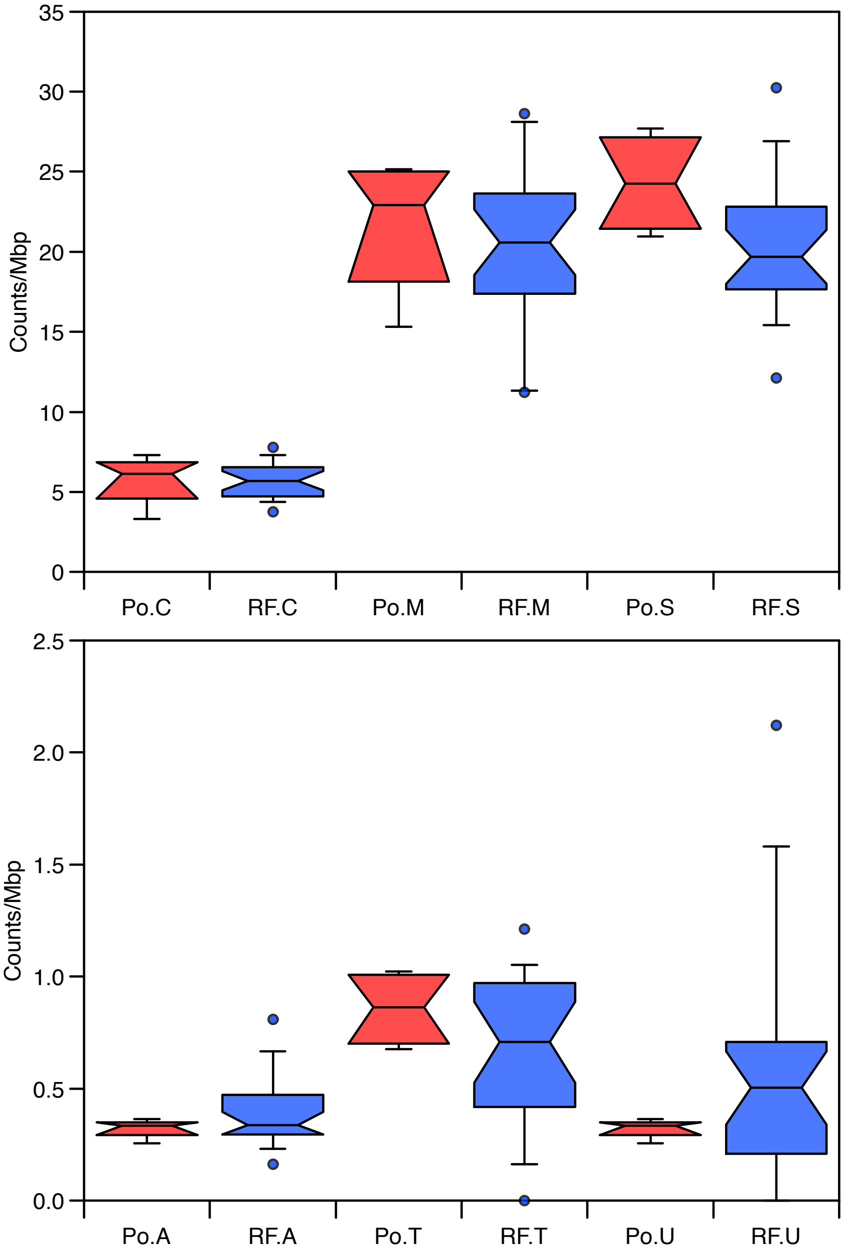
Supplementary Figure S4 PULs of the *Polaribacter* sp. Hel1_33_49 genome (all located on the larger of the two contigs). Numbers in genes indicate family affiliations of glycoside hydrolases, carbohydrate esterases, sulfatases and carbohydrate-binding modules. The asterisk indicates a likely sequencing error in an A-homopolymer stretch that results into two seemingly fused genes.



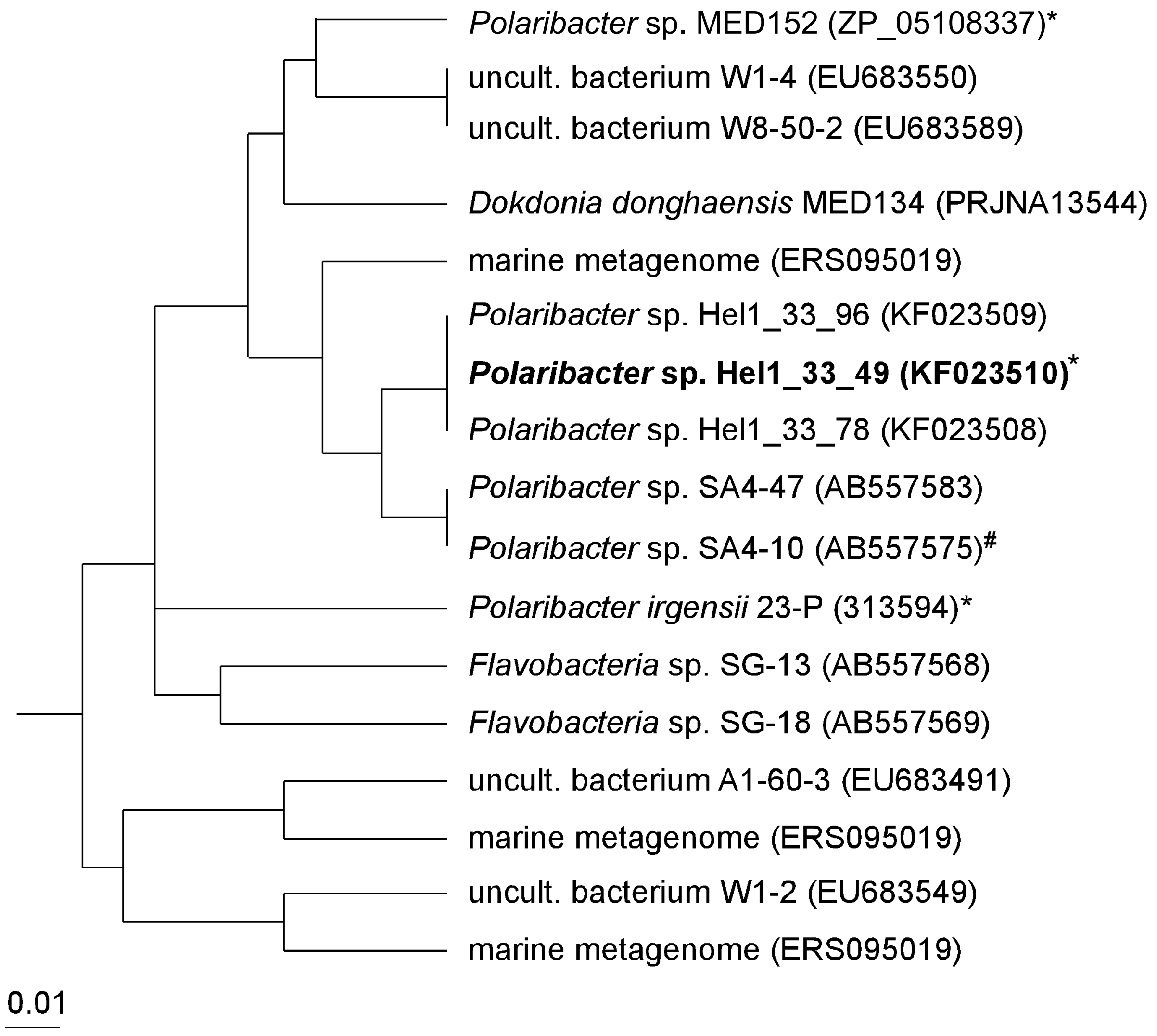
Supplementary Figure S5 PULs and a PUL-like gene cluster (E) of the *Polaribacter* sp. Hel1_85 genome. Superscript characters indicate contigs (a-c = from the largest down to smaller contigs). Numbers in genes indicate family affiliations of glycoside hydrolases, carbohydrate esterases, sulfatases and carbohydrate-binding modules.



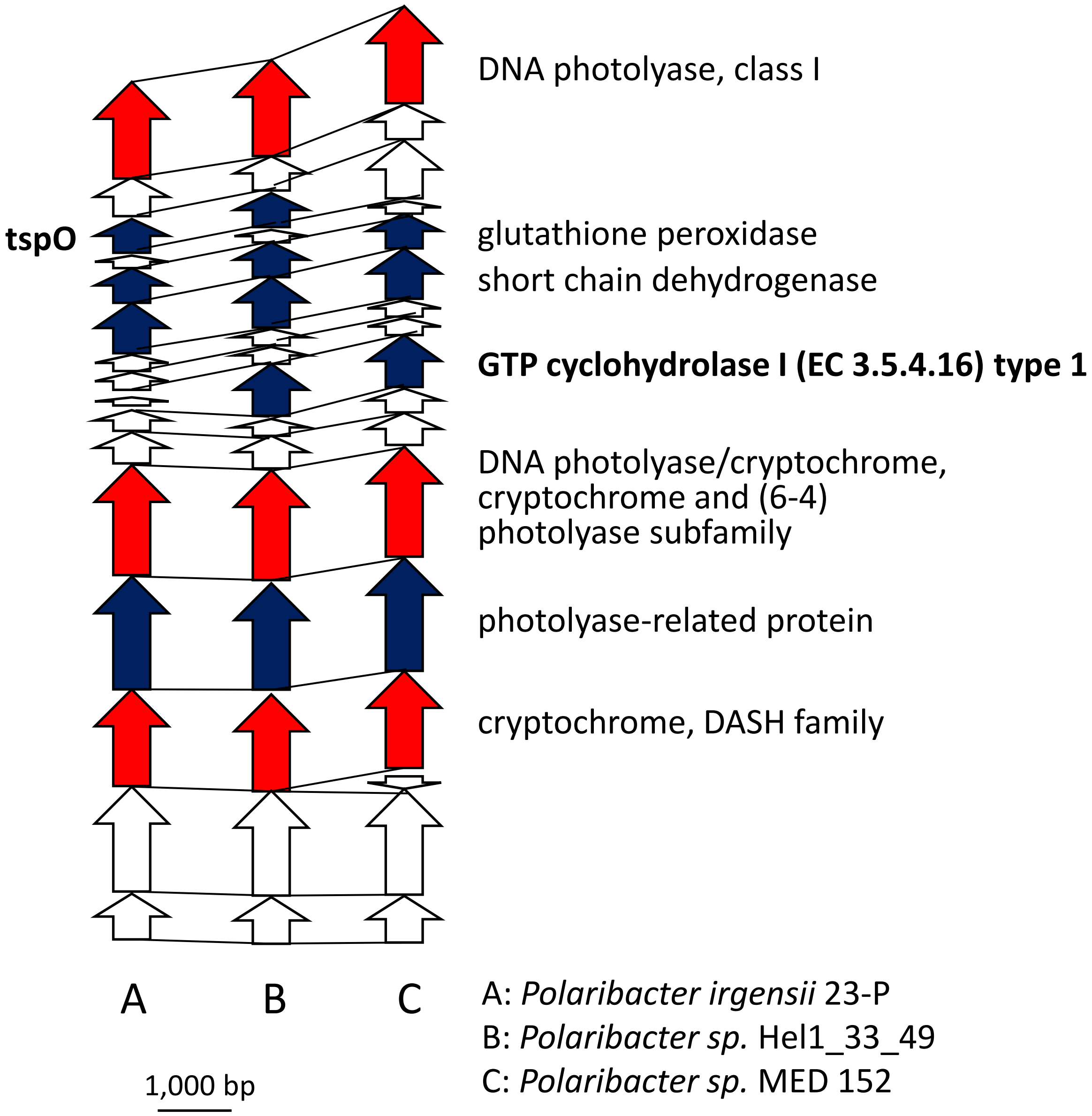
Supplementary Figure S6 Abundant peptidase families in 27 marine *Flavobacteriaceae* with sequenced genomes (Supplementary Table S3). Data are shown as box and whisker plots with boxes representing quartiles Q2 and Q3 and whiskers extending to 5% and 95% percentiles. Circles represent data outside these boundaries. Ninety different MEROPS families were found, but only families with at least three peptidases in the entire dataset are shown. Red triangles indicate the total of 27 families that were universally present in all *Flavobacteriaceae*.



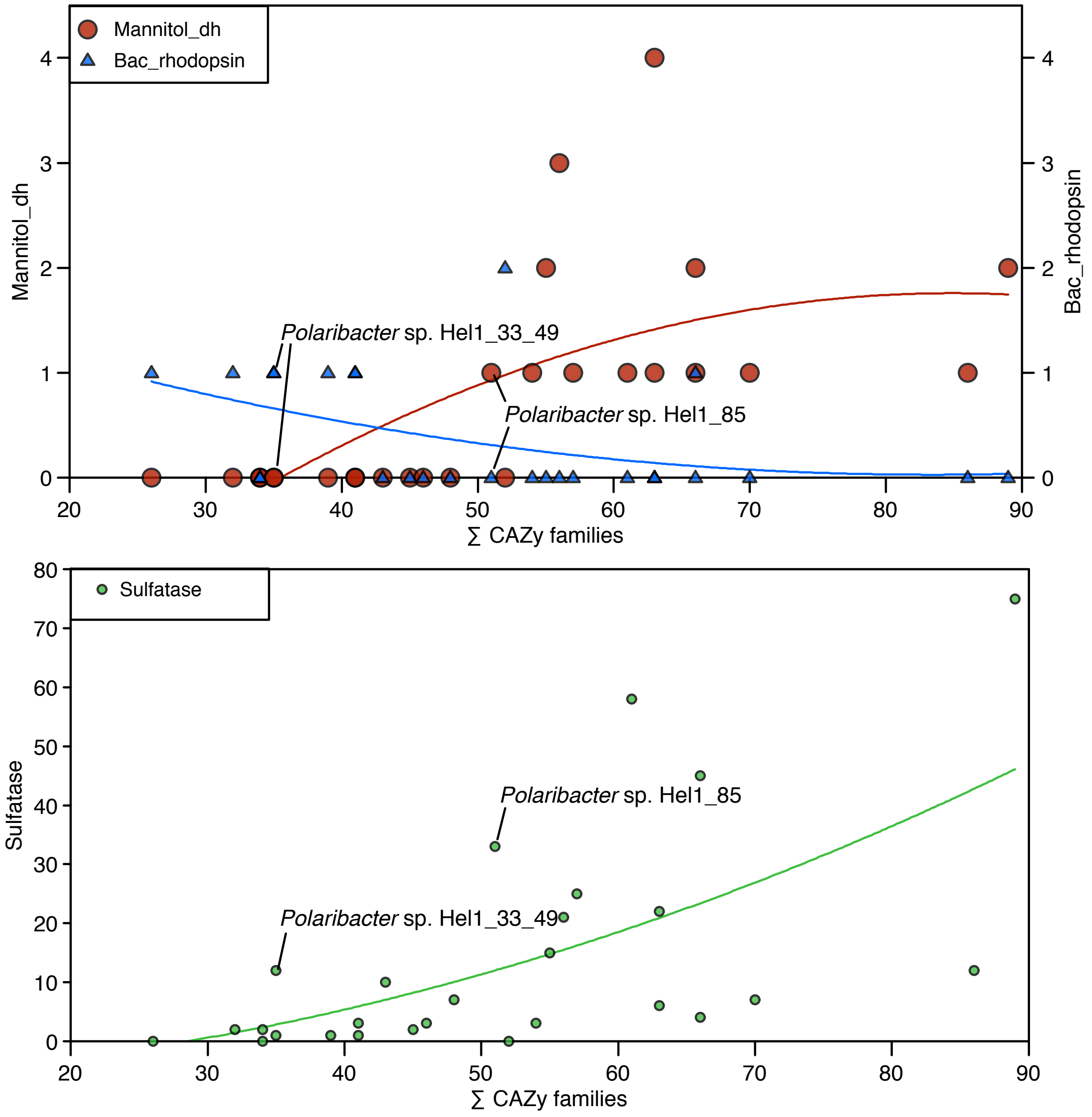
Supplementary Figure S7 Comparison of MEROPS categories (C-, M- S-, A-, T-, U-type peptidases) between *Polaribacter* species (Po) and other marine reference *Flavobacteriaceae* (RF) with sequenced genomes (Supplementary Table S3). Data are shown as notched box and whisker plots with boxes representing quartiles Q2 and Q3 and whiskers extending to 5% and 95% percentiles. Circles represent data outside these boundaries. The abundant cysteine- (C), metallo- (M), and serine- (S) peptidases are shown in the upper panel, and the less abundant aspartic- (A), threonine- (T), and unknown (U) type peptidases in the lower panel.



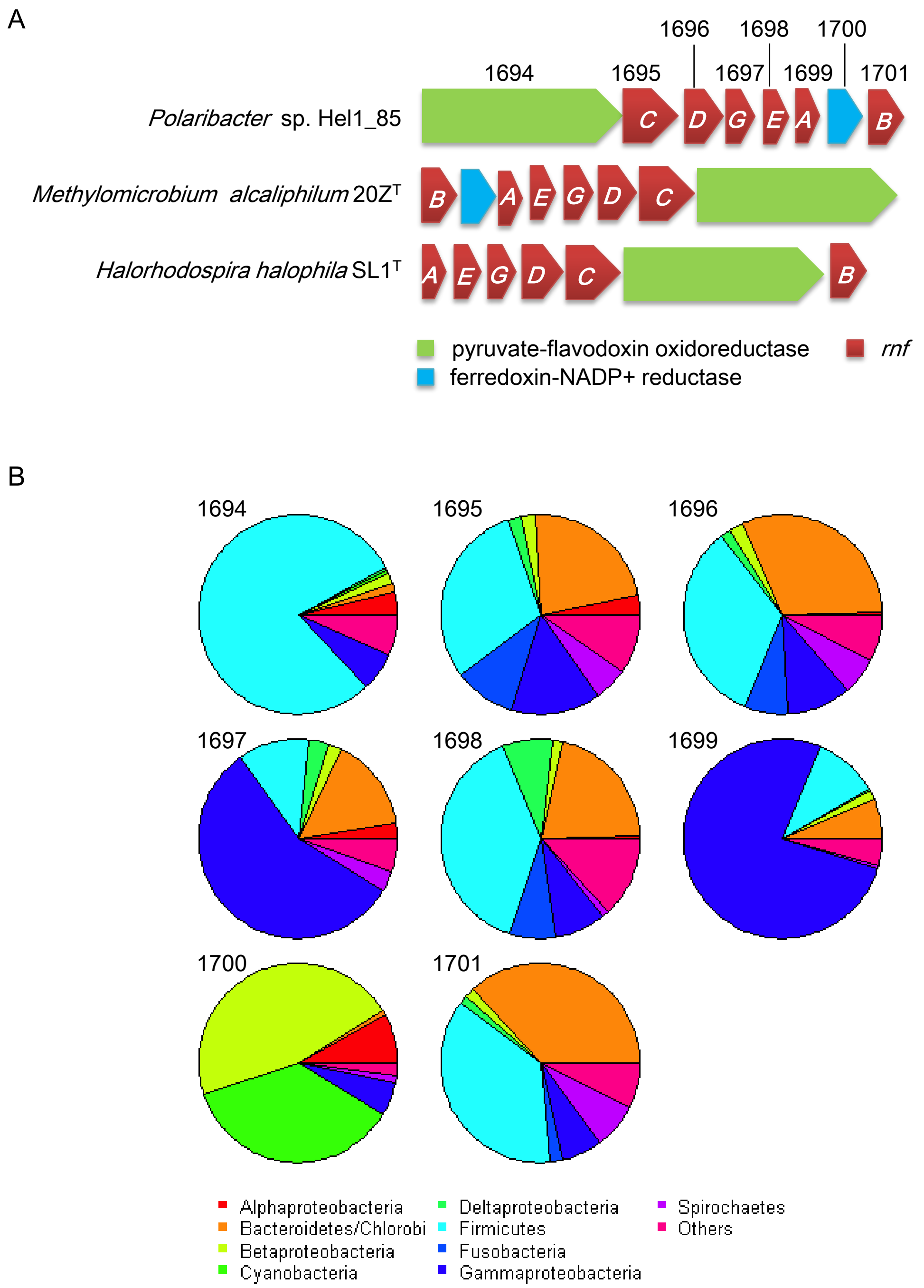
Supplementary Figure S8 Phylogenetic tree of proteorhodopsin (PR) genes sequences of *Polaribacter* sp. Hel1_33_49 and related *Flavobacteriaceae*. PR gene sequences were retrieved from Genbank and aligned using MAFFT. Full-length PR sequences were used to construct phylogenetic trees in Arb using a 40% base conservation filter with the neighbor-joining with Jukes-Cantor correction and the RAxML maximum likelihood methods. A consensus tree was built and partial PR sequences were subsequently added by parsimony. Strains were PR activity was shown are indicated by a hash; strains for which genomes are available are indicated by an asterisk. Bar: 0.01 substitutions per nucleotide position.



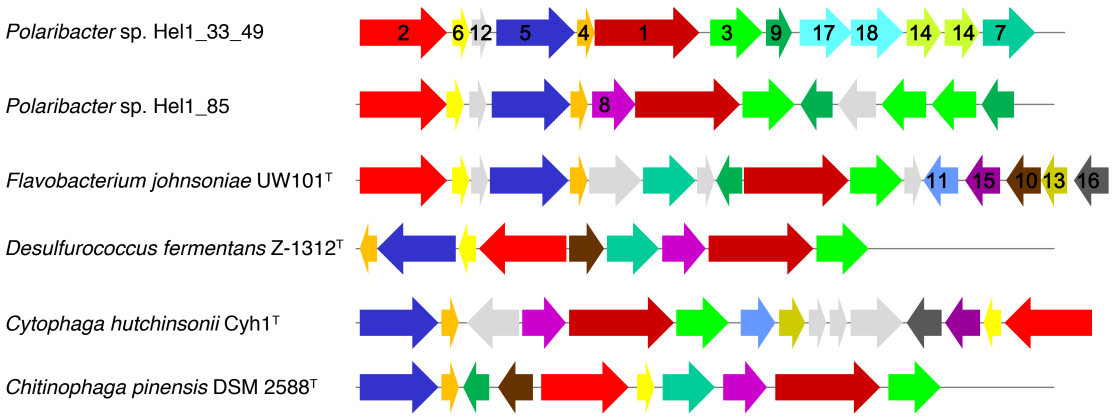
Supplementary Figure S9 Synteny of the DNA photolyase/cryptochrome (red) gene clusters among the three rhodopsin-containing *Polaribacter* strains 23-P^T (A), Hel1_33_49 (B), and MED152 (C). Genes in white are conserved hypotheticals or genes that belong to generic superfamilies, but for which the exact functions are unknown. Genes that are not present in all three strains are depicted in bold.



Supplementary Figure S10 Comparative genomics of 27 *Flavobacteriaceae* genomes (Supplementary Table S3): Relationship between mannitol dehydrogenase, bacteriorhodopsin and sulfatase gene copy numbers (based on matches to the Pfam profiles Mannitol_dh, Bac_rhodopsin with ≤ E-5 and sulfatase with ≤ E-13) and the number of CAZyme families (trend lines: 2nd order polynominal regressions).



Supplementary Figure S11 (A) Structure of the *rnf* operon of *Polaribacter* sp. Hel1_85 and the two most similar *rnf* operons in terms of best BLAST hits from *Methylomicrobium alcaliphilum* 20Z^T and *Halorhodospira halophila* SL1^T. Numbers above genes refer to locus tags of strain Hel1_85. (B) Distribution of phylum-level best BLAST hits for the *Polaribacter* sp. Hel1_85 *rnf* operon indicating lateral acquisition from a gammaproteobacterial species.



Locus	P. sp. Hel1_33_49	P. sp. Hel1_85	Annotation
	PHEL49_	PHEL85_	
2	846	2160	nitrite reductase (NAD(P)H), large subunit
6	845	2159	nitrate reductase (NAD(P)H), small subunit
12	844	2158	conserved hypothetical protein (DUF4202)
5	843	2157	multi-sensor signal transduction histidine kinase
4	842	2156	transcriptional regulator
1	841	2154	periplasmic nitrate reductase/nitrite reductase
3	840	2153, 2150, 2149	rubredoxin
9	839	2152, 2148	transcriptional regulator
17	838	_	nitrate ABC transporter, nitrate-binding protein
18	837	_	nitrate transporter, permease
14	836, 835	_	nitrate transporter, ATP-binding protein
7	834	_	conserved hypothetical protein
8		2155	nitrate/nitrite transporter
11	_	_	nitrate ABC transporter, ATP-binding protein
15	_	_	molybdenum cofactor biosynthesis protein MoaC / molybdenum cofactor biosynthesis protein MoaB
10	_	_	nitrate ABC transporter, permease protein
13	_	_	nitrate/nitrite transporter
16	_	_	uroporphyrinogen-III methyltransferase

Supplementary Figure S12 Clustered assimilatory nitrate reduction genes in the *Polaribacter* sp. Hel1_33_49 and sp. Hel1_85 genomes as well as in other *Flavobacteriaceae*.