Genomes of "*Spiribacter*", a streamlined, successful halophilic bacterium

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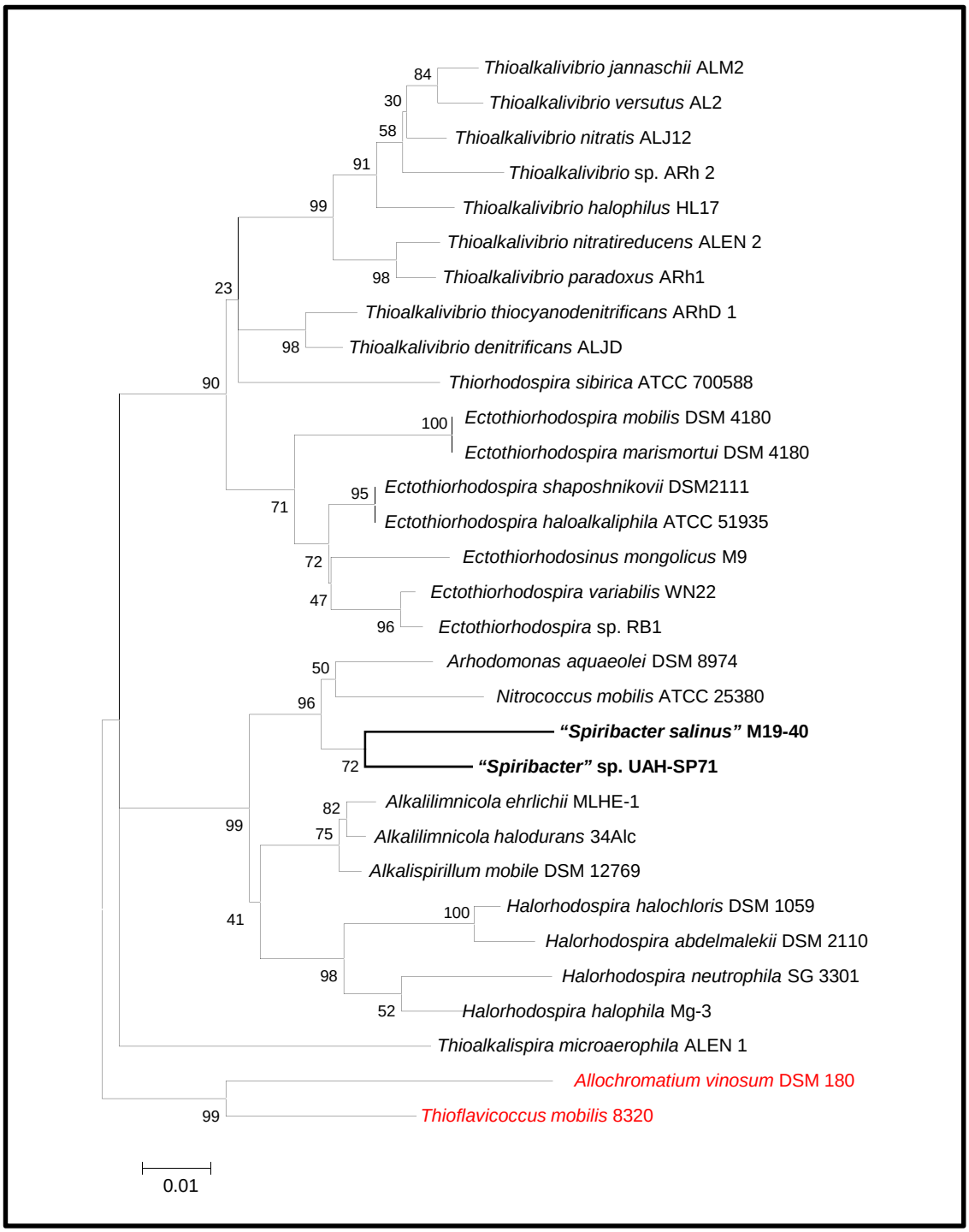
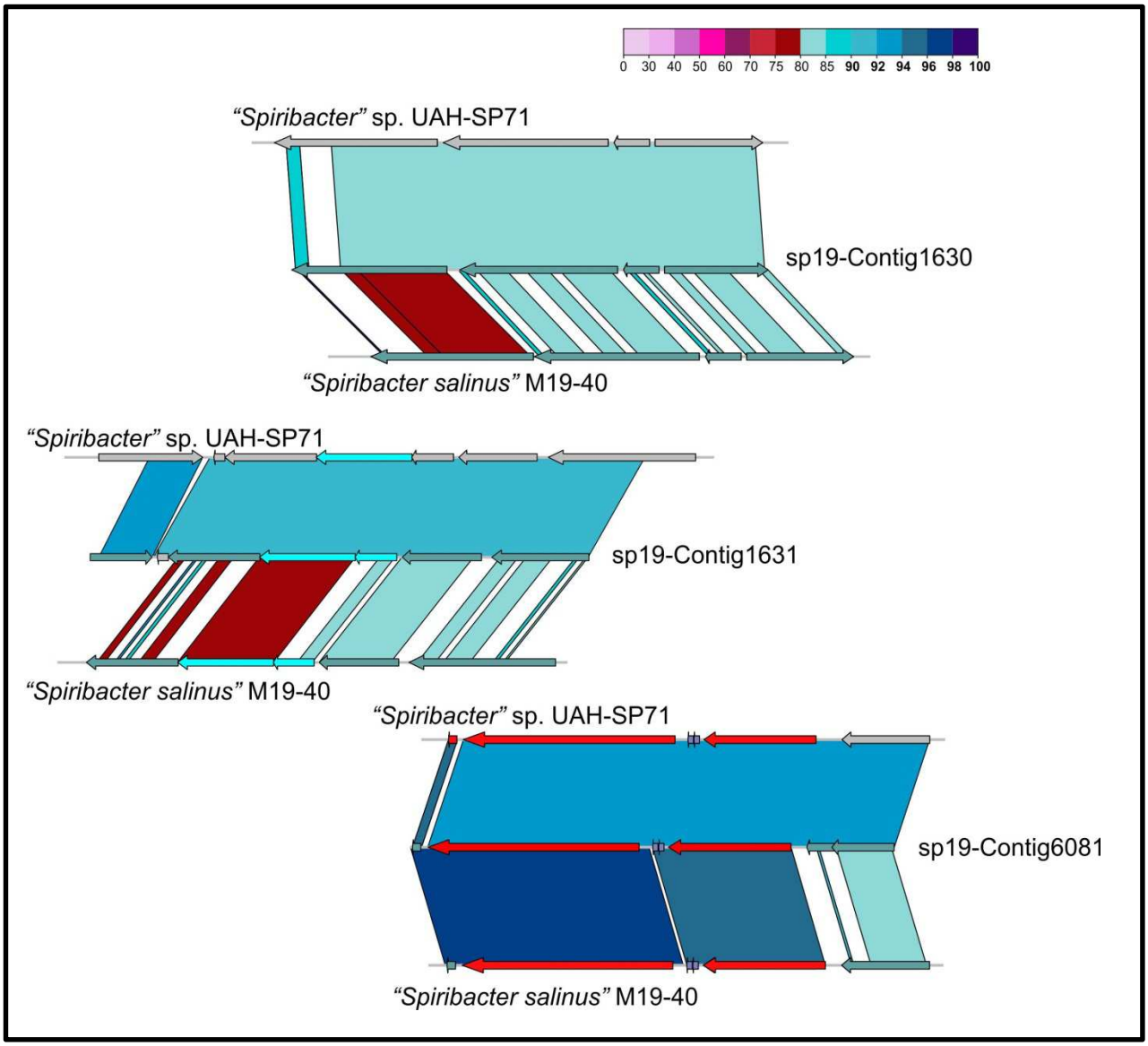
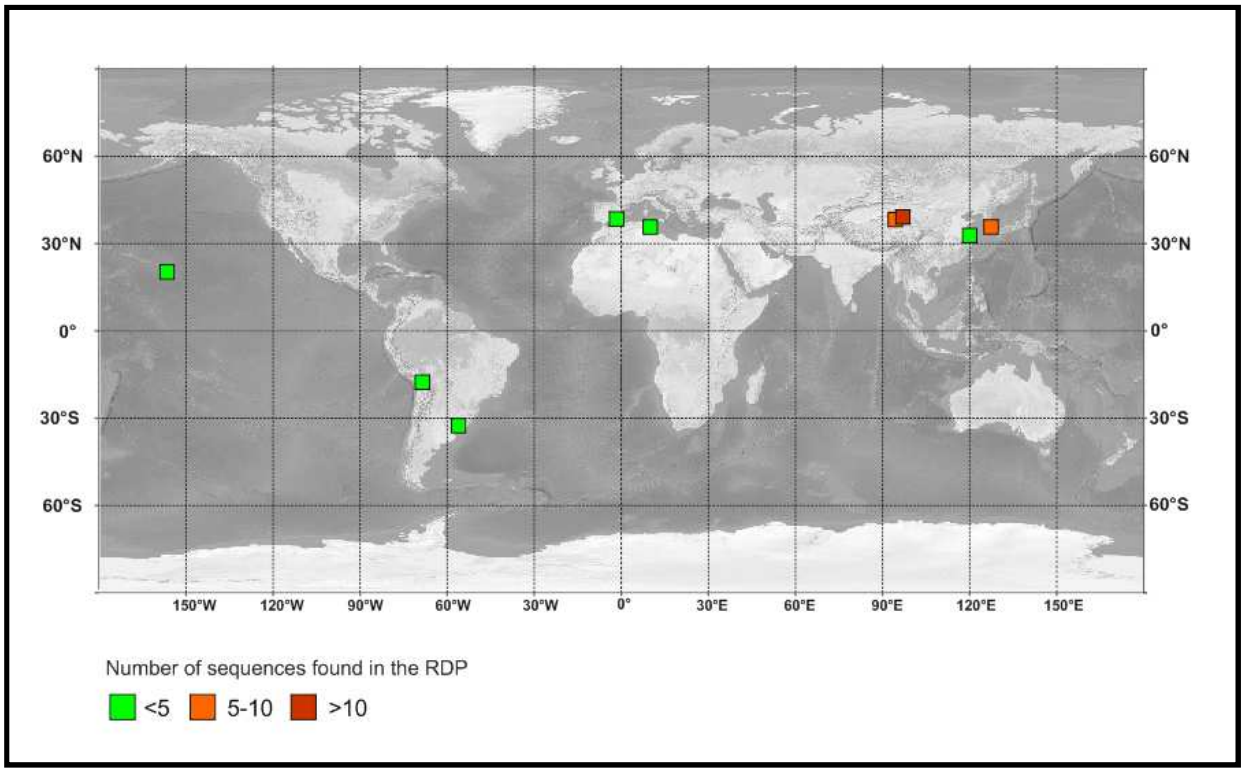
Running Head: "*Spiribacter*", a streamlined halophile



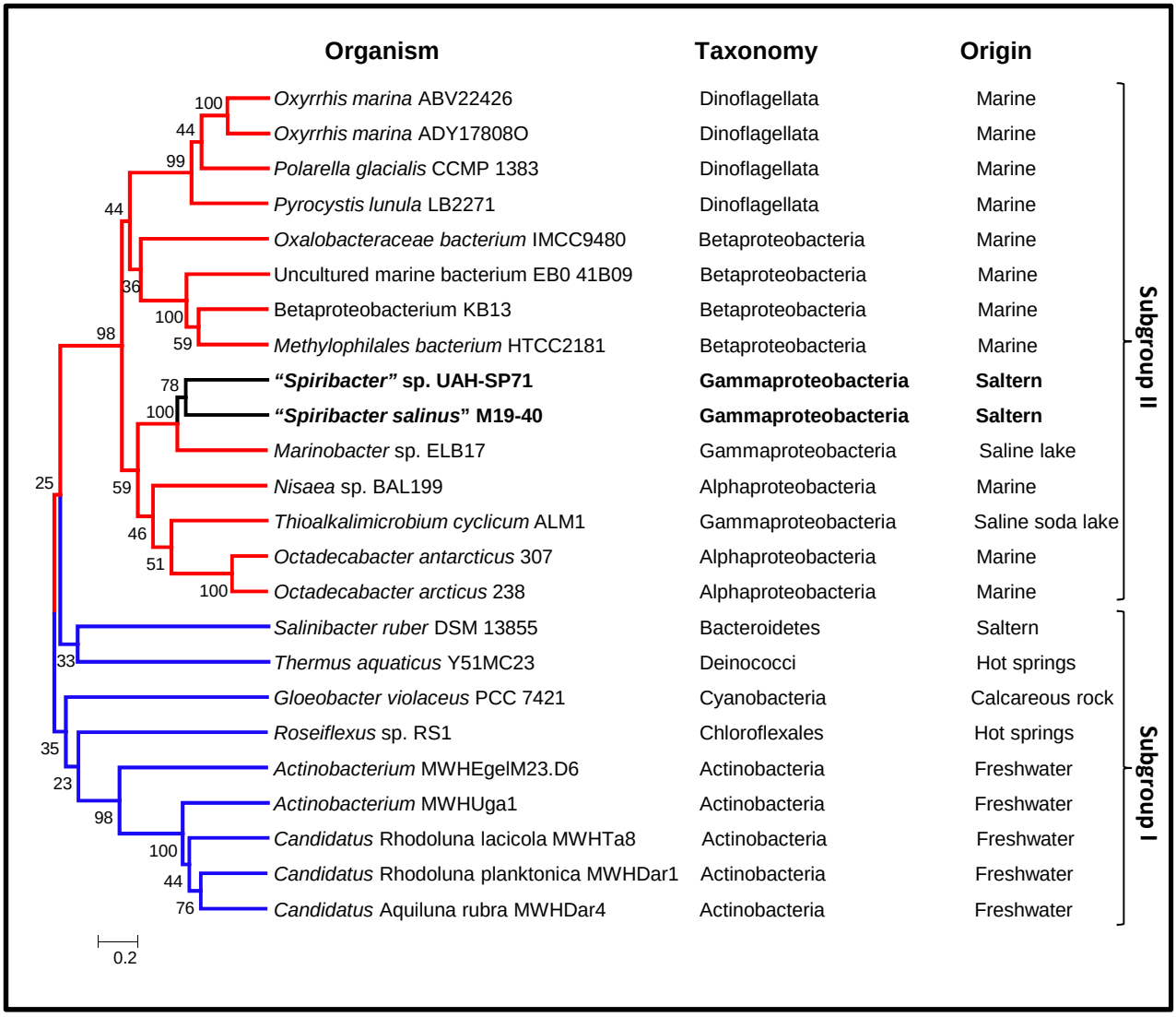
Additional Figure S1: 16S rRNA phylogeny. Maximum likelihood phylogenetic tree based on the comparison of 16S rRNA gene sequences of the *Ectothiorhodospiraceae*. *Allochromatium vinosum* DSM 180 and *Thioflavicoccus mobilis* 8320, belonging to the *Chromatiaceae* were used as outgroup and are shown in red. Bootstrap values are indicated at the nodes.



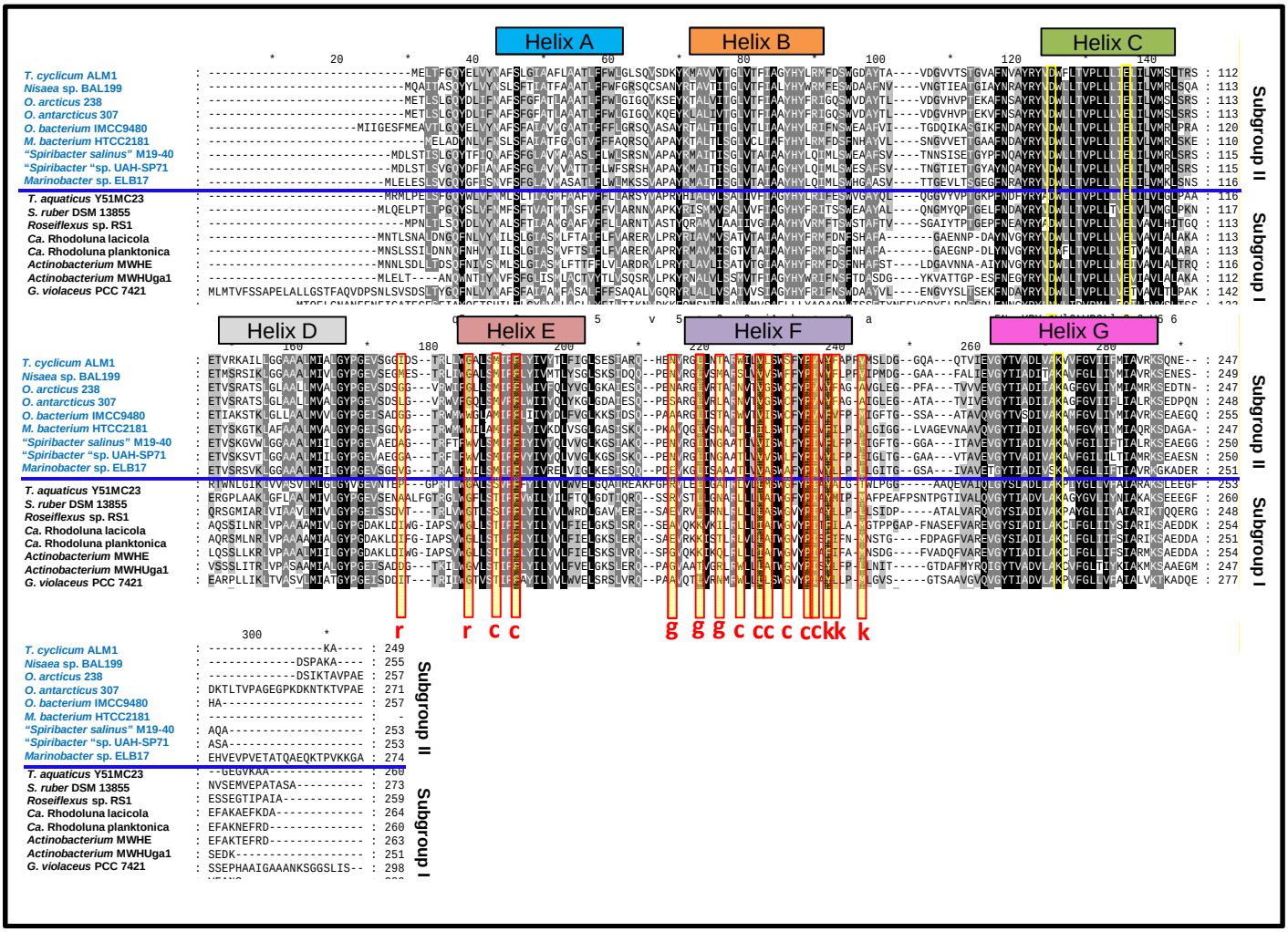
Additional Figure S2: BLASTN comparisons of metagenomic contigs from 19% Santa Pola to "*Spiribacter*" genomes. The metagenomic contigs are shown in the middle. A color key for the similarity is shown on the top right.



Additional Figure S3: Global distribution of Spiribacter 16S rRNA gene sequences. Locations where 16S rRNA gene sequences from the Ribosomal Database Project were found (>97% identical, >300 bp) are indicated by colored boxes. The color code indicates the number of sequences found at each location. The map is a modified version of a freely available map from http://www.naturalearthdata.com.



Additional Figure S4: Phylogenetic tree of the two xanthorhodopsins found in both "*Spiribacter*" with all the xanthorhodopsins available. Taxonomy and origin of isolation of each strain are also shown.



Additional Figure S5: Xanthorhodopsin amino acid sequence alignment. Multiple alignments of all the predicted aminoacid sequences of the two xanthorhodopsin subgroups. Rectangles over the sequence indicate predicted transmembrane regions. Proton acceptor and donor and the conserved lysine linked to the cofactor retinal are marked by a rectangle with a yellow line. Yellow rectangles with red line indicated the residues that interact with the keto-carotenoid identified by [69]. Maintaining nomenclature, the letters c, g, k and r, indicate contact with the chain, glucoside, keto group and ring of the carotenoid, respectively.