Figure S1. Multiple sequence alignments of putative transcriptional regulators FciA (A) and FciB (B), both containing an AraC-like α-helix-turn-α-helix (HTH, IPR018060) domain, and FciC (C) with a predicted ribbon-helix-helix (IPR010985 and IPR013321). Shading represents identical amino acid in at least 70% of the sequences. Protein domains, framed by a black rectangle, were determined using InterProScan against Synechococcus sp. RS9916 sequences, used as reference. Ab initio modeling using Phyre2 indicated that 77% of FciA (263 of 342 residues) and 50% of FciB (158 of 316 residues) from Synechococcus sp. RS9916 could be modeled with >90% confidence to the AraC/XylS family. Furthermore, 78% of FciC (42 of 55 residues) were modeled based on the CopG-like family (Gomis-Rüth et al., 1998).