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 2 **Supplemental Figure 10.** Congruence of maximum likelihood phylogeny of GlgA2 (**A**) and 16S RNA (**B**). To better appreciate the (relative)  
 3 congruence between GlgA2 tree (**A**) and 16SRNA tree (**B**), the same trees as figure S1 were positioned in front of each other. Parallel lines highlights  
 4 congruence while disruption of such lines highlights congruence disruption. The groups colored with the same color show an appreciable level of  
 5 topological congruence between their GlgA2 sequence (**A**) and their 16S RNA (**B**). Imperfect congruence between both trees can result either from  
 6 LGT among cyanobacteria or can result from signal erosion problems witnessed selectively in the GT5 glucan synthase phylogenies. Such

7 disruptions are more evident in the deepest branches. Low bootstrap values are due both to signal erosion and also to the patchy distribution of  
8 GlgA2.  
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