



Supplementary Figure S2. Maximum likelihood phylogeny of *Prochlorococcus* and *Synechococcus* proteins based on 100 resamplings of 100 randomly concatenated single-copy core proteins. Bootstrap values (total 100) were calculated using maximum likelihood (first value at each node) and neighbor joining (second value at each node), with dashes representing maximum likelihood topology unsupported by most of the neighbor joining trees.