Additional file 1. Phylogeny of chlorophycean taxa inferred using nucleotide data sets assembled from 69 protein-coding and 29 RNA-coding genes.

The tree presented here is the best-scoring ML tree inferred using the PCG12RNA data set under the GTR+Γ4 model. Support values are reported on the nodes: from left to right, are shown the BS values for the analyses of the PCG12RNA and PCG123degenRNA data sets. Black dots indicate that the corresponding branches received BS values of 95% in the two analyses; a dash denotes a BS support lower than 50%. The scale bar denotes the estimated number of nucleotide substitutions per site.