



supp. Fig. S1. Phylogenetic Bayesian consensus tree (WAG+F+Γ8+I model) based on 74 GAPDH sequences and 325 amino acid positions. The statistical support for internal nodes was determined by bootstrap analyses or posterior probabilities (BI; given as % values) and is indicated at the corresponding branches. Support values ≥ 30% and posterior probabilities ≥ 70% are shown. BI, Bayesian inference; ML, maximum likelihood; NJ, distance; MP, maximum parsimony. Capital letters at nodes specify the following statistical support values (BI|ML|NJ|MP): **GapB Streptophyta:** (A) 97|45|44|-; (B) -l-l-l-; (C) 76|41|37|30; (D) 89|l-l-; (E) 98|70|86|74; (F) -l40|45|31; (G) 100|l-l-l-; (H) -l-l-l-; (I) 100|55|l-40; (J) 100|72|75|59; (K) -l60|68|53; (L) 100|88|92|90; (M) 73|64|7|140; (N) 100|42|39|44; (O) 100|71|66|67; (P) 97|31|l-; (Q) 94|39|34|-; **GapA Streptophyta:** (A) 73|32|37|41; (B) 73|l-l-; (C) 100|92|94|92; (D) -l4|1|67|-; (E) -l-l-l-; (F) 72|l-l-; (G) 100|100|98|97; (H) 100|87|94|87; (I) 99|74|84|65; (J) 100|44|l-46; (K) -l-l-l-; (L) 100|88|91|77; (M) -l34|l-l-; (N) -l-l-l-; (O) 80|l-l-; (P) 100|99|100|100; (Q) 91|61|51|45; (R) 91|50|54|32; (S) -l-l-l-l-; (T) 82|31|l-l-; (U) 98|44|51|l-; (V) 99|49|l-l-; **GapA Chlorophyta:** (A) 100|100|100|100; (B) 74|57|47|60; (C) -l-l-l-; (D) -l-l-38; (E) 99|48|36|57; (F) 88|l-l-; (G) 99|64|81|46; **GapA Rhodophyta:** (A) 100|100|100|100; (B) -l-l-33; (C) -l49|l-47. **gap2 Cyanobacteria:** (A) 96|41|43|43; (B) 100|91|96|81; (C) 100|l-l-; (D) -l-l-; (E) 97|l-l-; (F) 100|43|33|-; (G) 100|100|100|100; (H) 91|l-57|-; (I) 100|98|100|98; (J) 96|70|50|43; (K) 80|l-l-; (L) 75|l-l-; (M) 99|35|62|-; (N) 100|51|l-52.