

### SUPPLEMENTARY FIGURE 3

Phylogenetic relationships of cyanobacteria derived from neighbor-joining analysis of amino acid sequences of the *trpA* (89 taxa, 235 characters), *trpB* (89 taxa and 395 characters), *trpC* (95 taxa and 233 characters), and *trpD* (84 taxa and 294 characters) genes. Numbers next to selected nodes represent non-parametric bootstrap support values based on 500 replicates but only those above 70% are marked. Scytonemin-operon gene homologue sequences are shown in blue type, supernumerary homologues (beyond housekeeping and scytonemin-associated) and those in remnant scytonemin operons are in green type.

