

Figure S1. The Δ -9 desaturases Likelihood/ Bayesian tree. Supported branches are labeled with corresponding values of bootstrap and posterior probability. Predicted subcellular locations are displayed.

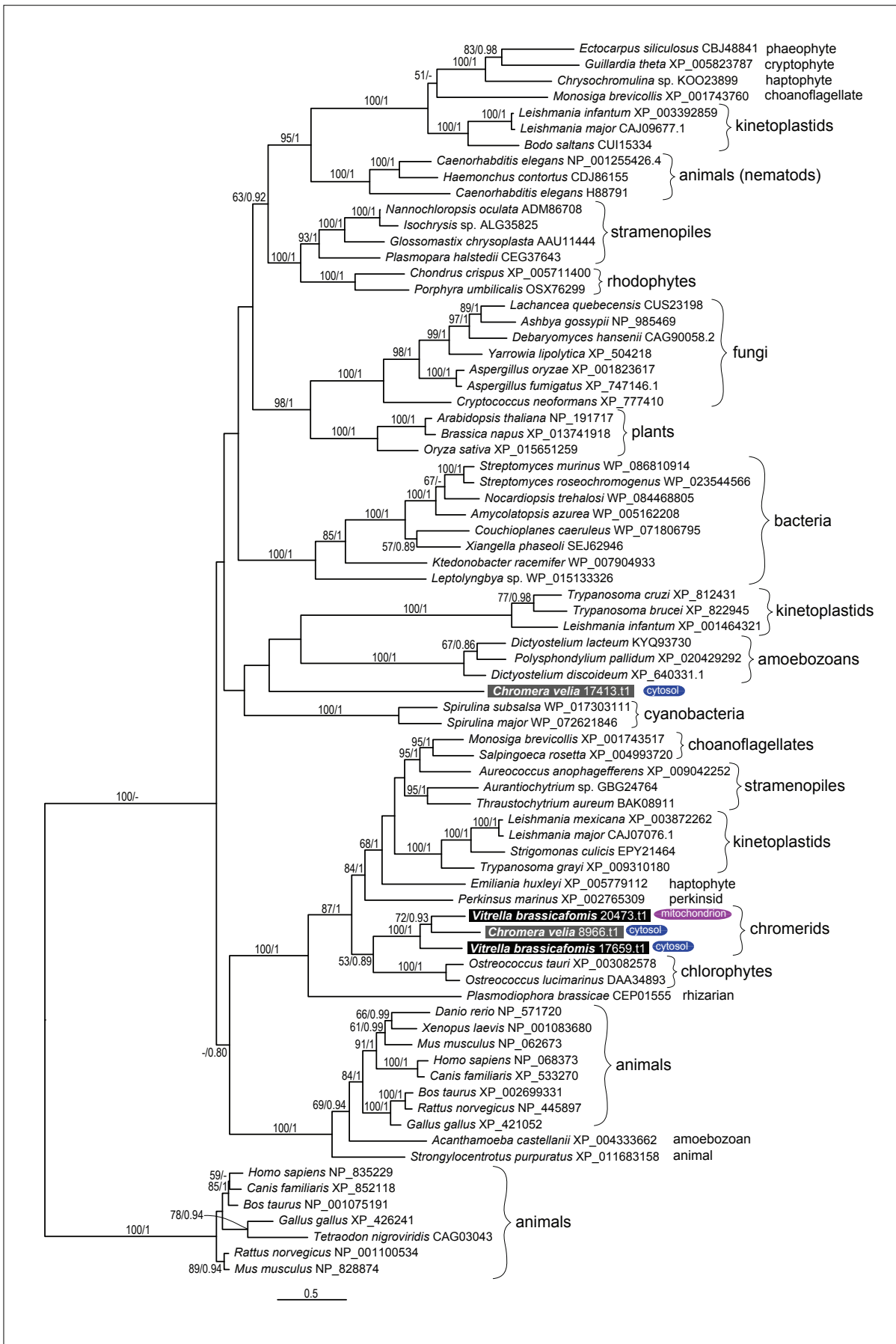


Figure S2. The $\Delta 5/6$ (front-end) desaturase Likelihood/ Bayesian tree. Supported branches are labeled with corresponding values of bootstrap and posterior probability. Predicted subcellular locations are displayed.

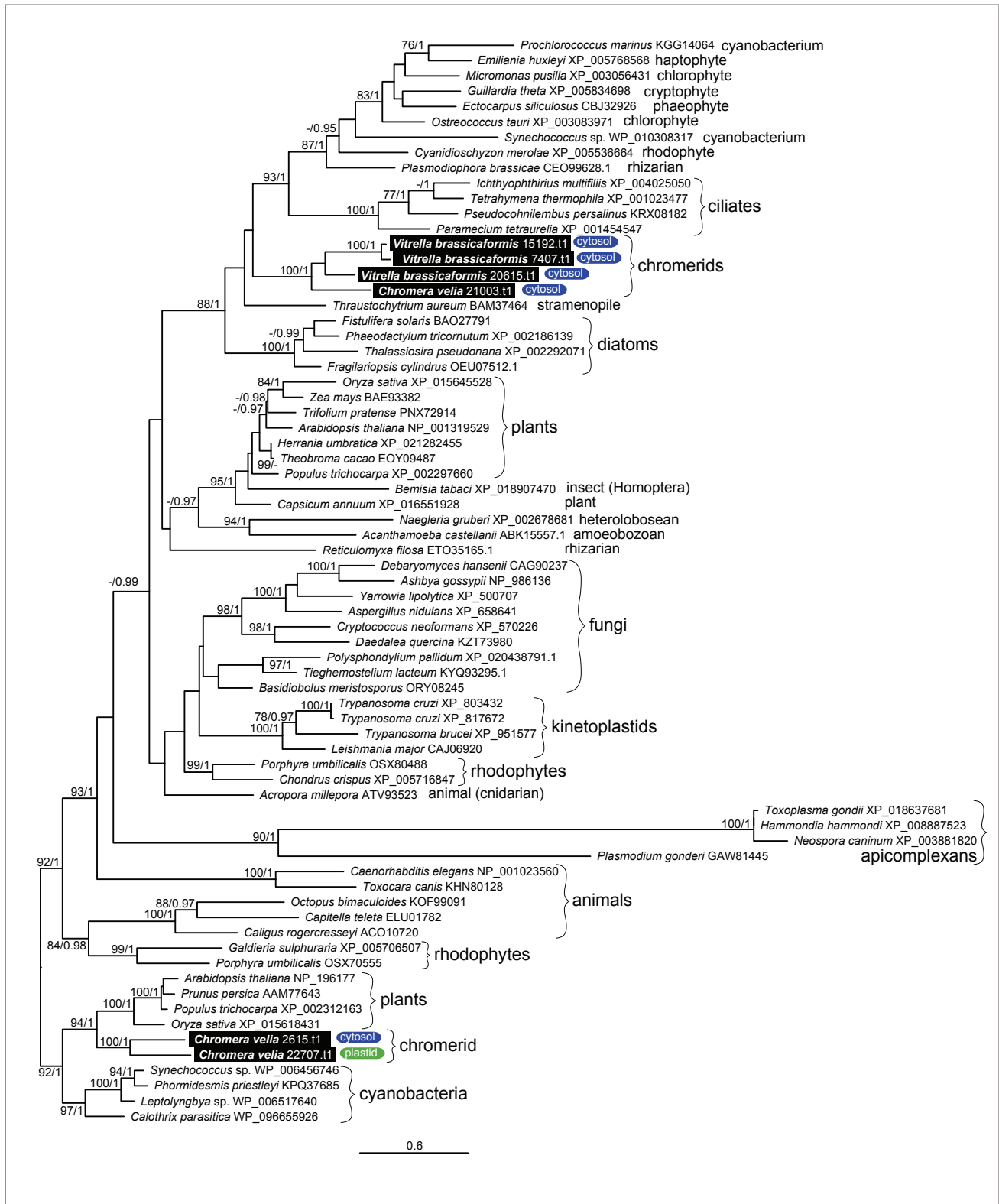


Figure S3. The omega ($\Delta_{12/15}$) desaturase Likelihood/ Bayesian tree. Supported branches are labeled with corresponding values of bootstrap and posterior probability. Predicted subcellular locations are displayed.

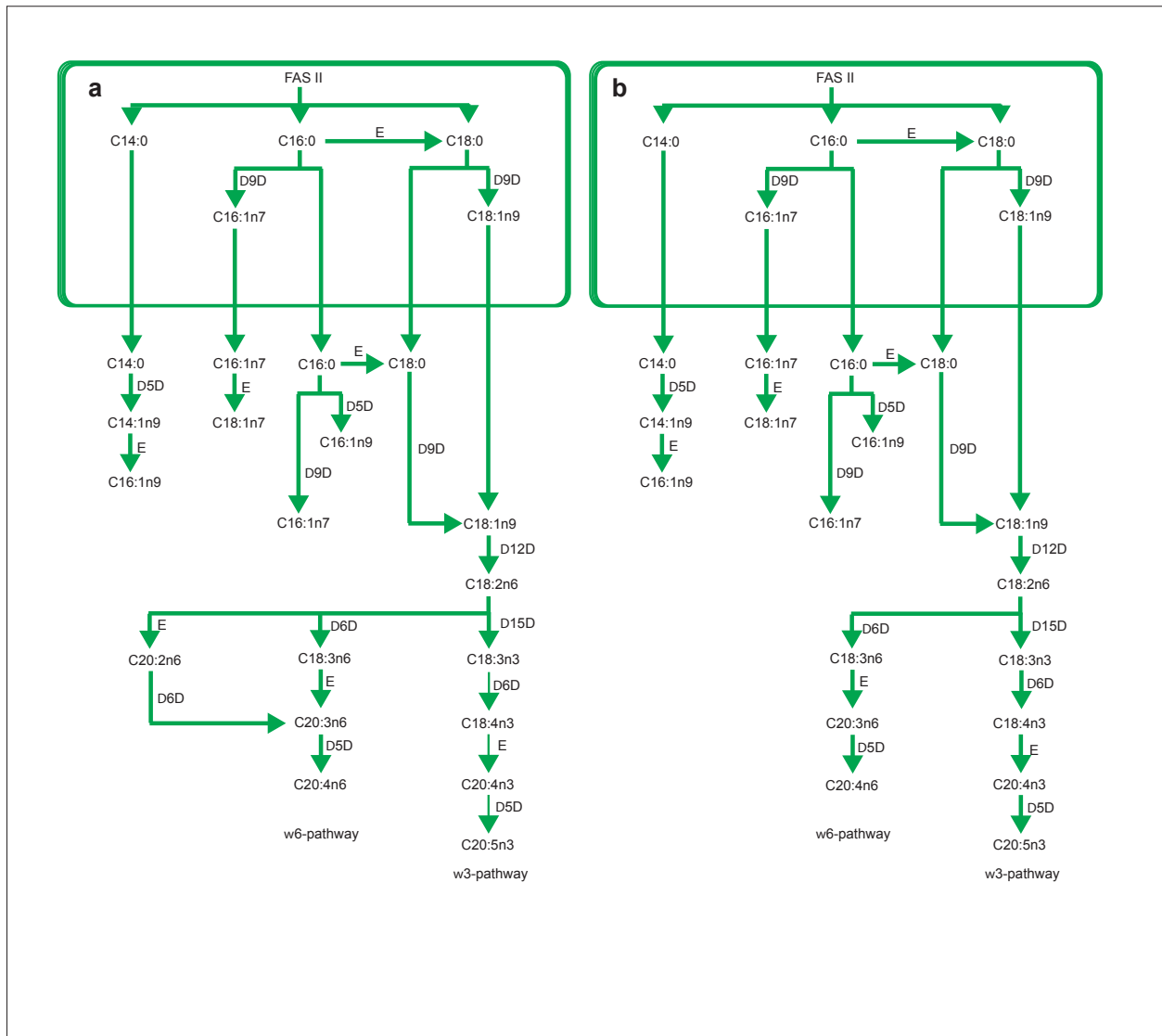


Figure S4. The model of fatty acid biosynthesis in *Chromera velia* (A) and in *Vitrella brassicaformis* (B).

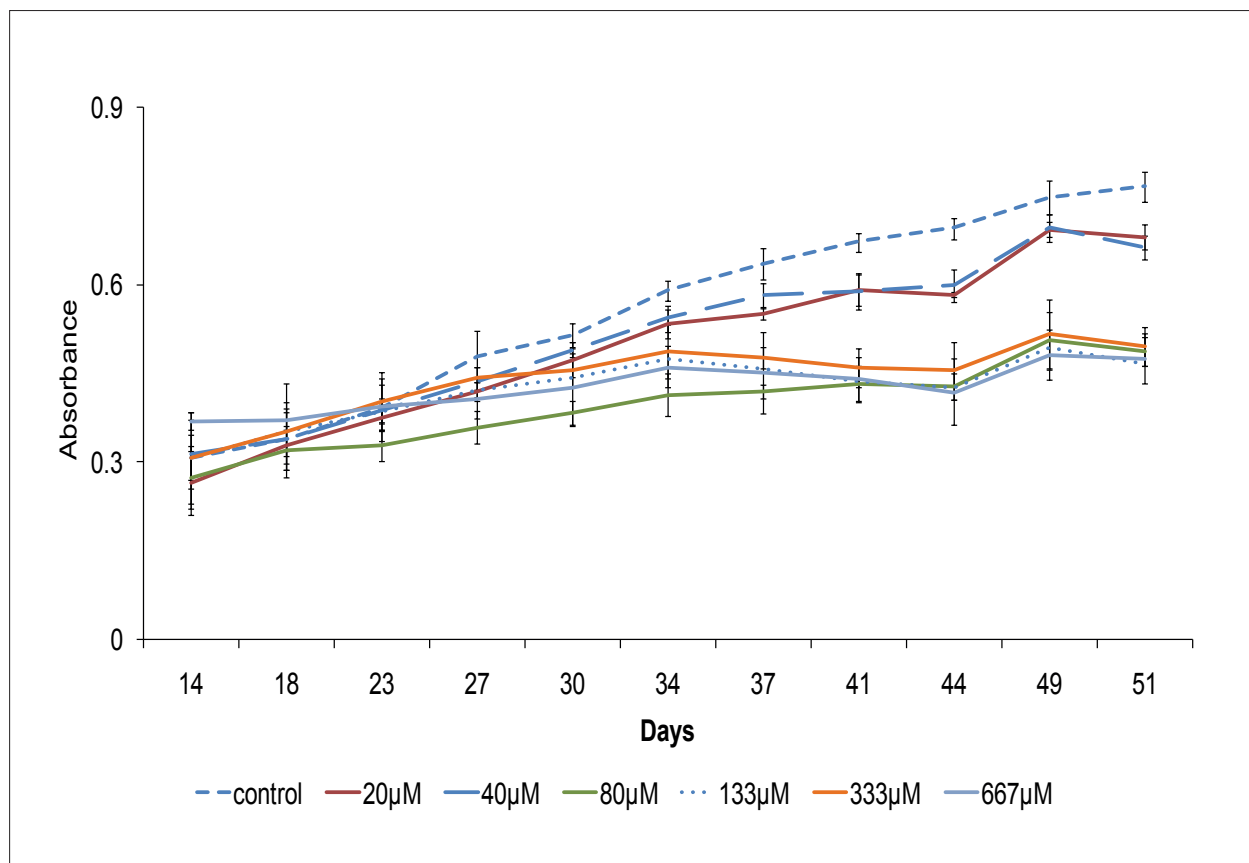


Figure S5. Growing curves of *Chromera velia* treated by the various concentration of Triclosan recorded by the Tecan instrument (n=5).

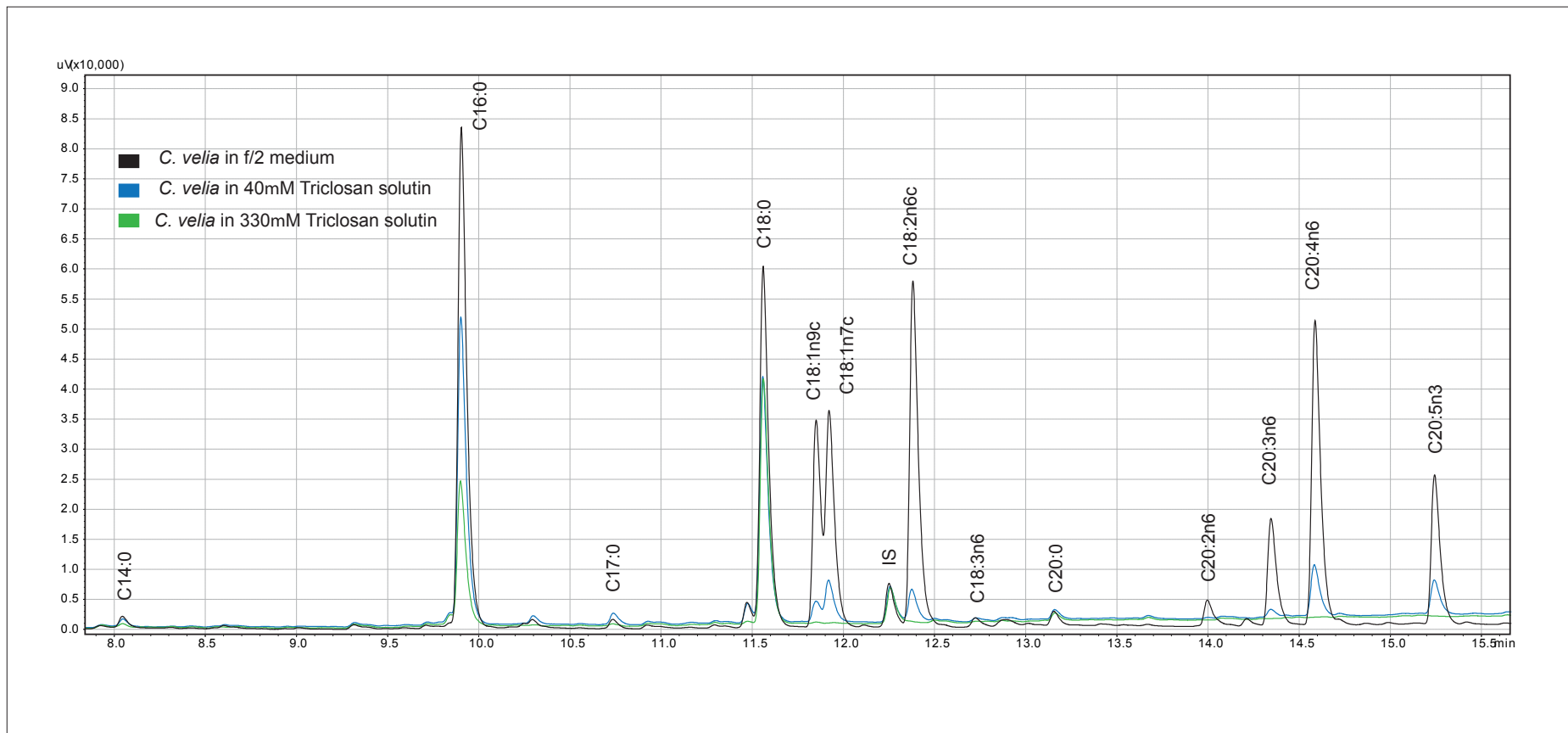


Figure S6. Spectra of fatty acid composition changes after Triclosan treatment obtained by GC FID

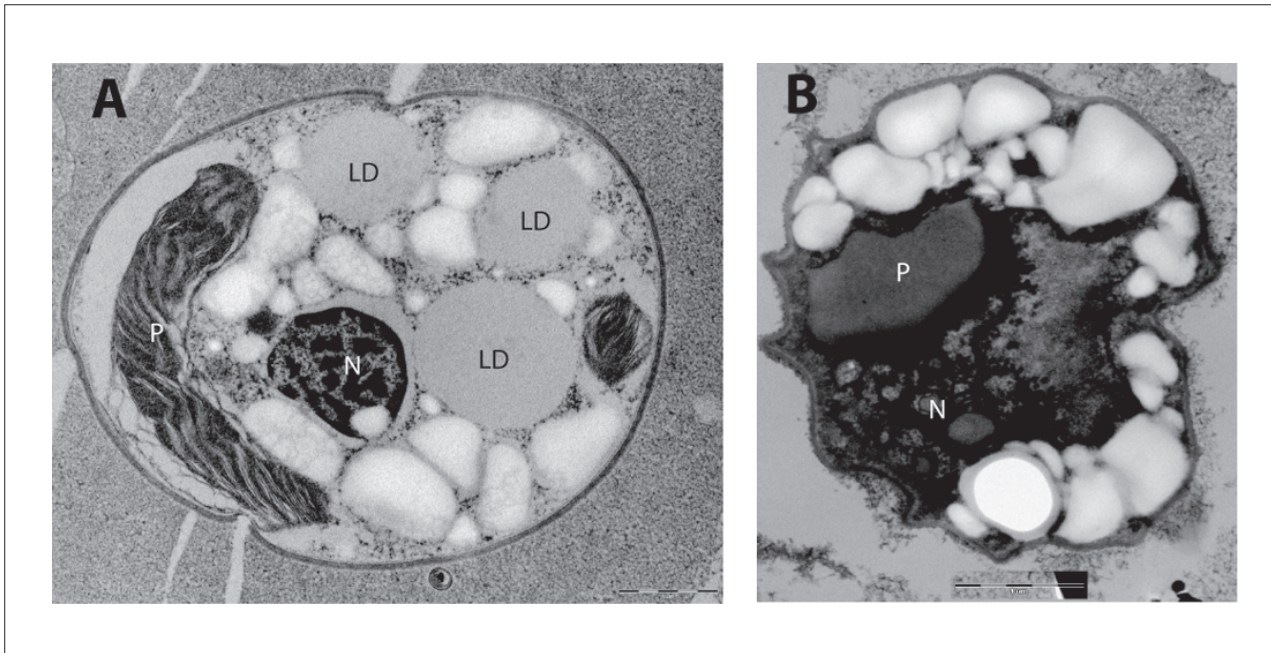


Figure S7. Transmission electron microscopy of *C. velia* grown in standard f/2 medium (A) and grown in f/2 medium with 333 μ M Triclosan (B), where the cell is deformed and the inner structure is collapsed. LD – lipid droplets; N – nucleus; P – plastid

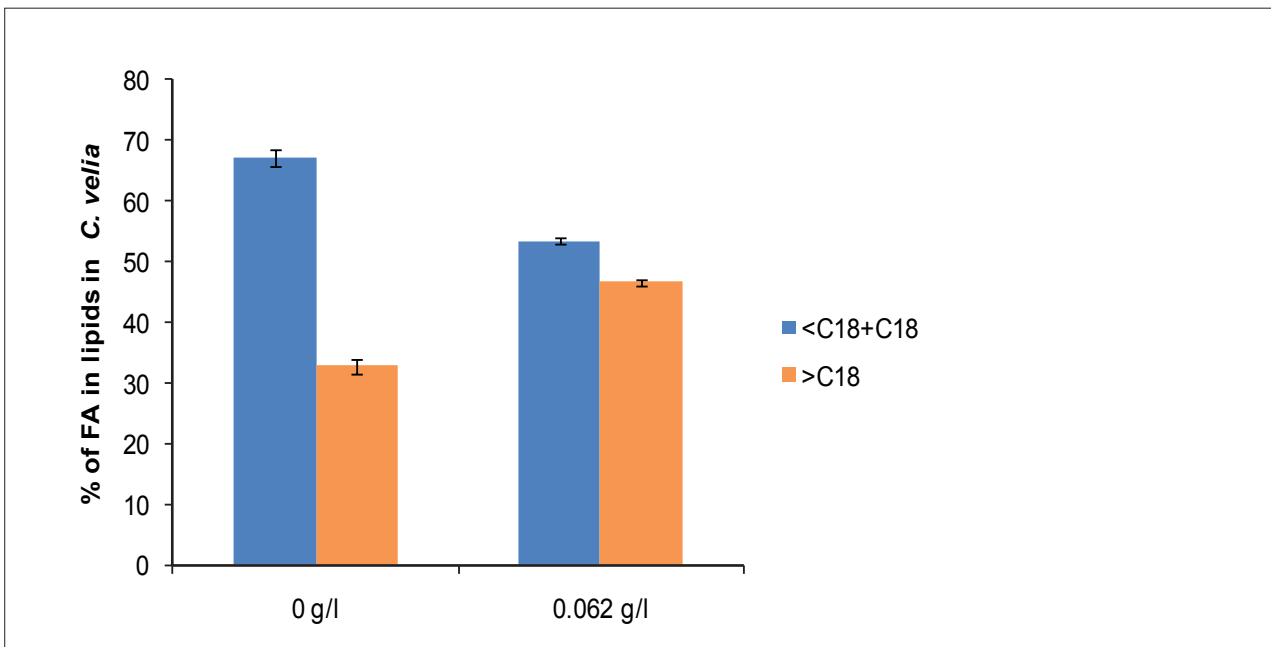


Figure S8. The ratio of fatty acids shorter than C18 and C18 (blue) and longer than C18 (orange) in *C. velia* during nitrogen deprivation and repletion (n=5). Data were obtained by GC FID.

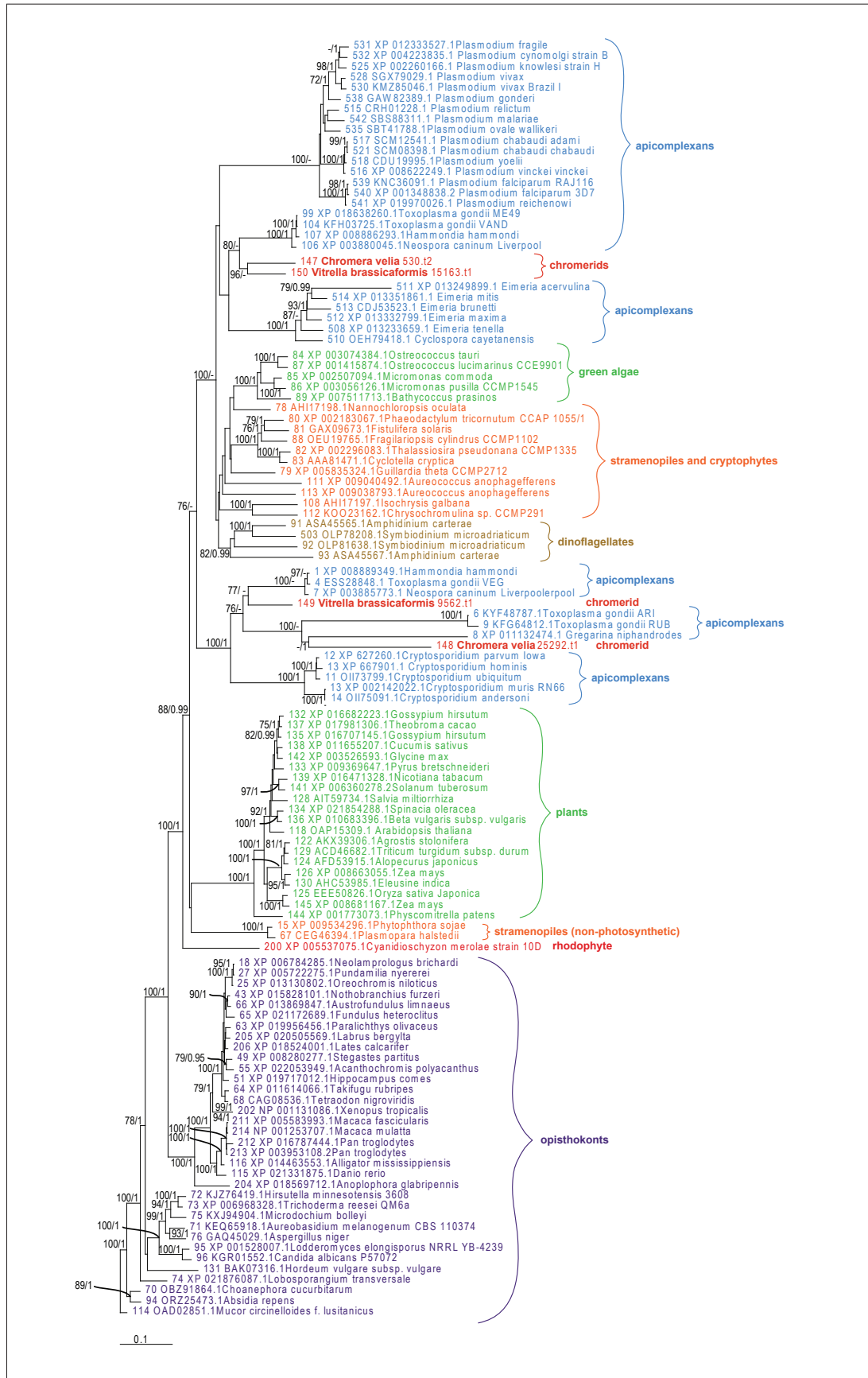


Figure S9. Maximum-likelihood phylogenetic tree of Acetyl-CoA decarboxylases. Supported branches are labeled with corresponding values of ML bootstraps and Bayesian posterior probabilities L.

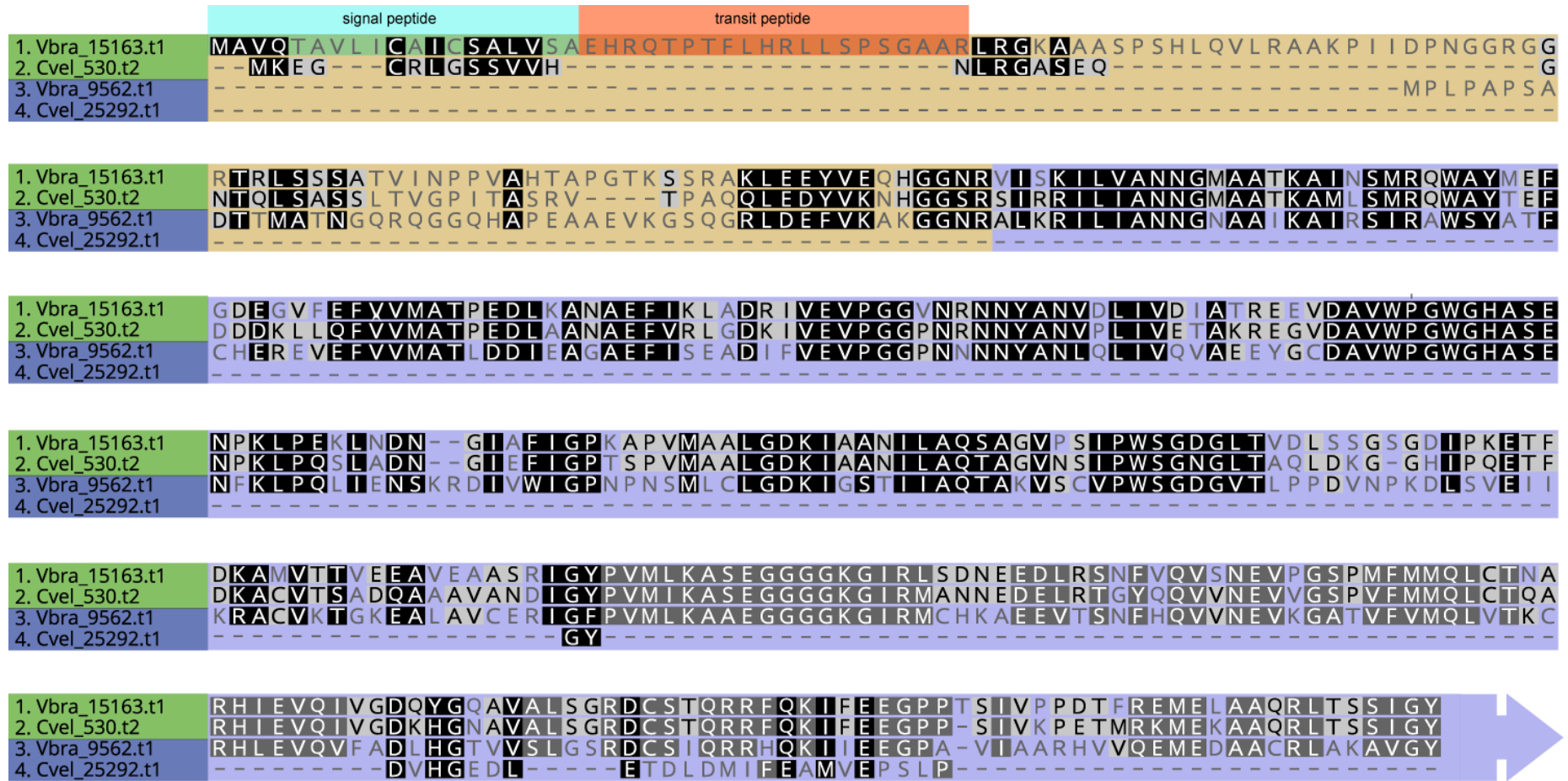


Figure S10. The alignment of ACCases of chromerids showing the first 408 amino acid residues with the N-terminal motif similarity shared between plastid-targeted gene variants. Plastid targeted variants are highlighted in green, cytosolic in blue. The bright blue field highlights the actual functional-domain part of the genes.