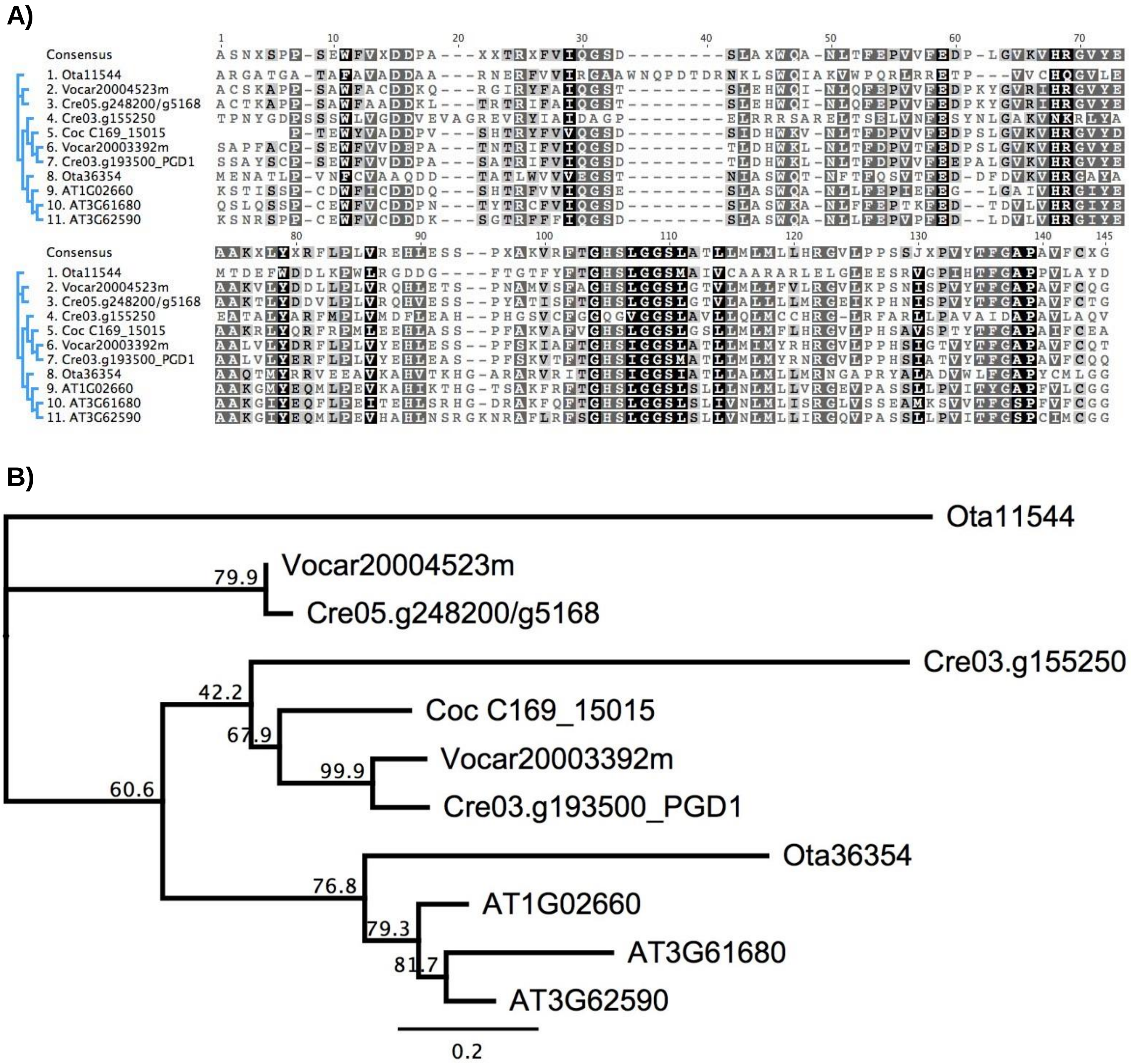

Figure S1 Phylogeny of *PGD1*-related genes. A) Alignments of N-terminal lipase domains. Shading is based on BLOSUM62 homology matrix. AT, *Arabidopsis thaliana*; Cre, *C. reinhardtii*; Coc, *Coccomixa subellipsoidea* C169; Ota, *Ostreococcus tauri*; Vocar, *Volvox carteri*. In addition to the lipase domain, *PDG1* and Cre05.g248200, but not Cre03.g155250, share a C-terminal homology domain. B) Bayesian tree based on N-terminal lipase domain alignments. Scale bar: gamma-corrected amino acid substitution rate based on WAG matrix per site.

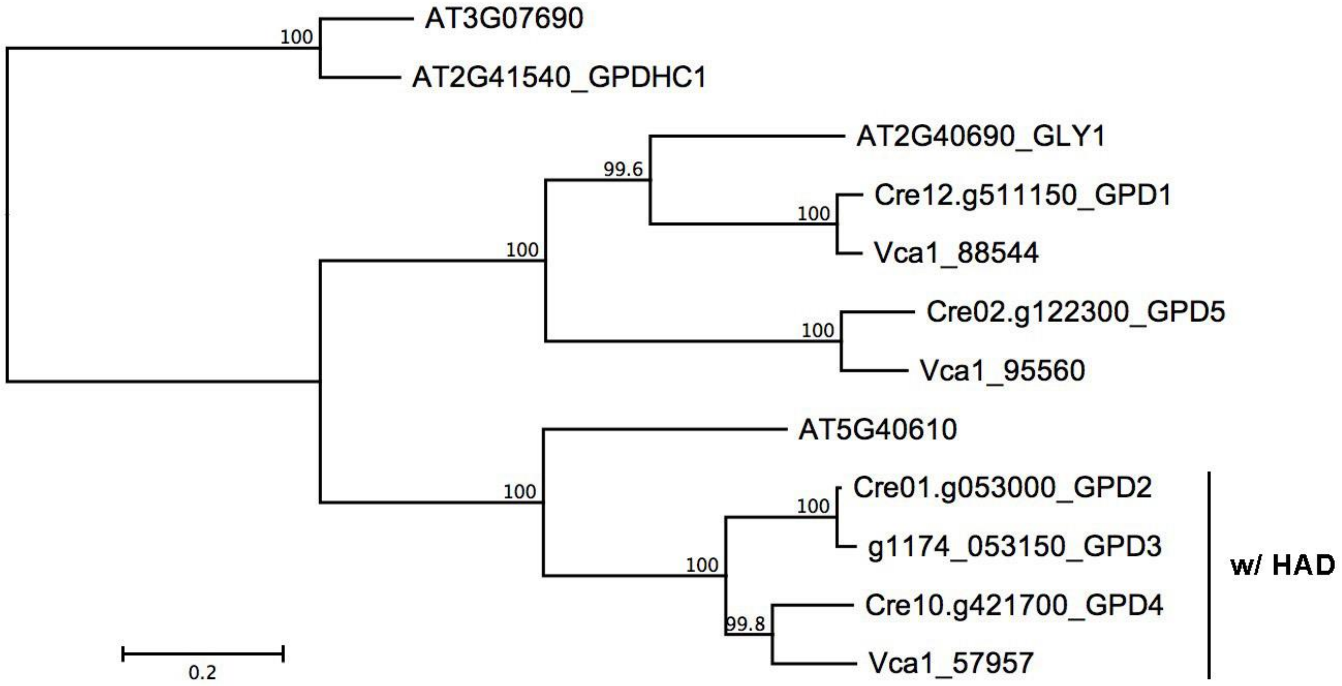

Figure S2 Neighbor-joining tree of the five glycerol-3-P dehydrogenase (*GPD*) genes in *C. reinhardtii* and their orthologues in *Volvox carteri* (Vca) and *Arabidopsis thaliana* (AT). HAD: genes including a HAD domain with homology to 3-phosphoserine phosphatase (PSP). Scale bar: Jukes-Cantor distance.

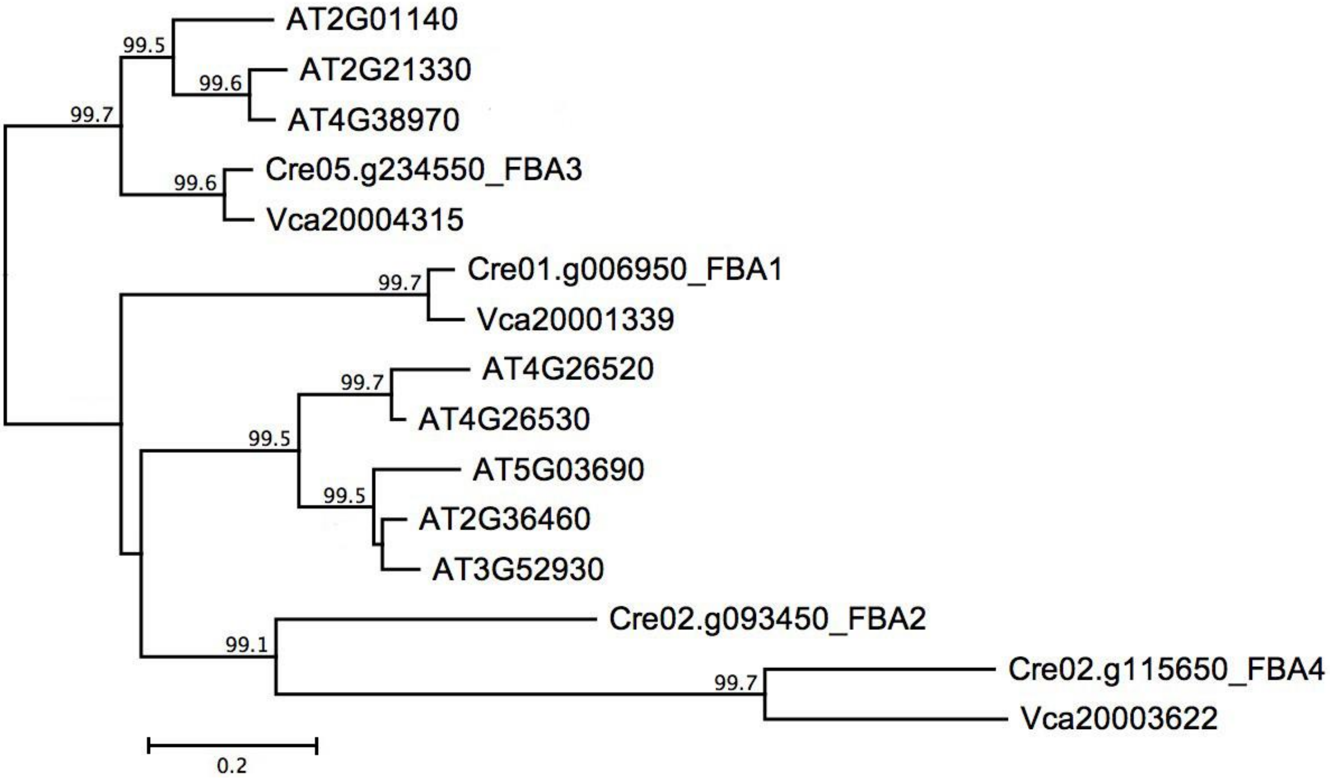

Figure S3 Bayesian consensus tree of the four fructose-1,6-bisphosphate aldolase (*FBA*) genes from *C. reinhardtii* and their ortholgues in *Volvox carteri* (Vca) and *Arabidopsis thaliana* (AT). Scale bar: gamma-corrected amino acid substitution rate based on WAG matrix per site.

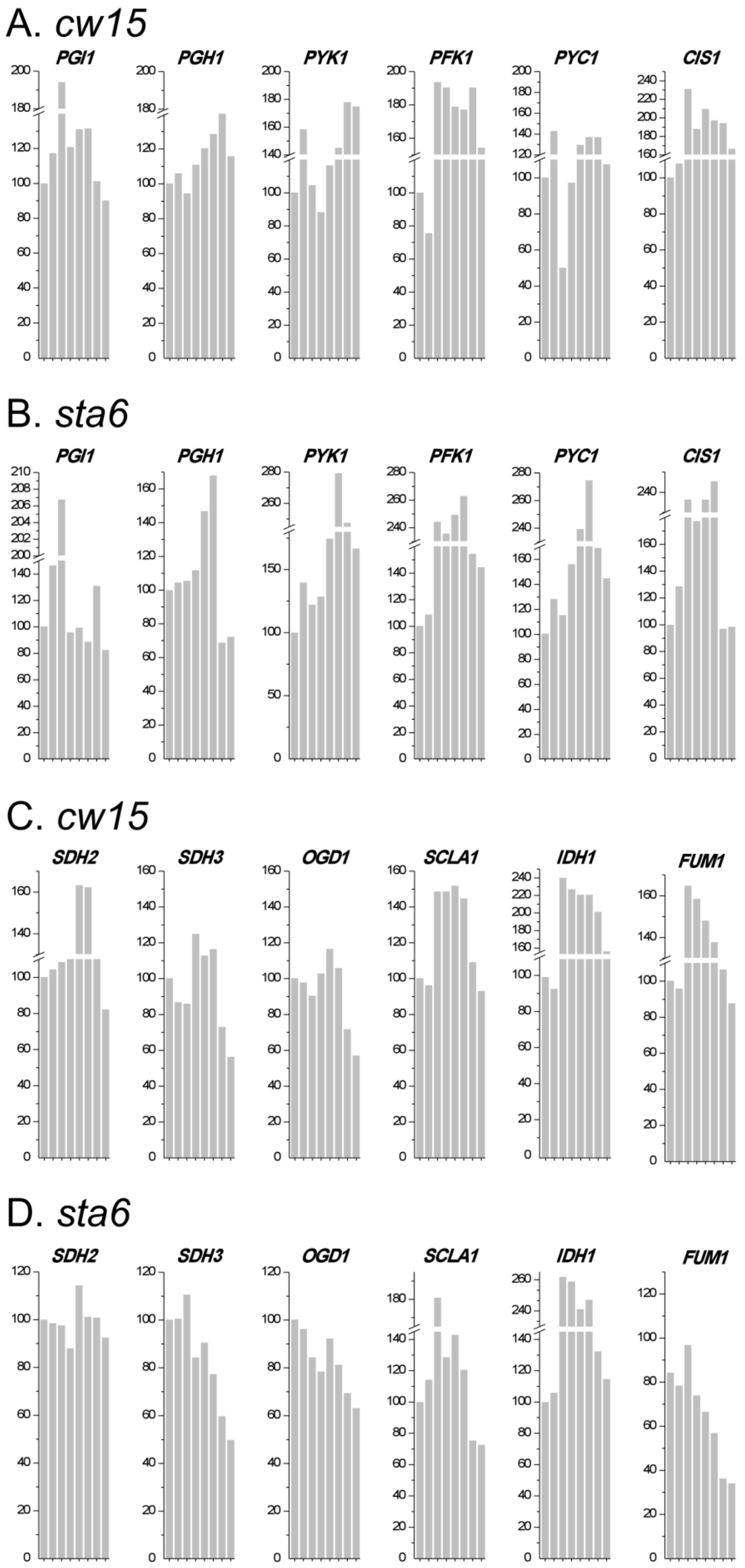

Figure S4 Expression profiles for genes in the same pathways as the "sensitive" genes displayed in Fig. 5 (see Fig. 5 legend for details).

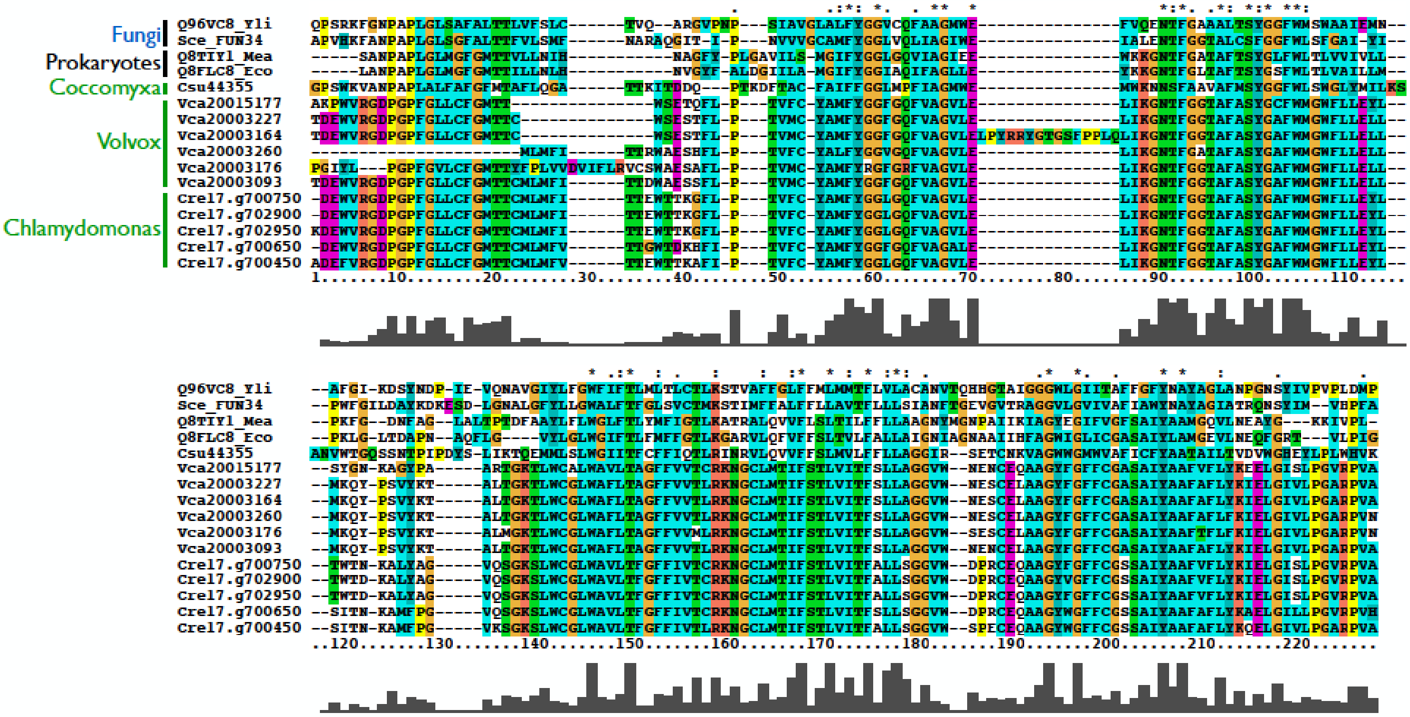

Figure S5A Alignment of pfam01184 domain from selected Grp1_Fun34_Yaah family proteins. See Supplementary Dataset 5 for full sequences of *Volvox* genes.

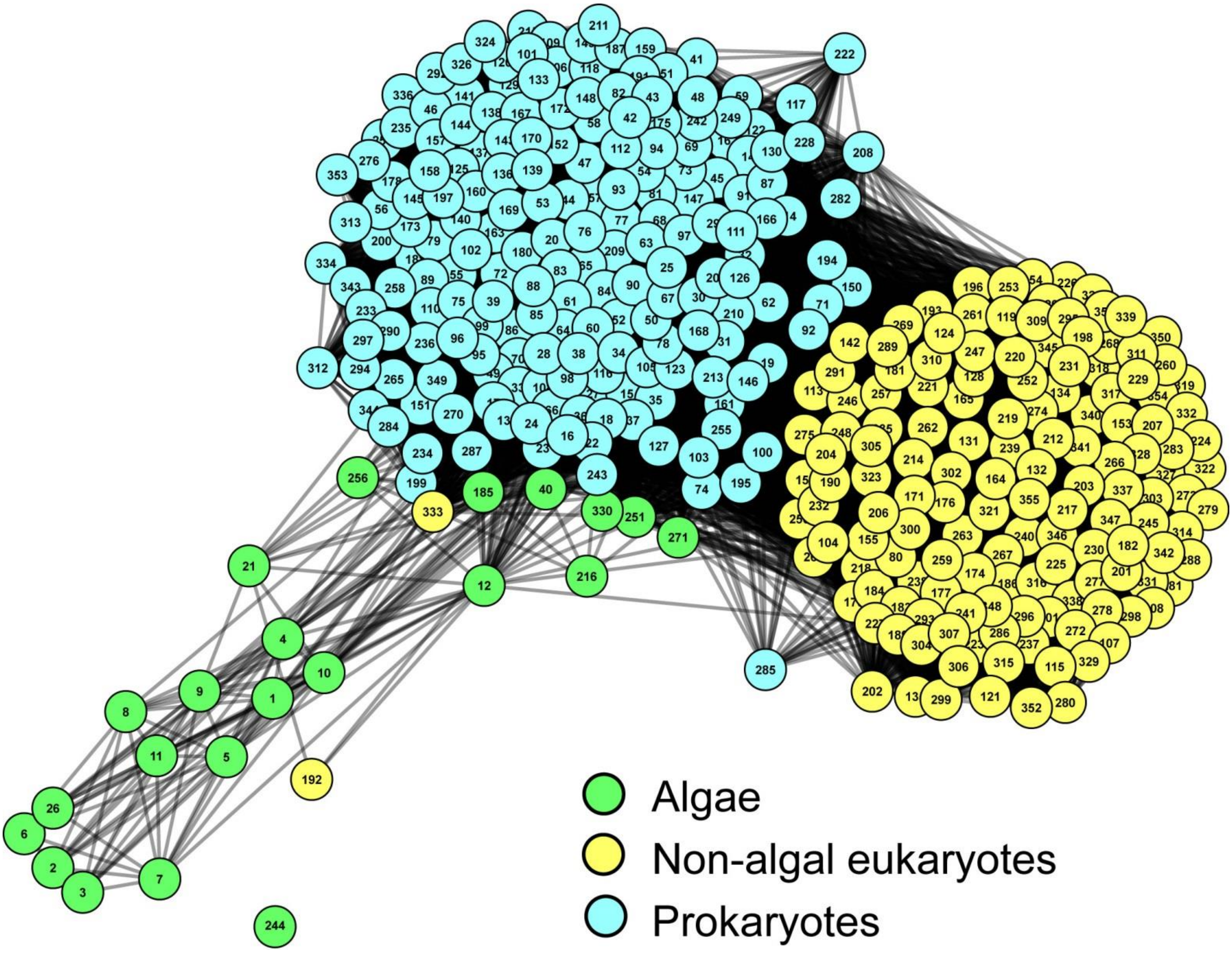

Figure S5B Similarity network of genes in the Grp1_Fun34_YaaH family (see Dataset 6 for key to numbers and protein sequences).

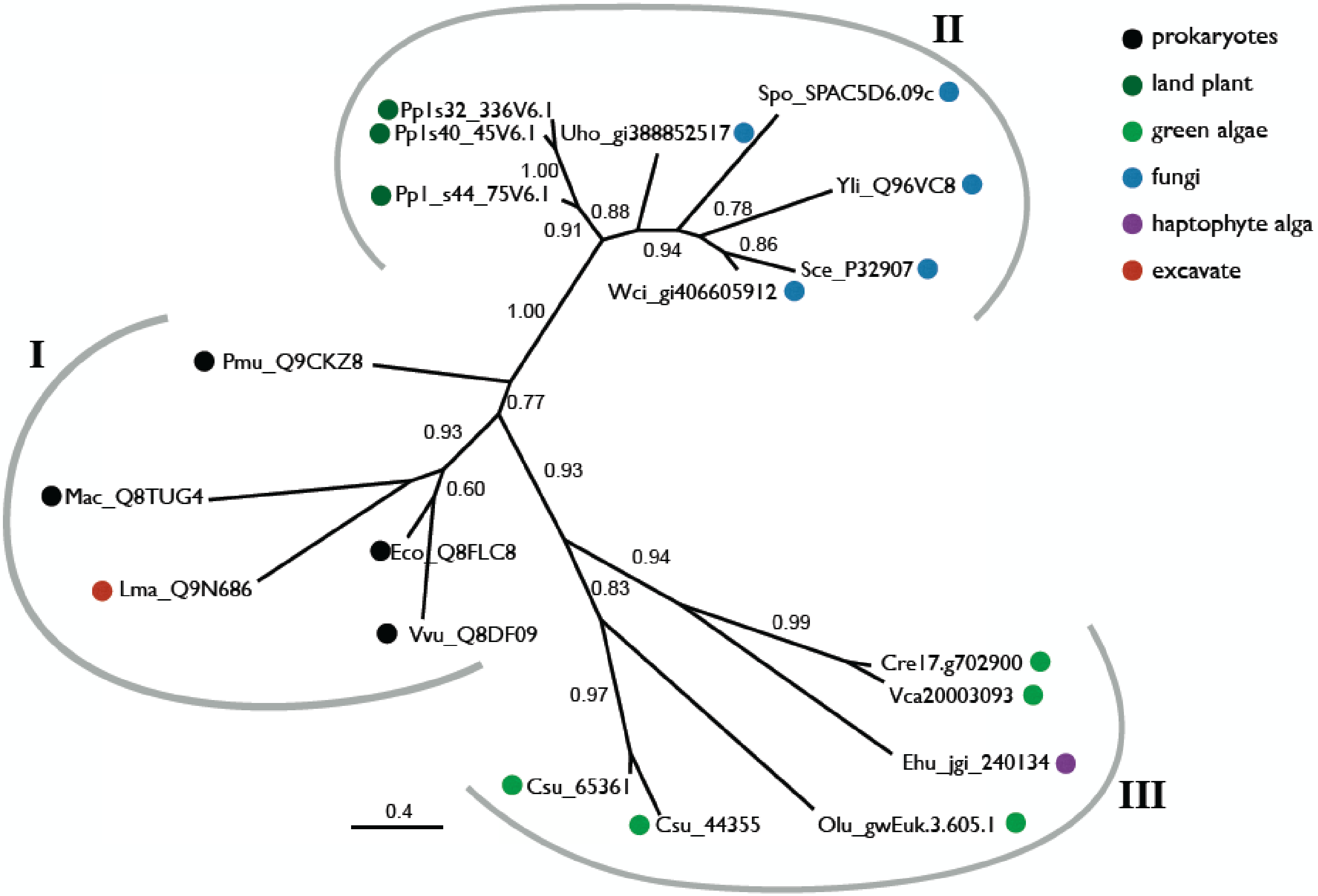

Figure S5C Unrooted maximum likelihood phylogeny queried with the pfam01184 domain. Approximate likelihood ratio test (aLRT) supporting values above 0.5 are shown at each branch. Species IDs: Cre, *Chlamydomonas reinhardtii*; Vca, *Volvox carteri*; Ehu, *Emiliania huxleyi*; Olu, *Ostreococcus lucimarinus*; Csu,*Coccomyxa subellipsoidea*; Vvu, *Vibrio vulnificus*; Eco, *Escherichia coli*; Lma, *Leishmania major*; Mac, *Methanosarcina acetivorans*; Pmu, *Pasteurella multocida*; Pp, *Physcomitrella patens*; Uho, *Ustilago hordei*; Spo, *Schizosaccharomyces pombe*; Yli, *Yarrowia lipolytica*; Sce, *Saccharomyces cerevisiae*; Wci, *Wickerhamomyces ciferrii.*

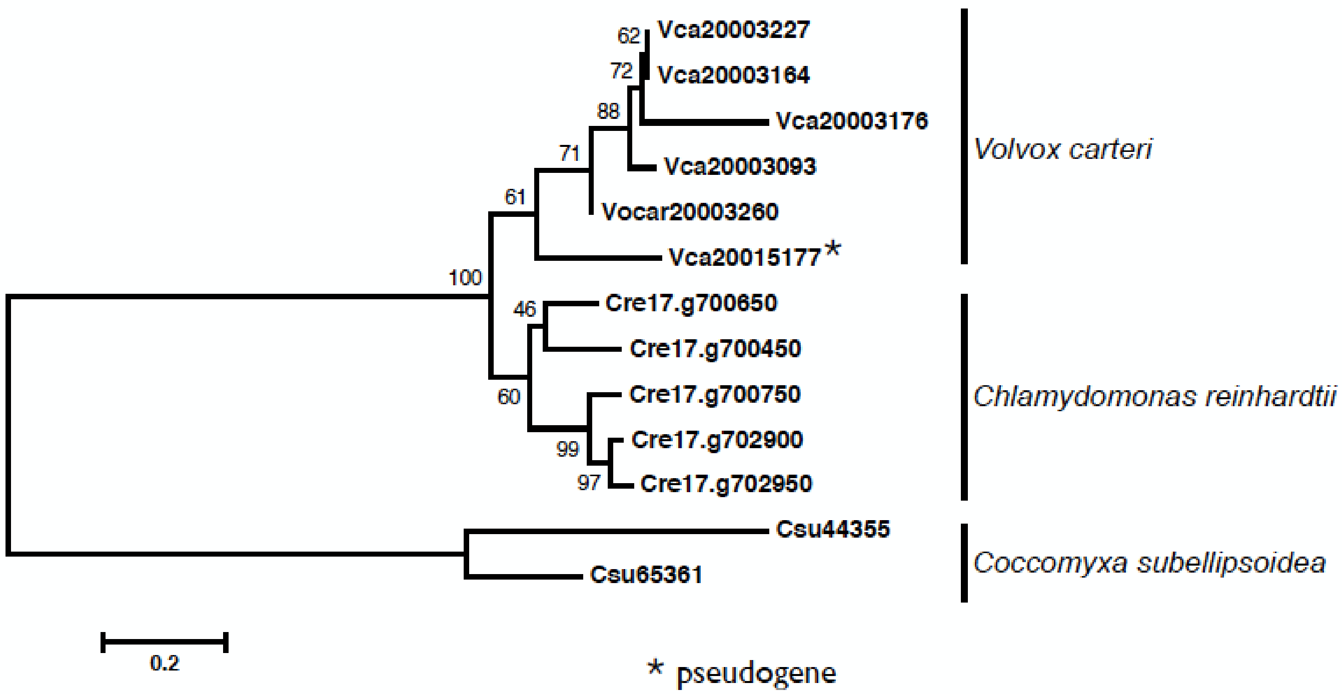

Figure S5D Neighbor-joining tree with bootstrap values from 500 replicates of Chlorophycean GPR1_FUN30_YaaH family members.