Supplementary Figure 1. Clustal W alignment of amino acid sequences surrounding the substituted residue of YGL1 paralogs and bacterial chlorophyll synthase orthologs. Accession number from expasy server (http://www.expasy.ch/); synthase type B and C indicate bacteriochlorophyll and chlorophyll synthase, respectively. Motif only in chlorophyll synthase is underlined; the arrow indicates the Pro-198 to Ser change in the *ygl1* mutant.