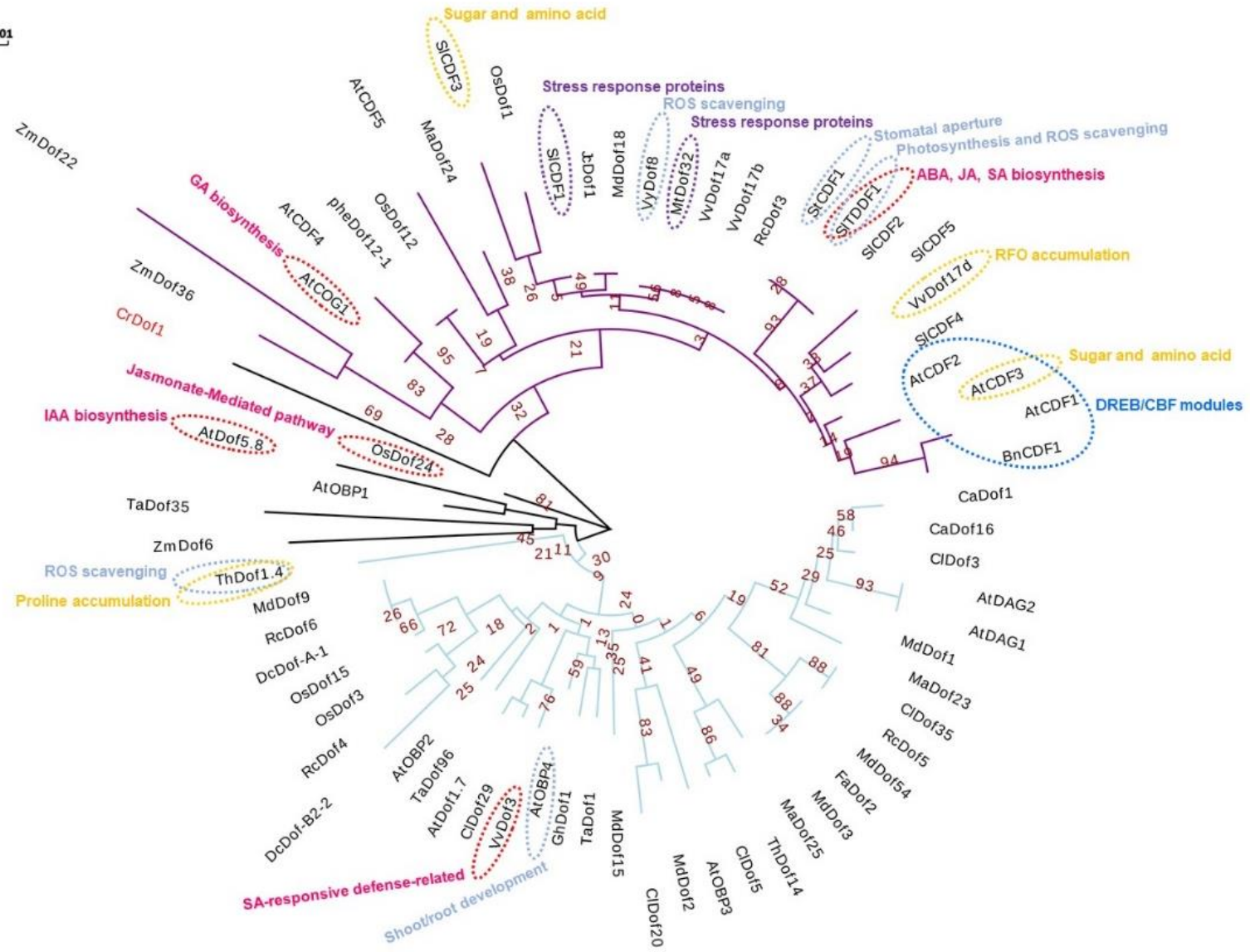**Figure S1** Neighbour-joining phylogenetic tree of selected stress- and hormone-related plant Dof transcription factors (Tables 1) with *C. reinhardtii* CrDOF1 as outgroup

Moreno-Risueno et al. (2007). The physiological function of Dof transcription factor are generally classified into ROS scavenging and others (lightblue), production of

compatible solutes (orange), hormone synthesis and signaling (pink), stress response proteins (light purple) and stress-response TFs (blue) and proteins (light purple). The

optimal tree with the sum of branch length = 3.47419992 is shown. The tree is drawn to scale, with scale bars representing branch lengths (number of substitutions per site).

The analysis involved 69 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 49 positions in the final dataset.

Evolutionary analyses were conducted in MEGA7 with Neighbour-joining method and 1000 bootstrap test replicates. Concordantly, other studies encompassing a wider range

of plants such as sorghum, rice, and grapes, among others also showed some clusters in common with our analysis (Kushwaha et al. 2011; Noguero et al. 2013). Mention here

that most hormone- and stress-related Dofs fall within 3 groups (of 6 total) according to the nomenclature of maybe Noguero et al. (2013).

Dof protein seq use in Fig. S1

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