



**Supplementary information, Figure S16** Unrooted phylogenetic tree of hemoglobin genes.

The consensus tree was generated based a multiple alignment of the CDS (coding sequence) from quinoa and Arabidopsis thalian. The codon alignment was generated by Muscle in MEGA7.0 and the tree was constructed using the neighbor-joining method with 1000 bootstrap replicates. Numbers at each branching point indicate that the local bootstrap values per 100 replicates.