



Figure S3 Phylogenetic analysis of PEPC genes. Phylogenetic hypothesis was derived from maximum parsimony analysis of the C-terminal fragments of PEPCs from *S. alfredii* (Sa_) and *Arabidopsis thaliana* (At_), *Zea mays* (Zm_), *Sorghum vulgare* (Sv_), *Saccharum officinarum* (So_), *Mesembryanthemum crystallinum* (Mc_), *Kalanchoë blossfeldiana* (Kb_), *Clusia venosa* (Cv_), *Clusia rosea* (Cr_), *Clusia schomburgkiana* (Cs_), *Clusia hilariana* (Ch_) and *Clusia aripoensis* (Ca_). The tree was rooted with *Saccharum officinarum*. Accession numbers are listed in Table S5.