



S2 Fig. The phylogenetic relationship of the TAFs group of the SAGA complex.

SAGA complex subunit protein sequences were used from At, *A. thaliana* (red circle); Dm, *D. melongaster*; Hs, *H. sapiens* (red square); Os, *O. sativa* (red diamond shape); Mm, *M. musculus*; Rn, *R. norvegicus*; Sc, *S. cerevisiae* (red triangle); Sp, *S. pombe*; Zm, *Z. mays*; Rc, *R. communis*; Pt, *P. trichocarpa*; Vv, *V. vinifera*; Al, *A. lyrta*; Mt, *M. truncatula*; Bd, *B. distachyon*; Sb, *S. bicolor*; Sm, *S. moellendorffii*; Pp, *P. patens*; Cr, *C. reinhardtii* and Ol, *O. lucimarinus*. Phylogeny reconstruction was analyzed by neighbour-joining statistical method based on the JTT matrix-based model. Test of phylogeny was analyzed by the bootstrap method (1,000 replicates). Evolutionary analyses were conducted in MEGA 6.06.