Supplementary information Figure S3 Evolutionary relationships of ZF (zinc-finger

motif)-containing PP2Cs. Sequence blast against existing sequenced genomes using

Arabidopsis PP2CA as query identified another fifty-six ZF-containing PP2CAs, all

from plants. PP2CA is highlighted in yellow. The evolutionary history was inferred

using the Neighbor-Joining method (Saitou & Nei, 1987). The evolutionary distances

were computed using the Poisson correction method and are presented in the units of the number of amino acid substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 171 positions in the final dataset. The optimal tree with the sum of branch length of 3.38593550 is shown. Evolutionary analyses were conducted in MEGA5 (Tamura et al, 2011). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree.

References

Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular biology and evolution* 4: 406-425

Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular biology and evolution* 28: 2731-2739