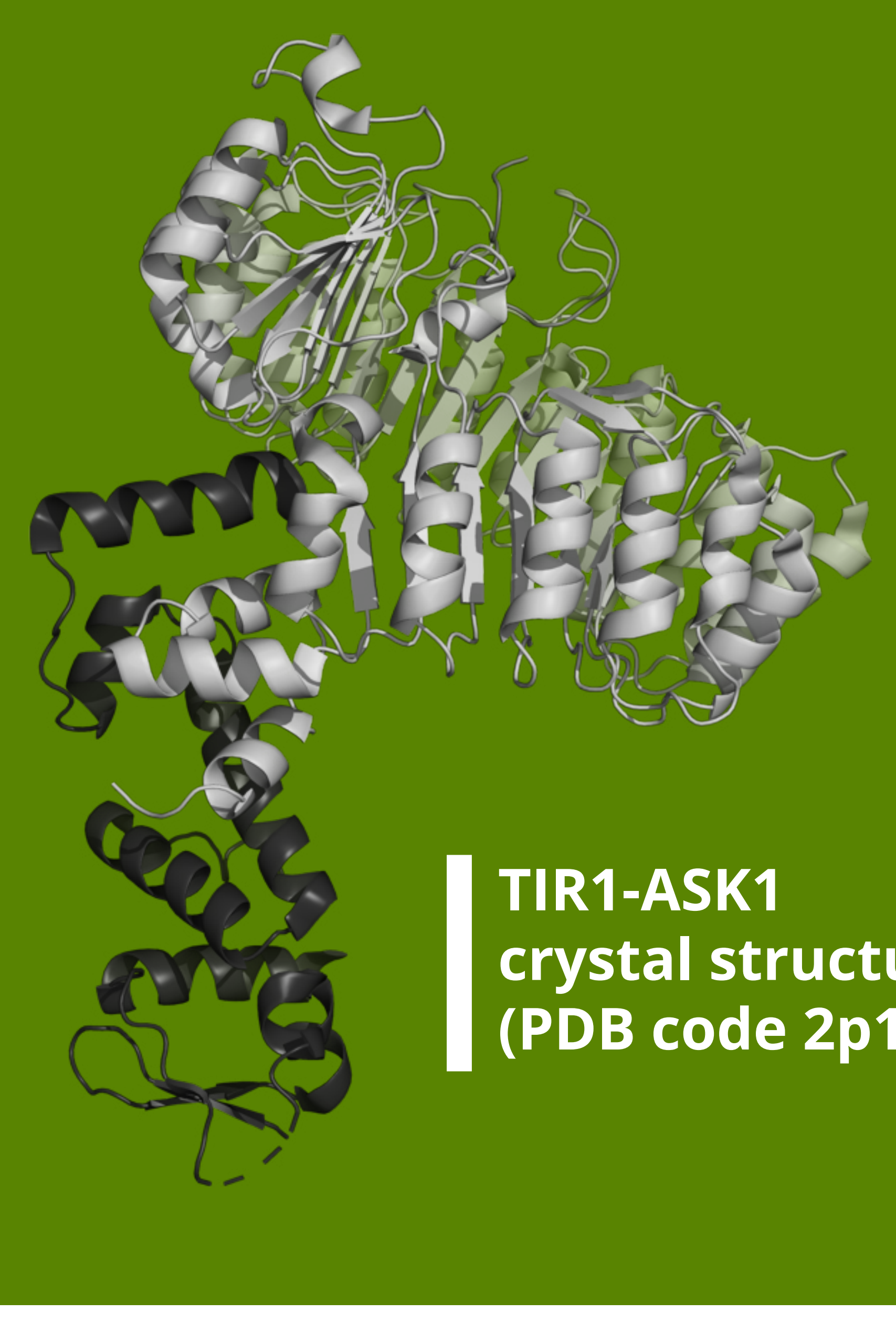
Adaptive and degenerative evolution of the *S-Phase Kinase-Associated Protein 1-Like* family in *Arabidopsis thaliana*

INTRODUCTION

Genome sequencing has uncovered tremendous sequence variation within and between species. In plants, in addition to large variations in genome size, a great deal of sequence polymorphism is also evident in several large multi-gene families, including those involved in the ubiquitin-26S proteasome protein degradation system. However, the biological function of this sequence variation is yet not clear.

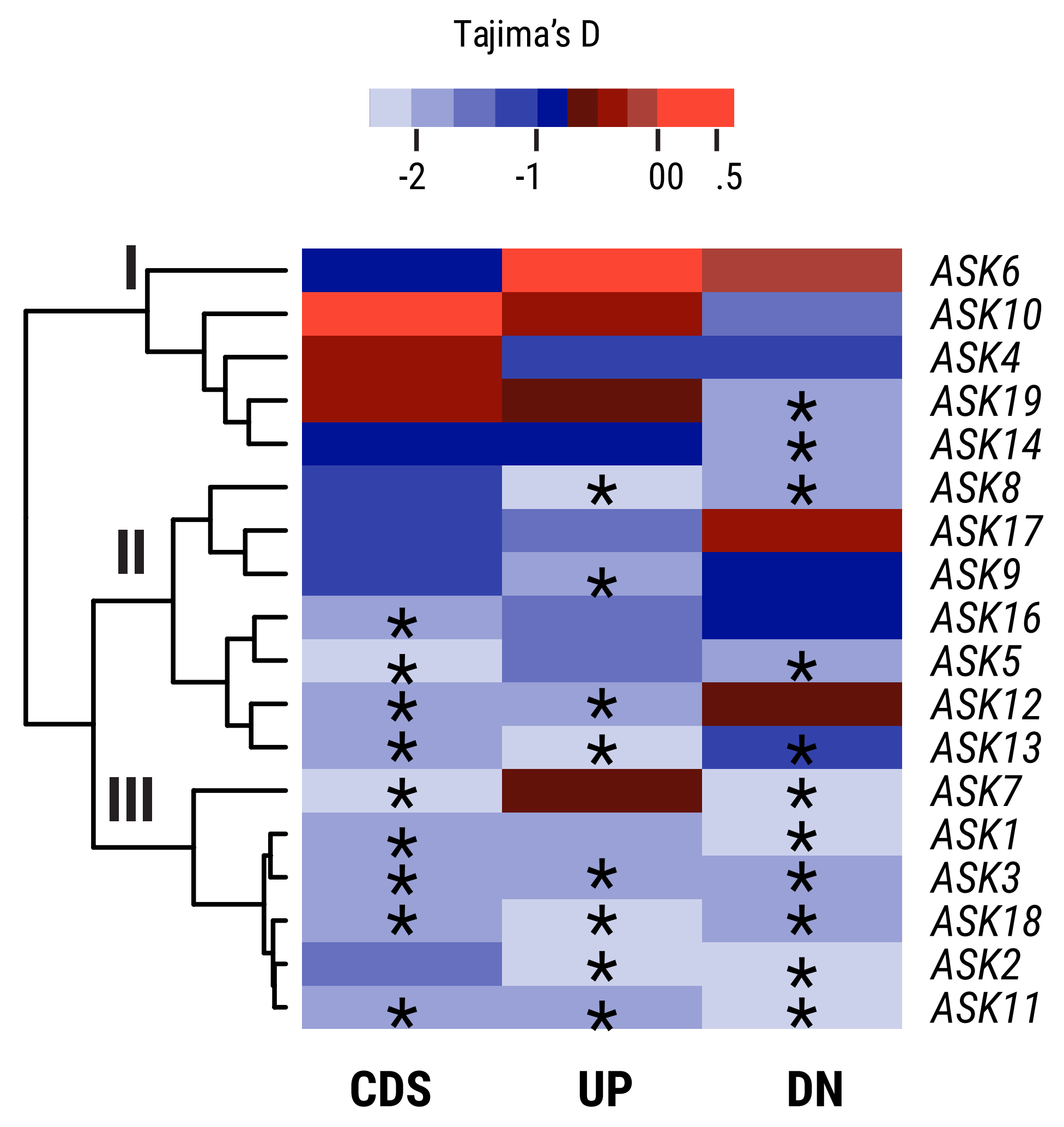


TIR1-ASK1 crystal structure (PDB code 2p1n)

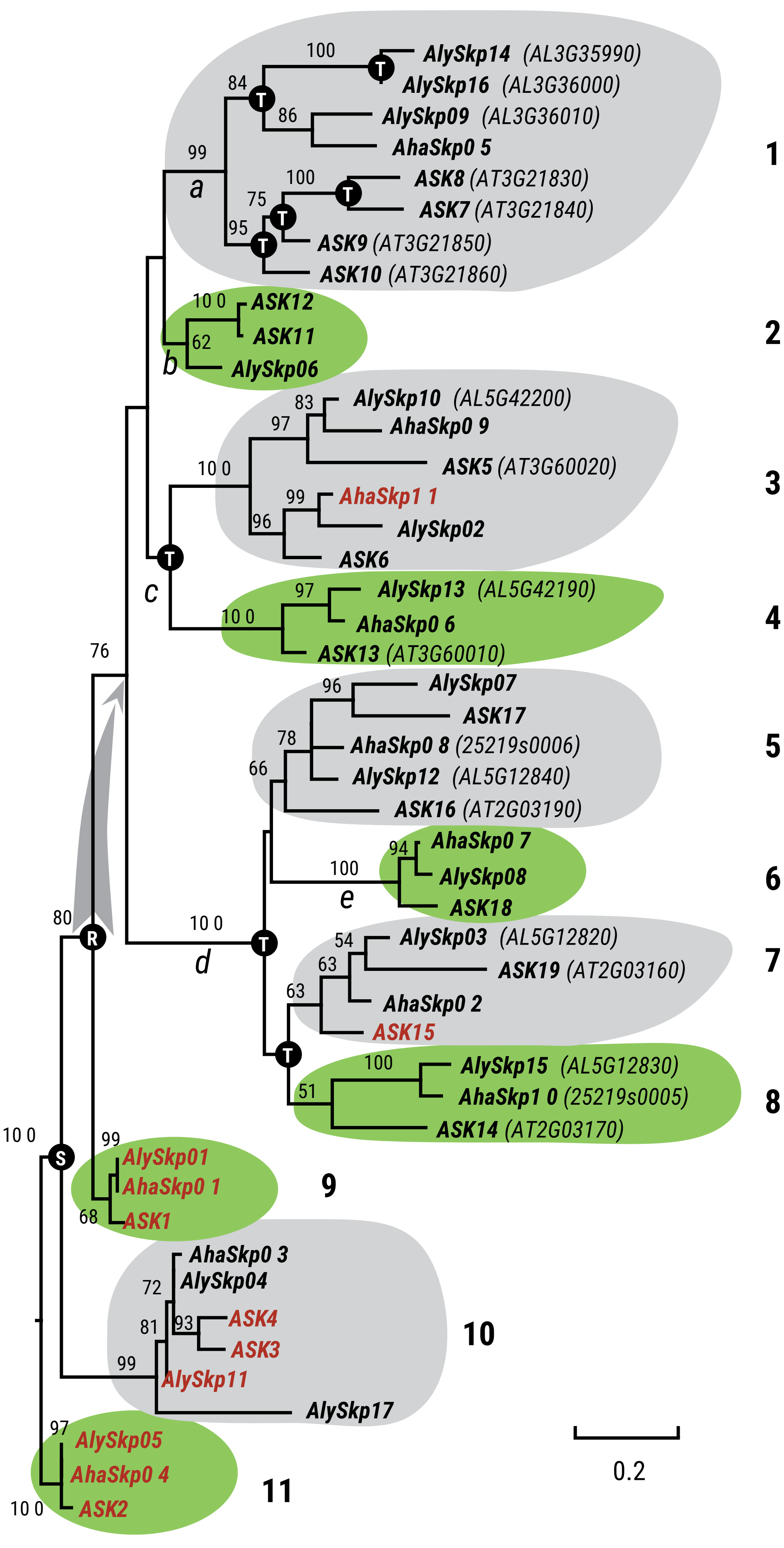
RESULTS

In this work, we explicitly demonstrated a single origin of retroposed *Arabidopsis Skp1-Like (ASK)* genes using an improved phylogenetic analysis. Taking advantage of the 1,001 genomes project, we provide several lines of polymorphism evidence showing both adaptive and degenerative evolutionary constraints of polymorphic mutations among and in *ASK* genes.

A heatmap representation of Tajima's D values demonstrating the differential evolutionary constraints of polymorphic mutations among *ASK* genes.

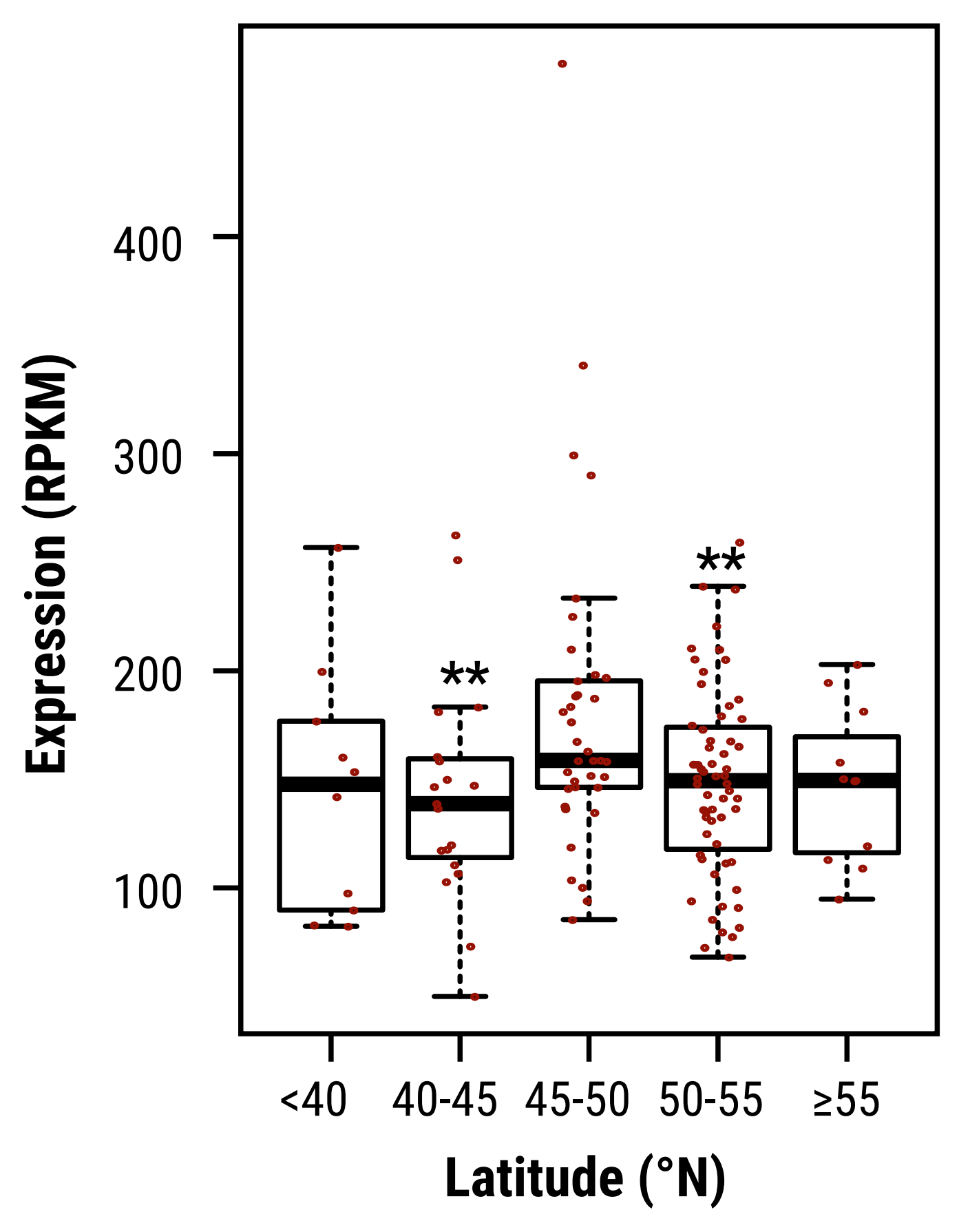


An improved phylogenetic analysis reveals one single origin of retroposed *Skp1* genes in the Arabidopsis genus.

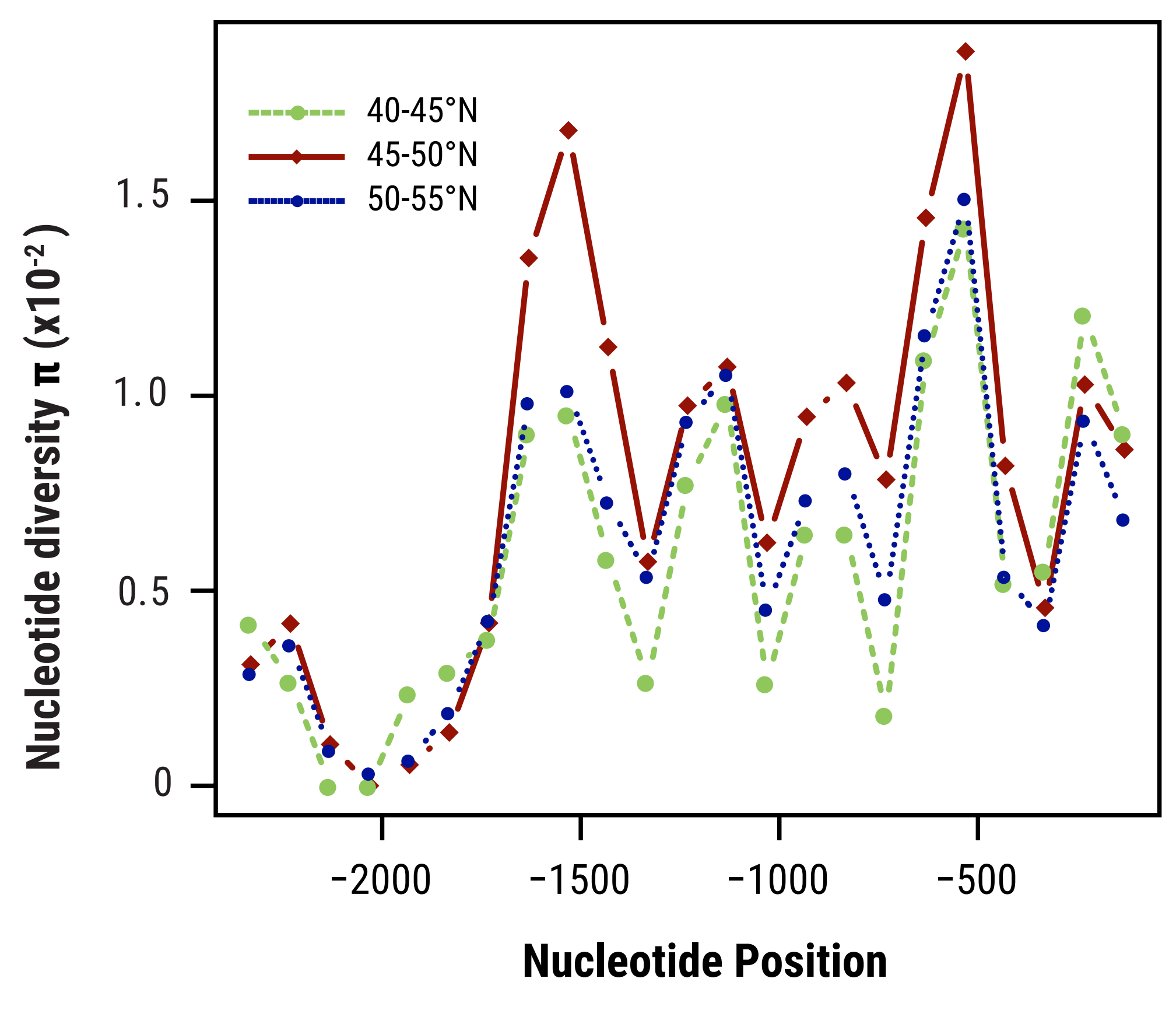


Yeast two-hybrid quantitative interaction assays further confirmed that recent neutral changes in the *ASK2* coding sequence weakened its interactions with some F-box proteins. The trend that highly polymorphic upstream regions of *ASK1* yield high levels of expression implied negative expression regulation of *ASK1* by an as-yet-unknown transcriptional suppression mechanism, which may contribute to the polymorphic roles of Skp1-CUL1-F-box complexes.

A. Latitudinal variation of *ASK1* expression. Asterisks indicate that the mean expression of the indicated group is significantly lower than that of the group within latitudes 45-50°N.



B. A window-slide polymorphic comparison of a 2.5 kb region upstream of the transcriptional start site of *ASK1* among populations from 3 latitudinal regions as in A.



CONCLUSION

Taken together, this study provides new evolutionary evidence to guide future functional genomic studies of SCF-mediated protein ubiquitylation.

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