

## Supplementary Figures

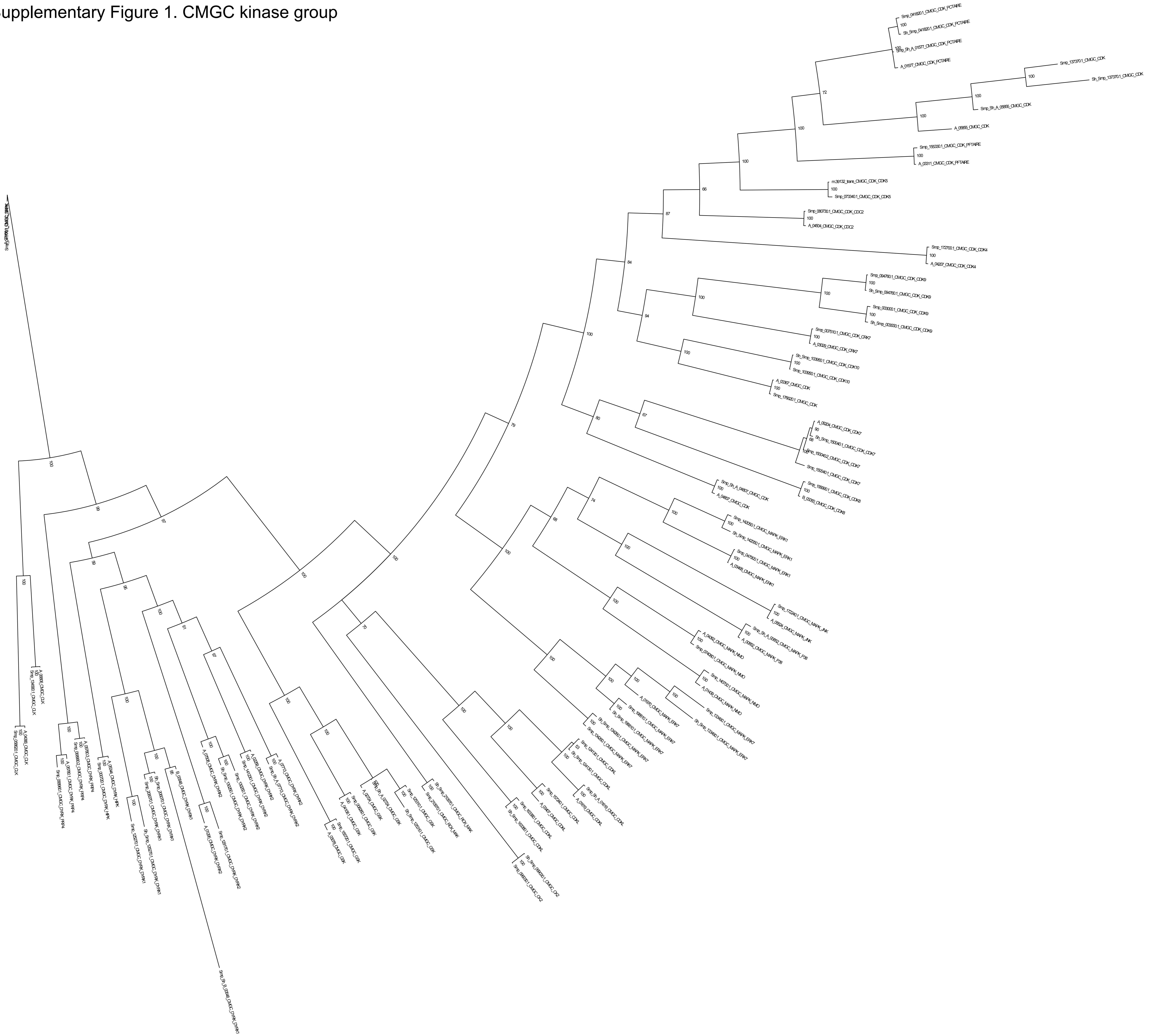
### Defining the *Schistosoma haematobium* kinome enables the prediction of essential kinases as anti-schistosome drug targets

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**Supplementary Figures 1 to 11. Phylogenetic analysis of individual eukaryotic protein kinase (ePK) groups and protein kinase-like (PKL) families of *Schistosoma haematobium* and *S. mansoni*.** Following the alignment of amino acid sequences representing CMGC, CAMK, AGC, Other, TK, STE, TKL, CK1, RGC groups and RIO and ABC kinase families, phylogenetic trees were constructed. High-resolution figures of individual trees including nodal support values and sequence identifiers are given.

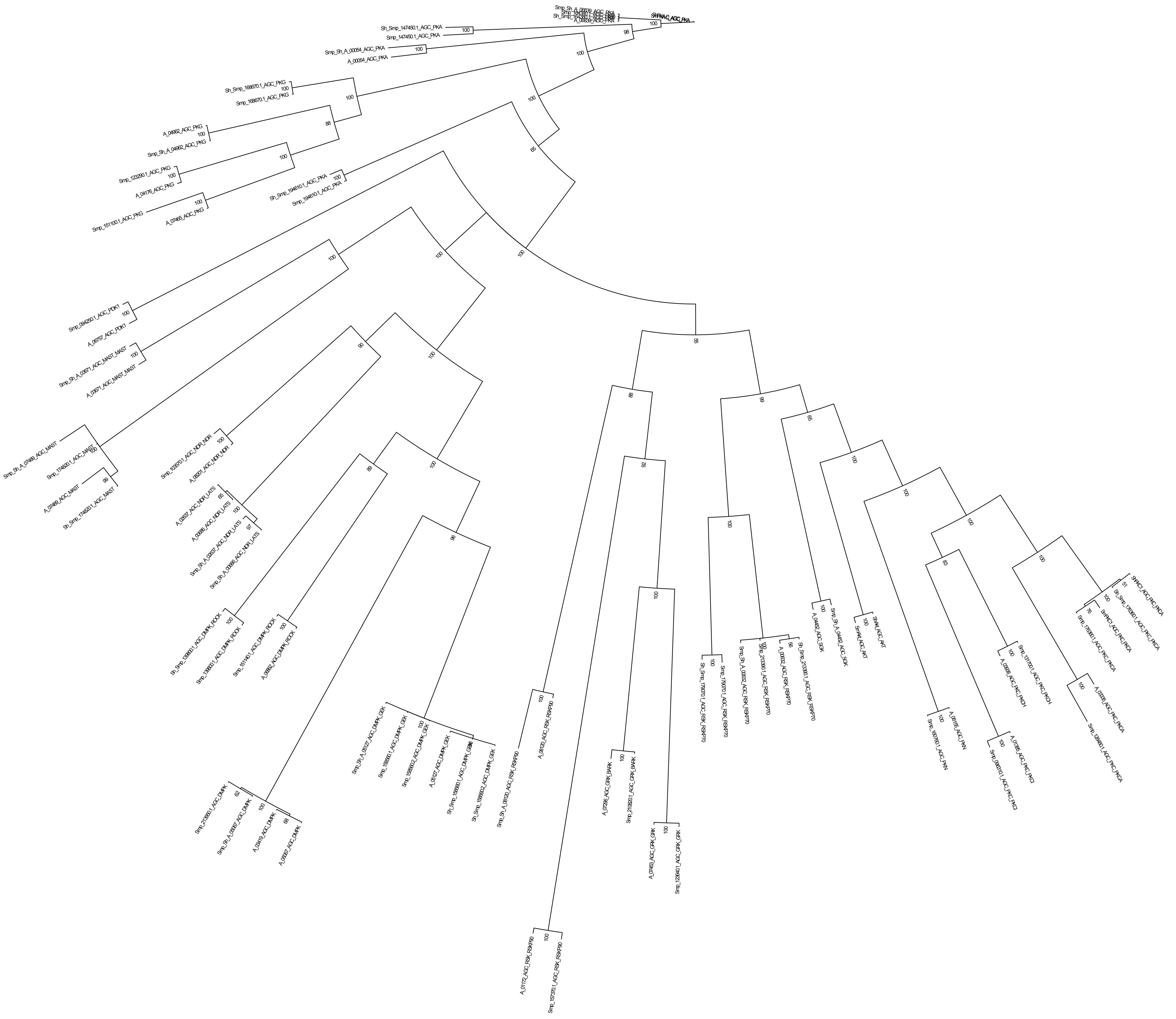
# Supplementary Figure 1. CMGC kinase group



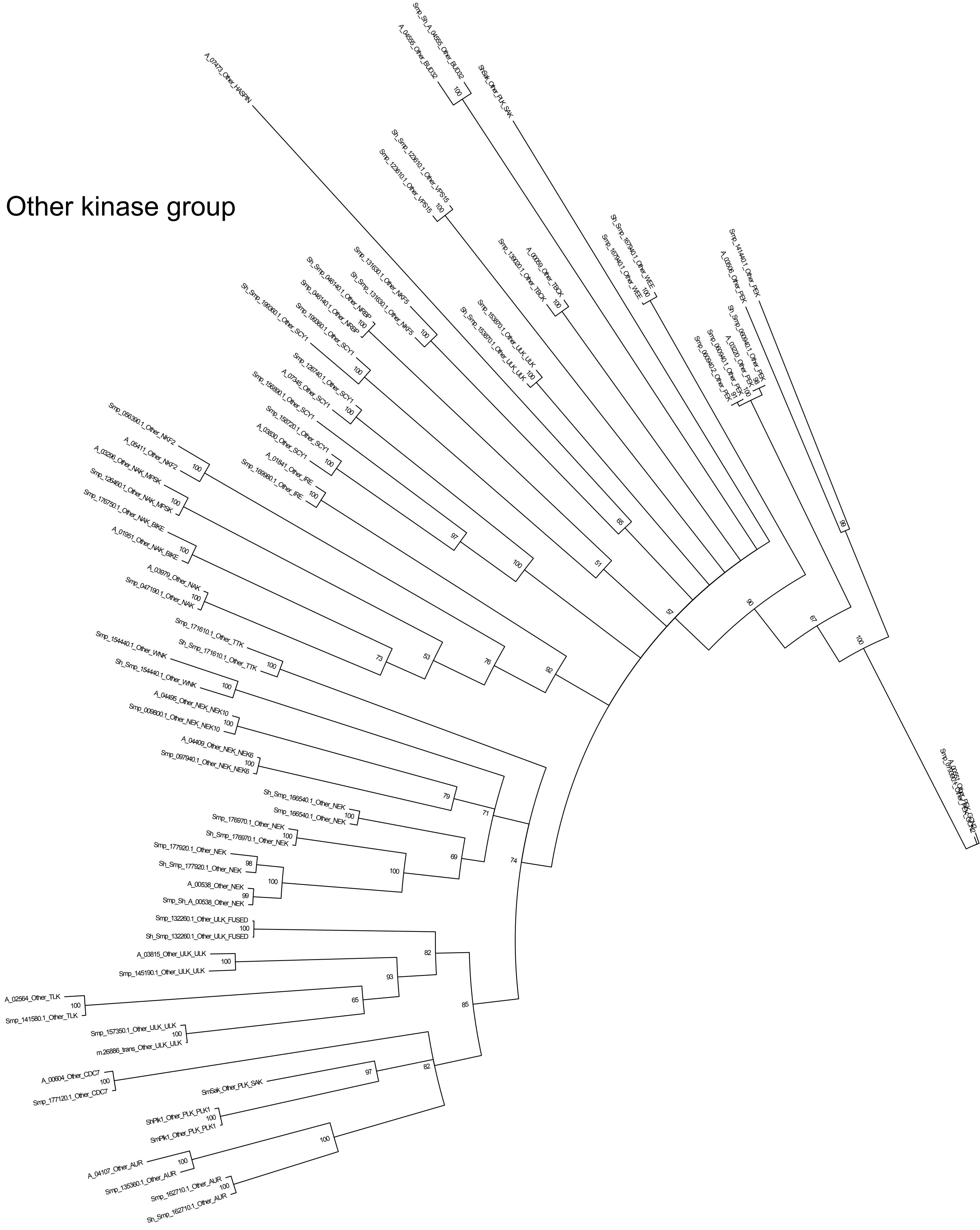
## Supplementary Figure 2. CAMK kinase group



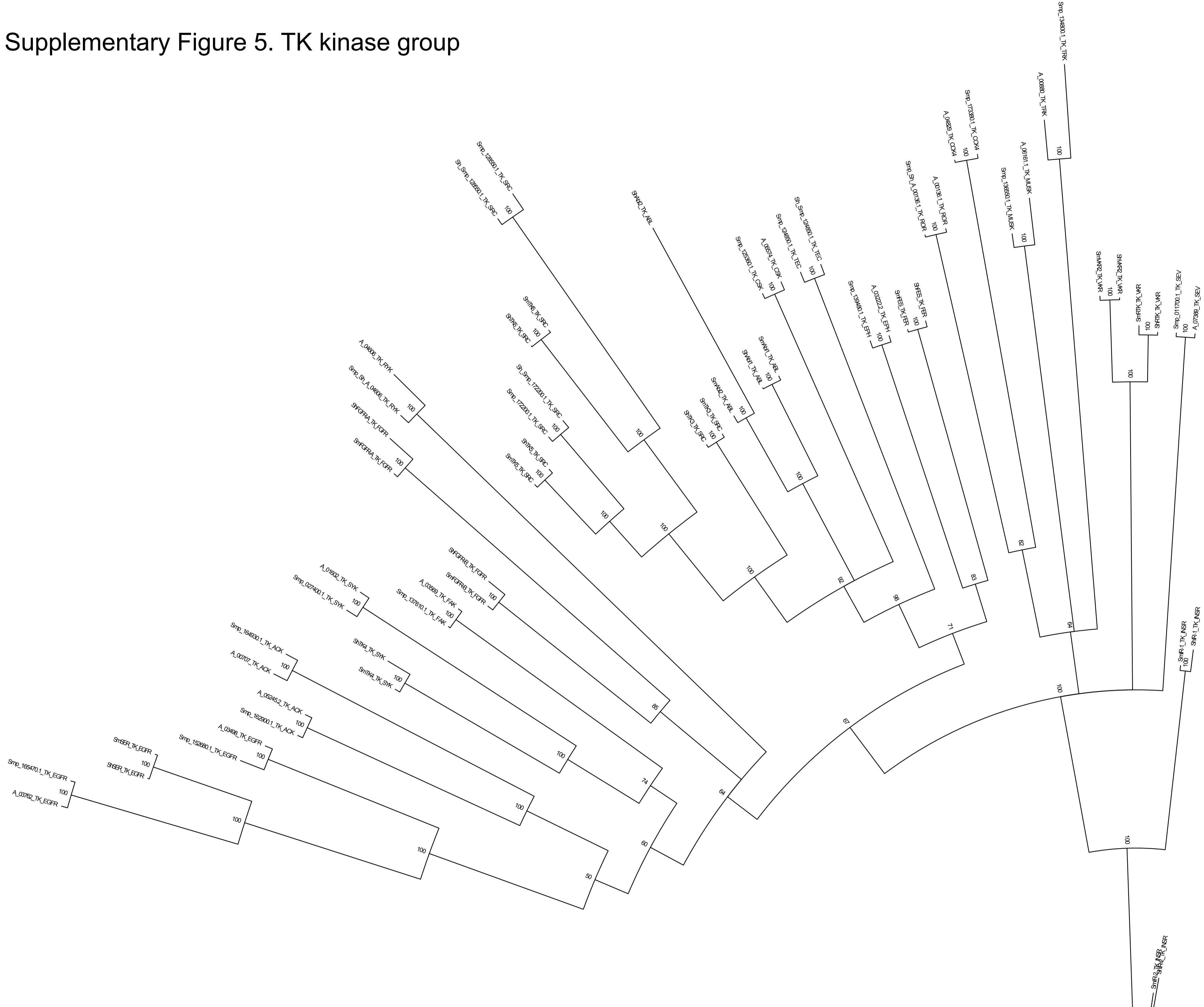
Supplementary Figure 3. AGC kinase group



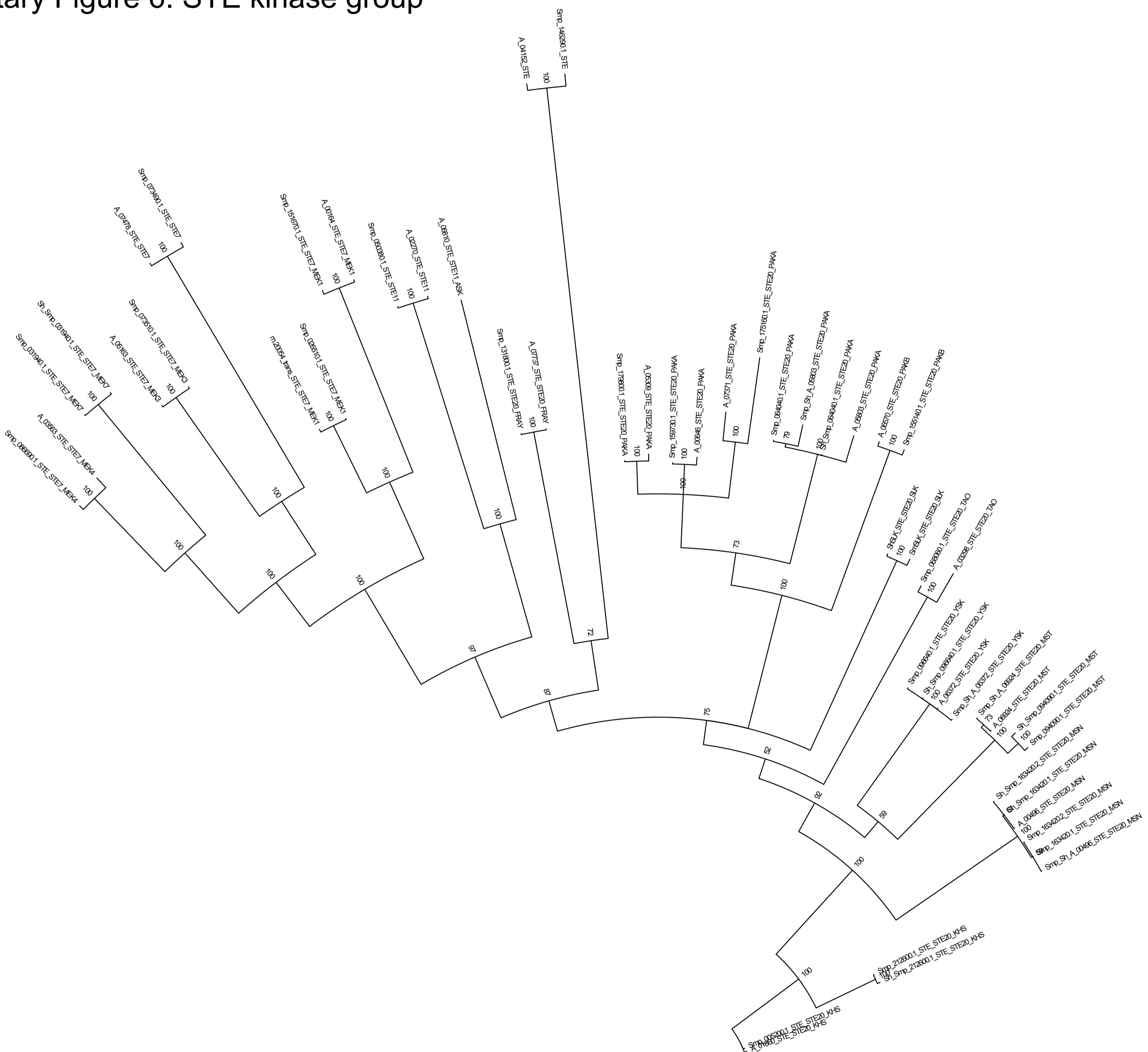
## Supplementary Figure 4. Other kinase group



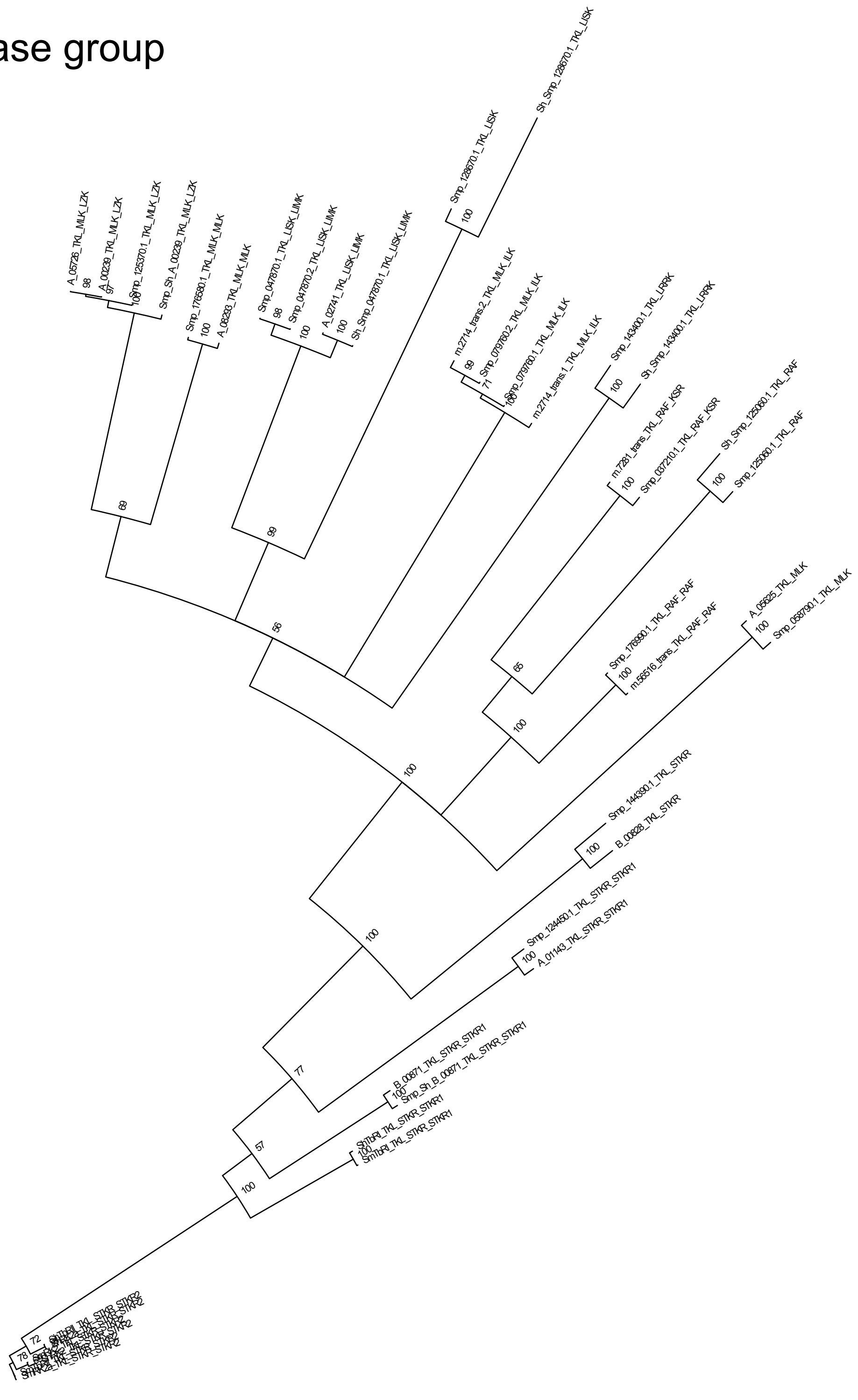
# Supplementary Figure 5. TK kinase group



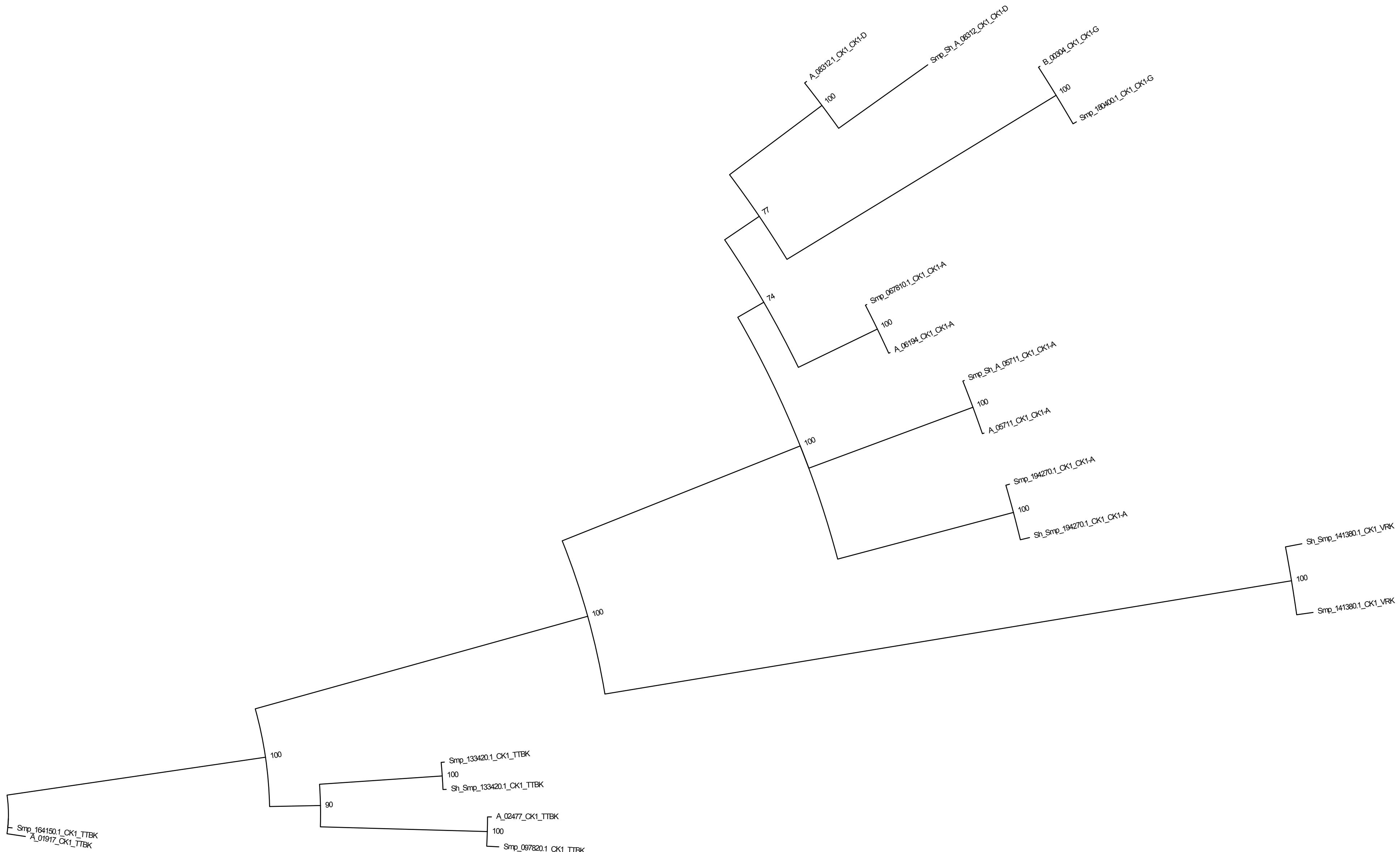
# Supplementary Figure 6. STE kinase group



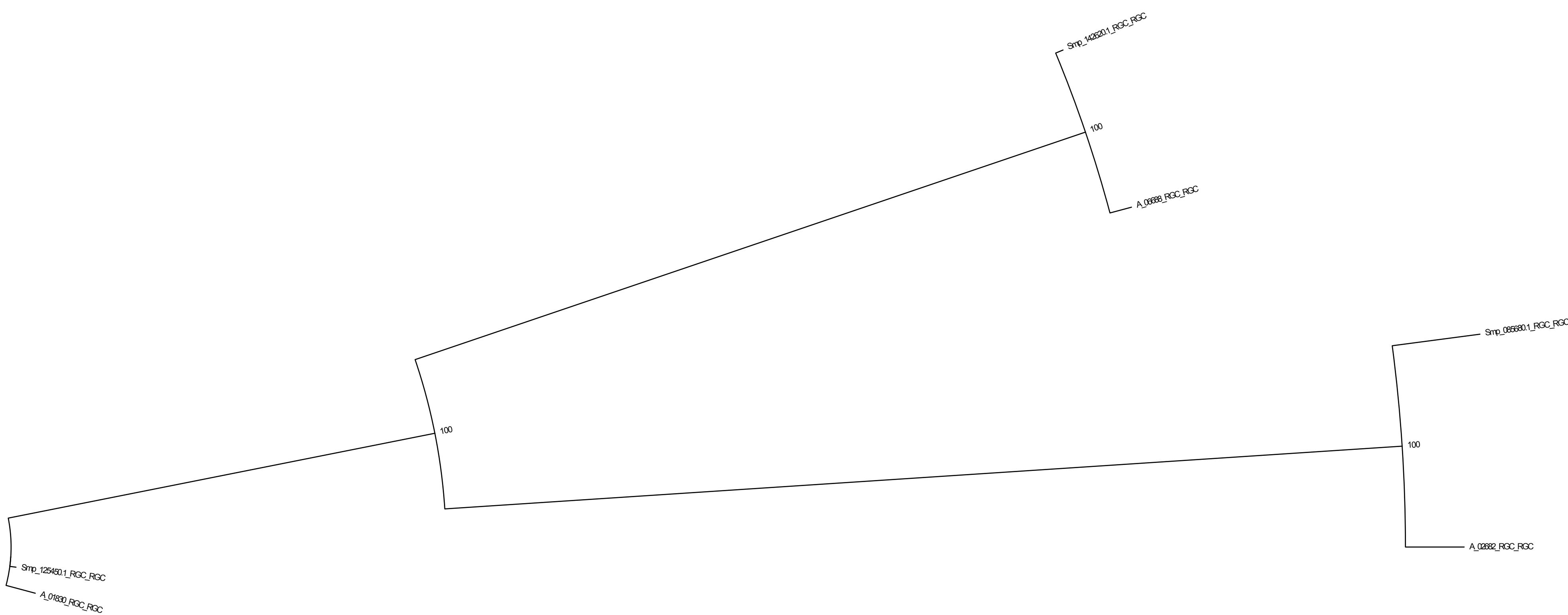
# Supplementary Figure 7. TKL kinase group



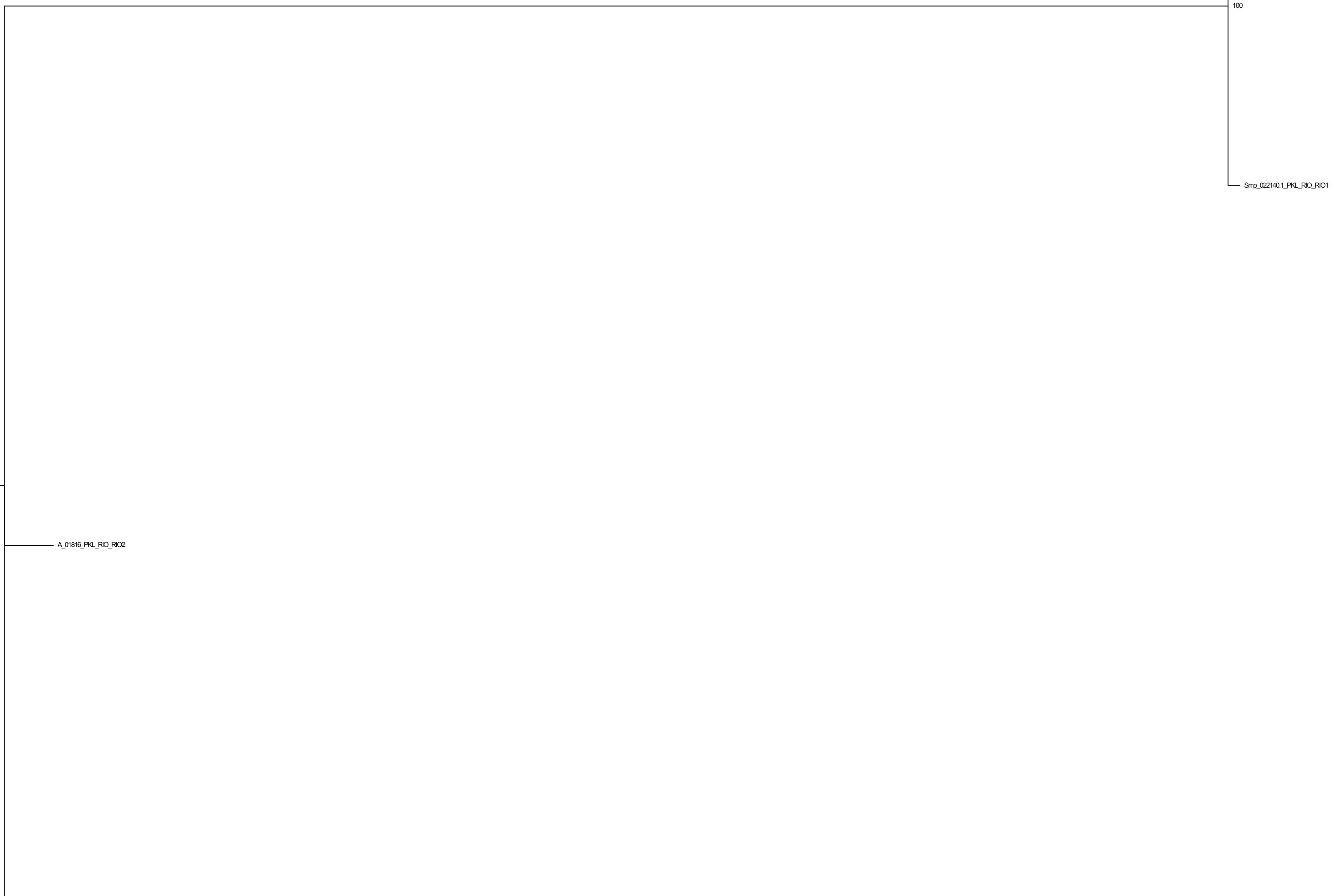
Supplementary Figure 8. CK1 kinase group



Supplementary Figure 9. RGC kinase group



## Supplementary Figure 10. RIO kinase family



## Supplementary Figure 11. ABC kinase family

