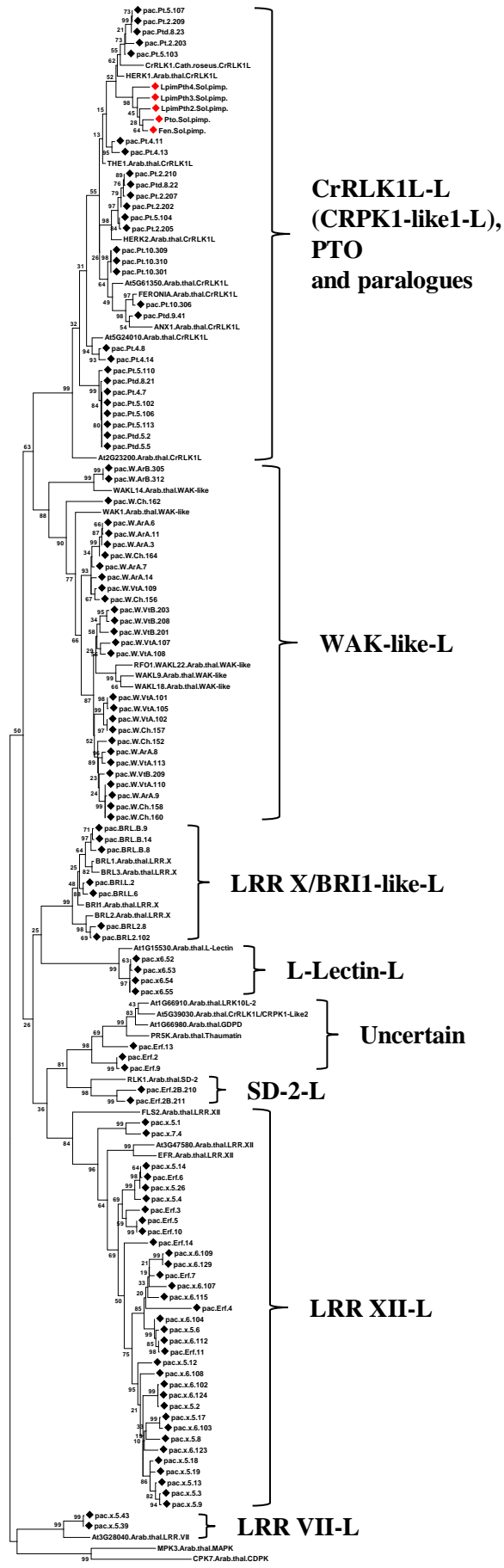


Additional file 10. Classification of *Pac* sequences based on maximum-likelihood (ML) phylogenetic analyses. Analyses were performed on the same dataset alignments used for crucial Neighbor-joining trees presented in this work (aa sequences). A1 and A2 match with Additional file 6B (all *Pac* sequences compared with homologous *Arabidopsis* RLK Pelles); B matches with Additional file 7 (*Arabidopsis* and rice CrRLK1L vs *Pac* CrRLK1L-L); C matches with Fig. 2 (*Arabidopsis* LRR XII vs *Pac* LRR XII-L); D matches with Fig. 3 (*Arabidopsis* WAK-like vs *Pac* WAK-like-L); E with Fig. 4 (*Arabidopsis* LRR X vs *Pac* LRR X-BRI1-L group). Editing matches that of counterpart figures.

All trees were inferred with Mega 6 except the one represented in A2 that was TREE PUZZLE-implemented. With regard to Mega 6 analyses, the percentage of trees in which the associated sequences clustered together in the bootstrap test (1,000 replicates) is shown for each node; trees are drawn to scale in the number of substitutions per site (scale at the bottom). TREE-PUZZLE analysis was conducted with 50,000 puzzling steps and quartet puzzling support values are shown for each node.

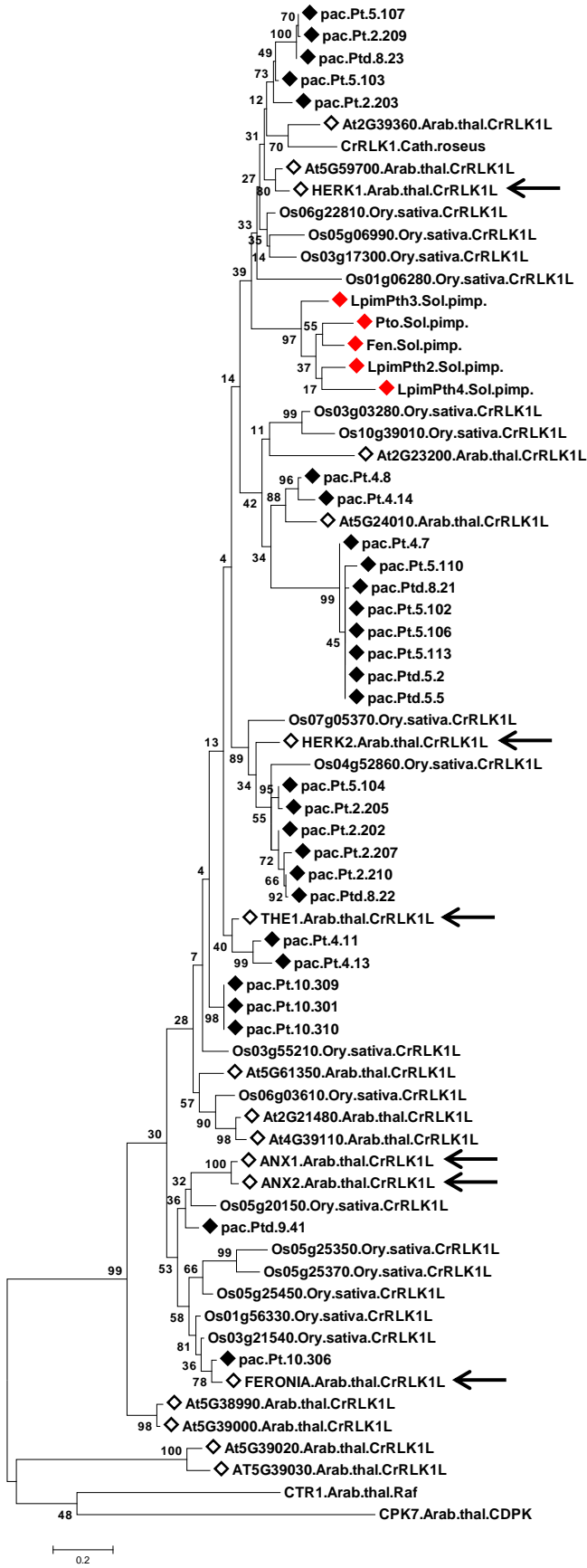
A1



A2



B

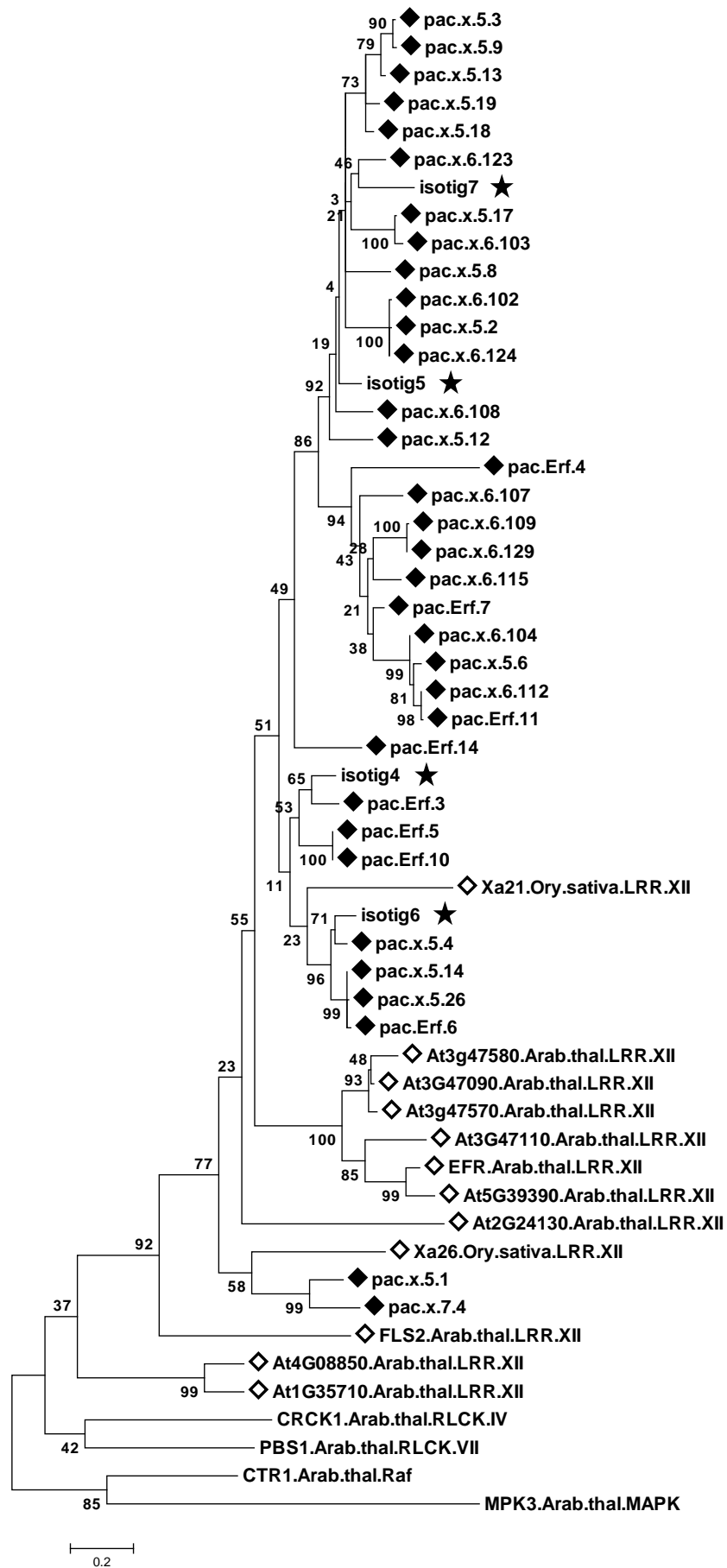


T

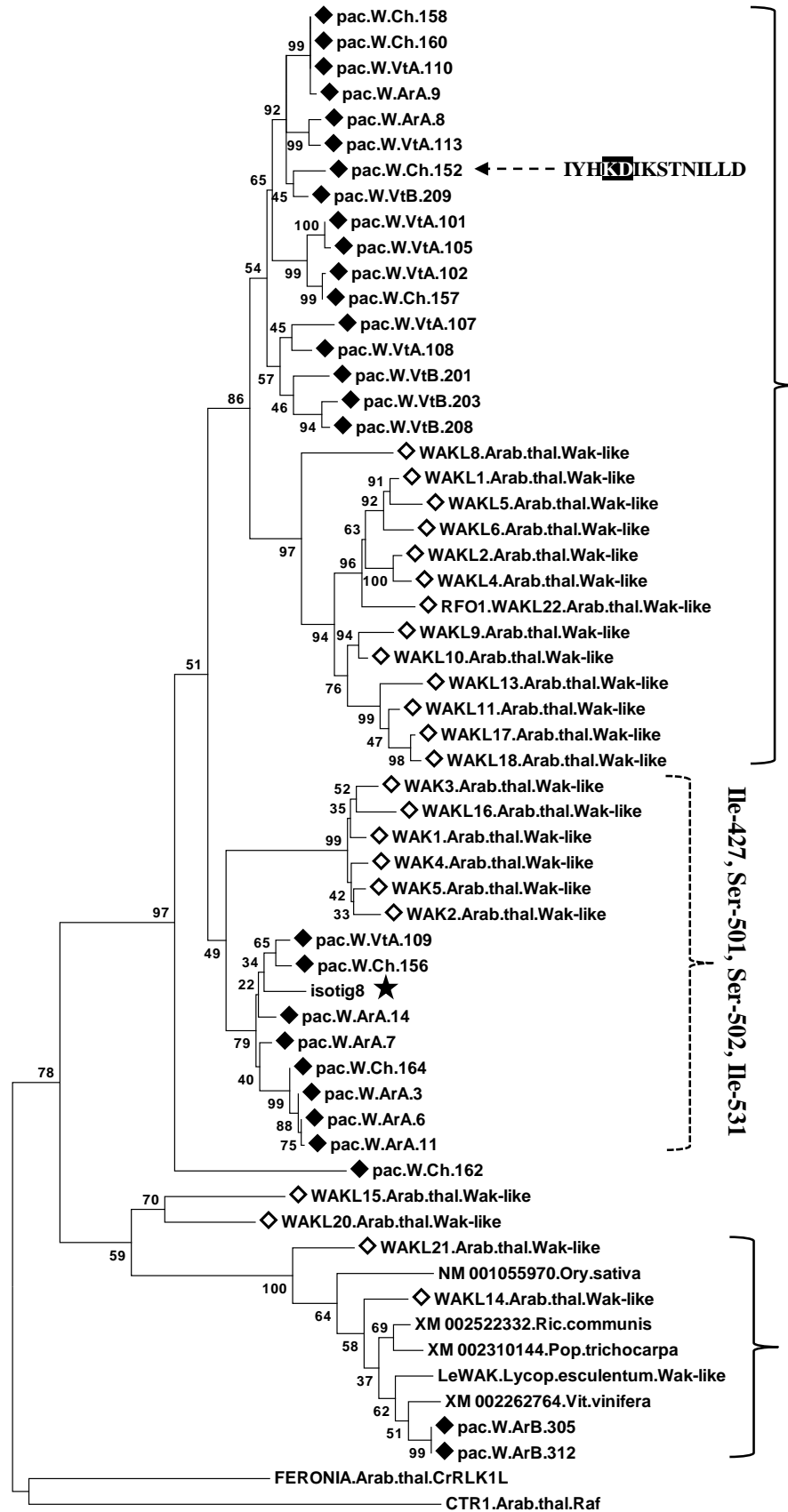
CRPK1-like1 (Shiu and Bleecker 2003)

CRPK1-like2 (Shiu and Bleecker 2003)

C



D



0.1

E

