

Additional file 17. Important residues of Wak-like located in the kinase domain region spanning subdomains VIB to VIII. The alignment shows the functional consensus derived from the Pto and BRI1 activation segment (subdomains VII and VIII) (Figure 6, Additional file 15) and its conservation in the WAK-like(-L) subfamilies of *Arabidopsis* and *Platanus × acerifolia* (*Pac*). Black-shaded residues define the Pto functional consensus and the identities with WAK-like(-L). BRI1 consensus residues shared with Pto consensus motif, are shaded black, the residue exclusive of BRI1 consensus is shaded grey. Shaded-grey gaps have been inserted in order to match sequences with BRI1 consensus. The figure also shows the RD and non-RD motif and the regions that are useful to infer the ser/thr, tyr and the dual phosphorylation specificities of protein kinases [42] (Additional file 14) [red-shaded residues (subdomain VIb) and the P+1 loop (subdomain VIII)].

