

**Additional file 16. Important residues of CrRLK1L 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 CrRLK1L(-L) subfamilies of *Arabidopsis* and *Platanus × acerifolia* (*Pac*). Black-shaded residues define the Pto functional consensus and the identities with CrRLK1L(-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/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)].

