

Additional file 8. Unwanted RLK/Pelles of *Platanus × acerifolia* (*Pac*). Sequences were obtained with primers aimed at isolating members of LRR XII subfamily. **A** Neighbor-joining tree based on the aa sequences of *Pac* (pac, ♦), the nearest RLK/Pelle members of *Arabidopsis* (◇) and other unknown, homologous sequences of rice and poplar. Analysis was based on the kinase domain region spanning subdomains I/II to the beginning of VIII. See caption of Figure 1 for details on the representation of the tree. **B** Multiple alignment of RD motif (shaded grey), non-RD motif (shaded black) and an atypical variant of the non-RD-Asp (shaded black). **C** Phylogenetic analysis was ambiguous in determining the homology relationship of pac.Erf.2, pac.Erf.9 and pac.Erf.13 with the *Arabidopsis* RLK/Pelle subfamilies GDPD, LRK10L-2, CRPK1-like2 (i.e. CrRLK1L) and Thaumatin. The table thus shows the identity and similarity values and number of gaps derived from the pairwise comparison of these sequences with one *Arabidopsis* relative for each subfamily which, in preliminary analyses, were the nearest sequences.

Plane tree genes				
	Arabidopsis homologs	aa id. (%)	aa sim. (%)	Gaps (%)
pac.Erf.13	At1G66910.LRK10L-2	61.5	74.3	3/148 (2.0)
	• 149 PR5K.Thaumatin	58.7	73.3	4/150 (2.7)
	• I/II→VIII At1G66980.GDPD	62.2	76.4	3/148 (2)
	At5G39030.CRPK1-like-2	60.1	74.3	3/148 (2)
pac.Erf.2	At1G66910.LRK10L-2	56.1	75.7	3/148 (2.0)
	• 149 PR5K.Thaumatin	55.5	75.3	3/146 (2.1)
	• I/II→VIII At1G66980.GDPD	54.1	73.6	3/148 (2)
	At5G39030.CRPK1-like-2	54	72.7	7/150 (4.7)
pac.Erf.9	At1G66910.LRK10L-2	55.4	75.0	3/148 (2.0)
	• 149 PR5K.Thaumatin	54.8	74.7	3/146 (2.1)
	• I/II→VIII At1G66980.GDPD	53.4	73	3/148 (2.0)
	At5G39030.CRPK1-like-2	51.4	70.9	3/148 (2.0)

C

