

**Additional file 5. The extracellular domain of *Platanus × acerifolia* (*Pac*) RLK/Pelles.** Pairwise comparison between selected gene fragments obtained in this work, and the overlapping RLK/Pelle isotigs extracted from a 454 FLX dataset of a *Platanus × acerifolia* (*Pac*) transcriptome (Pilotti M., Brunetti A., Iacono M. and Pindo M. unpublished data). **A** Spanning regions and identity values. **B** The isotigs display a region 5'-upstream the kinase domain, which includes putative extracellular domains typical of the RLK/Pelle subfamilies dealt with in this work (output data from Pfam). This is a confirmation of the phylogenetic identification of the gene fragments. A SMART analysis predicted in a confident manner transmembrane domains in all the isotigs, which were located upstream the kinase domain and downstream the putative extracellular domains.

## A

PCR gene fragments (length, nt)	Classification at the subfamily level	Isotigs KF208644-KF208653 (length, nt)	Spanning region	Identity score (nt)	Indel
pac.pt.10.306 (535)	CrRLK1L	1 (2322)	535	99.81	1 (1nt)
pac.ptd.5.2 (533)	CrRLK1L	2 (1707)	533	99.81	-
pac.pt.2.210 (533)	CrRLK1L	3 (2499)	533	100	-
pac.Erf.3 (493)	LRR XII	4 (2406)	493	89.05	1 (3nt)
pac.x.5.19 (496)	LRR XII	5 (2778)	496	91.13	-
pac.x.5.4 (487)	LRR XII	6 (3165)	487	93.43	-
pac.x.6.123 (502)	LRR XII	7 (1131)	502	88.25	1 (1nt)
pac.W.Ch.156 (503)	WAK-Like	8 (2283)	503	88.47	-
pac.BRI.L.2 (825)	LRR X-BRI1	9 (1071)	136 <sup>a</sup>	100	-
pac.BRL2.102 (832)	LRR X-BRL	10 (2109)	832	99.76	-

<sup>a</sup> pac.BRI.L.2 overlapped the isotig in head-to-tail fashion

## B

<i>Pac</i> (S1s/43) RLK/Pelle Isotigs	Classification	Domain with significant matches <sup>1</sup>	E-value	Domain with insignificant matches <sup>a</sup>	E-value
1	CrRLK1L	Malectin like (80-444) Pkinase (574-772)	3.6e-64 3.2e-44	SKG6 (473-513)	0.2
2	CrRLK1L	Malectin like (2-132) Pkinase (229-502)	1.1e-16 1.1e-46		
3	CrRLK1L	Malectin like (10-347) Pkinase (498-768)	9.8e-54 7.8e-47		
4	LRR XII	LRR8 (291-351) Pkinase (483-789)	1.4e-06 3.4e-43	LRR8 (1-56) LRR4 2 copies (170-218) LRR8 (221-279)	5.8e-05 9e-05 0.001
5	LRR XII	LRRNT 2 (53-92) LRR6 (487-509) LRR4, 2 copies (513-552) LRR8 (561-620) Pkinase (727-921)	1.1e-11 0.18 1.9e-06 4.9e-07 6.9e-33	LRR8 (120-180) LRR8 (192-252) LRR4 (313-365) LRR8 (367-428) LRR4 (440-477)	0.0003 9e-05 0.14 0.00044 0.06
6	LRR XII	LRRNT2 (47-87) LRR8 (189-249) LRR4 (534-579) Pkinase (727-1027)	6e-12 2.5e-07 1e-06 3.2e-40	LRR8 (118-177) LRR8 (413-473) LRR4, 2 copies (582-623)	6.7e-05 0.025 0.00045
7	LRR XII	LRR1 (13-34) LRR8 (36-95) Pkinase (202-373)	0.22 2.5e-10 5.1e-31		
8	WAK-Like	GUB WAK bind (46-157) EGF-CA (312-352) Pkinase (439-709)	7.2e-28 4e-07 1.5e-51	EGF3 (272-305)	0.054
9	LRR X-BRII	LRR8 (120-178)	4.5e-07	LRR6 (1-24) Pkinase (318-355)	0.099 0.011
10	LRR X-BRL	LRR4 (178-225) Pkinase 406-689	9.3e-07 1.6e-43	LRR4 (14-61) LRR4 (62-106) PgaD (312-379)	4.5e-05 2.8e-06 0.012

<sup>a</sup>: domain names

Pkinase: Protein kinase

Malectin like: Carbohydrate-binding protein of the endoplasmic reticulum

LRR: Leucine rich repeat

LRRNT: Leucine rich repeat N-terminal

GUB WAK bind: Wall-associated receptor kinase galacturonan-binding

EGF-CA: Calcium-binding epidermal growth factor

EGF3: Epidermal growth factor

SKG6: Transmembrane alpha-helix