

Figure S3

		P	P	
A.thaliana	1	MGCFSCFDS	SSDDEKLN	PF-----VD
G.max	1	MGCFSCFDS	SSSKEDHNL	PF-----RPO--H
R.communis	1	MGCFSCFDS	REEETLNP	PF-----QK--S
P.trichocarpa	1	MGCFSCFDS	REEEKLNQ	PF-----EKQ--S
S.lycopersicum	1	MGCFSCFDS	KEDEKLN	PF-----KKD--R
O.sativa	1	MGCFSCFDS	PAEEQLNPKVGGPYG-GGSSSSAAAAAYGGGGSS	AGRHGERGGYPDLHH
Z.mays	1	MGCFSCFDS	PADEQLNPKFGGAGGYGGTSSAVAAYGN	TGAGVSIGRHGDR--GYPL--
P.taeda	1	MGCFSCFDS	RSSKKS	PKSPK-----SSMED
P.patens	1	MGCFSCFDS	KPKERKPLK	PF-----RDDNNS

A.thaliana	24	GQKK	QSTVTSNNISGLPSGGEKLS	SKTNG-GSKRELLPRD---GLG	QIAAHTFAFREL
G.max	22	QPNQ---	PLPSQISRLPSGADKLSRS	SNG-GSKRELQQPPP---TVQ	IAAQTFTFREL
R.communis	22	DDRK	QSLTESSNISKLSGADRLRS	RSNG-RSKRELPSPKDGPV	PGVNMIAAQTFTFREL
P.trichocarpa	22	VDLK	QTLPPVSSNISKLSGADRFK	RSNNGEQSKRELPSPKD--	APGVNIAAHTFTFREL
S.lycopersicum	22	DDSDRK	QPEP-PSNISRLSSGADRLK	IRSNG-GSKREFLGLKD--	APDVQIAAHTFTFREL
O.sativa	60	HHQQ	QQLPMAAPRVEKLSAGA	EKTRVKSNA--ILREPS	APKD--ANGNVISAQTFTFREL
Z.mays	57	---	QAPMAAPRVEKLSAAA	EKARVKSNG--LTK	EALVPKD--ANGNAISAQTFTFREL
P.taeda	23	TKAG	QSAASSTHAAKDP	PESIKSKPSFDS--RRE	MS--RD---GSQHTAAQTFTFREL
P.patens	26	RDGQ	SAAANPVAQISKLP	SGTCNSK-KYDAKGS	FDKKEPQRE---GSTHIAAQTFTFREL

		I		II	III
		95			
A.thaliana	80	AAATMNFH	PDTFLGEGGFRVYKGR	LDST-----GQVVAVKQLDR	NGLQGNREFLV
G.max	73	AAATKNFR	PESFVGE	GGFRVYKGRLETT-----	AQIVAVKQLDR
R.communis	81	AAATKNFR	QESFVGE	GGFRVYKGRLETT-----	GQVVAVKQLDR
P.trichocarpa	80	AAATKNFR	PCEFLGEGGFRVYKGR	LEST-----GQVVAVKQLDR	NGLQGNREFLV
S.lycopersicum	78	AAATNNFR	PESFVGE	GGFRVYKGRLEPS-----	GQVVAVKQLDR
O.sativa	116	ATATRNFR	PCEFLGEGGFRVYKGR	LEST-----GQVVAIKQLNR	DGLQGNREFLV
Z.mays	109	ATATRNFR	PCEFLGEGGFRVYKGR	LEST-----GQVVAIKQLNR	DGLQGNREFLV
P.taeda	75	AAATKNFR	PECLLGE	GGFRVYKGRLEST-----	GQVVAVKQLDR
P.patens	82	AAATKNFR	PECLLGE	GGFRVYKGRLENTGQARVLS	GWLQVVAVKQLDR

		III	IV	V	VIa
A.thaliana	131	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEALDWNTRMKI
G.max	124	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEPLDWNTRMKI
R.communis	132	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEPLDWNTRMKI
P.trichocarpa	131	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEPLDWNTRMKI
S.lycopersicum	128	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEPLDWNTRMKI
O.sativa	167	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEALDWNTRMKI
Z.mays	160	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEALDWNTRMKI
P.taeda	126	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKEPLDWNTRMKI
P.patens	142	EVLMLSL	LHHPNLVNLIGYCADGDQ	RLLVYEFMPLGSLEDHLHDL	PPDKECLDWNTRMKI

		VIa	VIb	VII	VIII
A.thaliana	191	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPTGDKSHVSTRV
G.max	184	AVGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPVGDKSHVSTRV
R.communis	192	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPTGDKSHVSTRV
P.trichocarpa	191	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPTGDKSHVSTRV
S.lycopersicum	188	ASGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPTGDKSHVSTRV
O.sativa	227	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDESHPKLS	SDFGLAKLGPVGDKSHVSTRV
Z.mays	220	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDESHPKLS	SDFGLAKLGPVGDKSHVSTRV
P.taeda	186	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPVGDKSHVSTRV
P.patens	202	AAGAAK	GLEYLHDKANPPVIYR	DFKSSNILLDEGFHPKLS	SDFGLAKLGPVGDKSHVSTRV

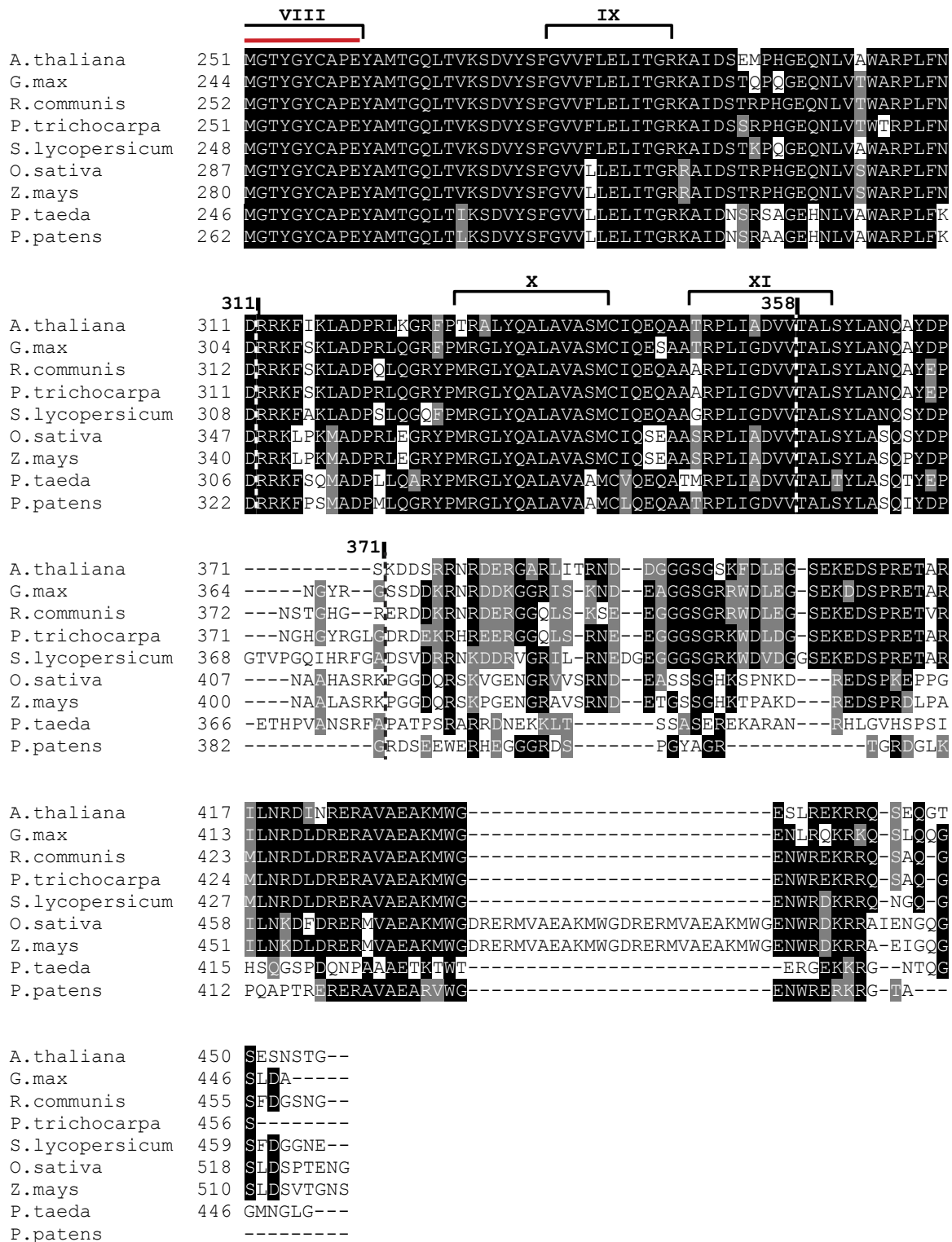


Figure S3. Alignment of PBS1 Orthologues. Amino acid sequences were aligned using ClustalW2, with default parameters selected. The alignment output was converted to a visual representation using Boxshade 3.21 using the default parameters. Conserved protein kinase domains of PBS1 are indicated with brackets above the alignment. Potential palmitoylation (P) sites are indicated above the alignment. The position of the N- and C-terminal truncations of PBS1 are indicated above the alignment with a vertical line and the position of the terminal amino acid. The activation segment is indicated by the red bar and the site of cleavage by AvrPphB is indicated by a vertical arrow within the red bar.