Table S1. Sequences of primers for generation Y2H, BiFC and *in vitro* kinase assay constructs.

Name	Nucleotide sequence from 5′ to 3′ [a]	Orientation	Use
ML3564	CCGGAATTCTCCTTCAAAGACGACAATCTC (*Eco*RI)	Forward	In generation of plasmids pAT1103, pAT1114
ML3565	CGCGGATCCTCAATTTACTTCTCCCCCCACA (*Bam*HI)	Reverse	In generation of plasmid pAT1103
ML3566	CCGGAATTCTCCTTCAAAGACGACAATCTC (*Eco*RI)	Forward	In generation of plasmids pAT1104, pAT1115
ML3567	CGCGGATCCTCAATTTACTTCTTCCCCCACA3 (*Bam*HI)	Reverse	In generation of plasmid pAT1104
ML3568	CCCCCCGGGGATGTACAGAGAGCGAGGAGG (*Xma*I)	Forward	In generation of plasmid pAT1096
ML3569	CCGCTCGAGTCAGGGCTTGTGAAGTTTGA (*Xho*I)	Reverse	In generation of plasmid pAT1096
ML3570	CCGGAATTCATGCAGAAGCATGGTTTT (*Eco*RI)	Forward	In generation of plasmid pAT1097
ML3571	CCGCTCGAGTCAAGAAGAGTCTTTGTCTTT (*Xho*I)	Reverse	In generation of plasmid pAT1097
ML3572	CCGGAATTCATGGAAGGAGGAGGAGCTG (*Eco*RI)	Forward	In generation of plasmid pAT1098
ML3573	CCGCTCGAGCTACTGCTGATACTCAGGGTTAAA (*Xho*I)	Reverse	In generation of plasmid pAT1098
ML3574	CGCGGATCCCGATGGAAAACAATGGTGCTGA (*Bam*HI)	Forward	In generation of plasmid pAT1099
ML3575	CCGCTCGAGCTATTCCAACATCTGATGATCCT (*Xho*I)	Reverse	In generation of plasmid pAT1099
ML3576	CCGGAATTCATGGAGCGCTATGAGATCCT (*Eco*RI)	Forward	In generation of plasmid pAT1100
ML3577	CCGCTCGAGTTAAATAGGACACACAAATTCAC (*Xho*I)	Reverse	In generation of plasmid pAT1100
ML3578	CGCGGATCCCGATGGAACGGTATGAGAT (*Bam*HI)	Forward	In generation of plasmid pAT1101
ML3579	CCGCTCGAGTCACAATGCACAGACAA (*Xho*I)	Reverse	In generation of plasmid pAT1101
ML3580	CCGGAATTCATGGATCGGGCGGCGTTGAC (*Eco*RI)	Forward	In generation of plasmid pAT1102
ML3581	CCGCTCGAGCTATATGGCATACACTATCTC (*Xho*I)	Reverse	In generation of plasmid pAT1102
ML3608	CGCGGATCCTTCCATTTGTGAGTCACTGC (*Bam*HI)	Reverse	In generation of plasmid pAT1114
ML3609	CCGGAATTCGCCATTCATGGATTTGCCAG (*Eco*RI)	Forward	In generation of plasmid pAT1116
ML3610	CGCGGATCCGTTTGACTCACAGATGTCACG (*Bam*HI)	Reverse	In generation of plasmid pAT1116
ML3611	CCGTCTAGAATGGAAGGAGGAGGAGCTG (*Xba*I)	Forward	In generation of plasmid pAT1119
ML3612	CGCGGATCCCGGGCCCTACTGCTGATACTCAGGGTTAA (*Bam*HI)	Reverse	In generation of plasmid pAT1119
ML3613	CGCGGATCCATGGAACGGTATGAGAT (*Bam*HI)	Forward	In generation of plasmid pAT1120
ML3614	CCGCTCGAGCGGGCCTCACAATGCACAgACAA (*Xho*I)	Reverse	In generation of plasmid pAT1120
ML3615	CCGCTCGAGATGGAAGGAGGAGGAGCTG (*Xho*I)	Forward	In generation of plasmid pAT1121
ML3616	CGCGAATTCCTACTGCTGATACTCAGGGTTAAA (*Eco*RI)	Reverse	In generation of plasmid pAT1121
ML3617	CGCCTCGAGATGGAACGGTATGAGAT (*Xho*I)	Forward	In generation of plasmid pAT1122
ML3618	CGCCTCGAGATGGAACGGTATGAGAT (*Xho*I)	Reverse	In generation of plasmid pAT1122
ML3150	CTCGAGGACGACAATCTCACCGTCAC (*Xho*I)	Forward	In generation of plasmid pAT963
ML3129	TGGGGGAAGAAGTAAATTGACTCGAG (*Xho*I)	Reverse	In generation of plasmid pAT963

[a] Restriction sites are underlined and shown in parentheses.

Table S2. Kinase-specific phosphorylation sites of Class II GmACBPs predicted by GPS 6.0.

Phosphosite position	Code	Phosphopeptide sequence [a]	Score	Kinase family
49	T	AAAETTTTTRDDAVS	0.0615	CK
57	S	TRDDAVSSDARPFEE	0.3391	CK
78	S	HGSVRNDSDGDYDDD	0.4620	CK
120	S	RLSQKVSSDVQLQLY	0.0784	CK
140	T	ATEGPCSTPQPSPLK	0.2057	CK
179	T	YIDIVTETYPTWLDG	0.0536	AGC
182	T	IVTETYPTWLDGSSL	0.0533	AGC
193	S	GSSLRNKSGDSGGHG	0.3440	CK
250	S	KCIENGVSMNLKDSE	0.0910	CK
256	S	VSMNLKDSEGRTPLH	0.1242	CK

[a] Phosphorylation sites are in red.

Table S3. Kinase-specific phosphorylation sites of Class II GmACBPs predicted by EPSD 1.0.

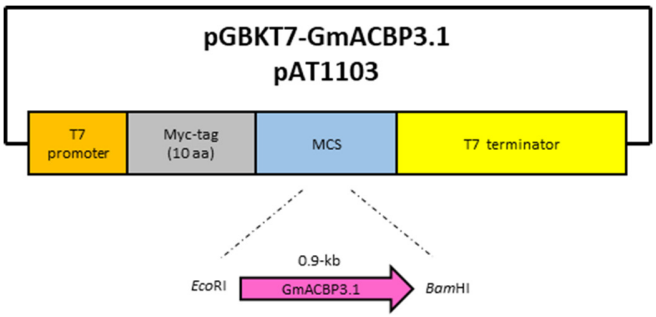
Phosphosite position	Code	Phosphopeptide sequence [a]	Score	Kinase family
56	S	TTRDDAVSSDARPFE	0.007	AGC/CK
57	S	TRDDAVSSDARPFEE	0.007	CK
66	S	ARPFEEESMVAEHGS	0.997	CK
73	S	SMVAEHGSVRNDSDG	1	AGC
78	S	HGSVRNDSDGDYDDD	1	CK/AGC

[a] Phosphorylation sites are in red.

Table S4. Kinase-specific phosphorylation sites of Class II GmACBPs predicted by NetPhos 3.1.

Phosphosite position	Code	Phosphopeptide sequence [a]	Score	Kinase family
18	S	GLIFSYLLA	0.539	CLK
30	S	SIVVSFKDD	0.707	AGC
37	T	DDNLTVTRA	0.438	AGC
49	T	ETTTTTRDD	0.5	AGC
56	S	DDAVSSDAR	0.616/0.576	AGC /CK
57	S	DAVSSDARP	0.566	CK
66	S	FEEESMVAE	0.509	CK
78	S	VRNDSDGDY	0.583	AGC
92	S	EGVESTELD	0.689	CK
93	T	GVESTELDE	0.625	CK
115	S	ADRLSQKVS	0.822/0.665	AGC /PIKK
120	S	QKVSSDVQL	0.625	CK
140	T	GPCSTPQPS	0.588/0.585/0.502	CDK/MAPK/GSK
144	S	TPQPSPLKM	0.642/0.5	CDK/ GSK
149	T	PLKMTARAK	0.779	AGC
187	S	WLDGSSLRN	0.697	AGC
188	S	LDGSSLRNK	0.803	AGC
193	S	LRNKSGDSG	0.515	AGC
213	T	PVFSTFVYE	0.553	CK
222	S	EEYGSDSQM	0.644/0.515	CK/CLK
224	S	YGSDSQMEA	0.633/0.632	CK/PIKK
256	S	NLKDSEGRT	0.995	CK
293	T	NDGQTPLHY	0.501	MAPK
319	S	ADIYSKDND	0.525	CK

[a] Phosphorylation sites are in red.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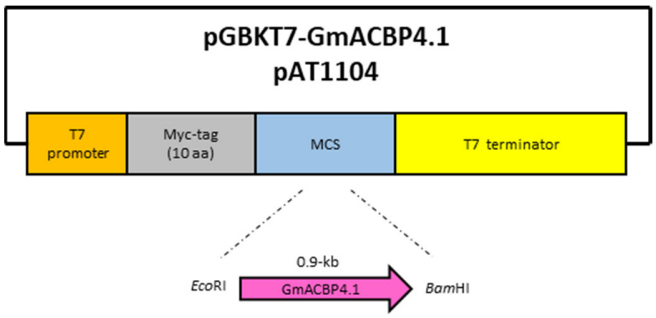
BamHI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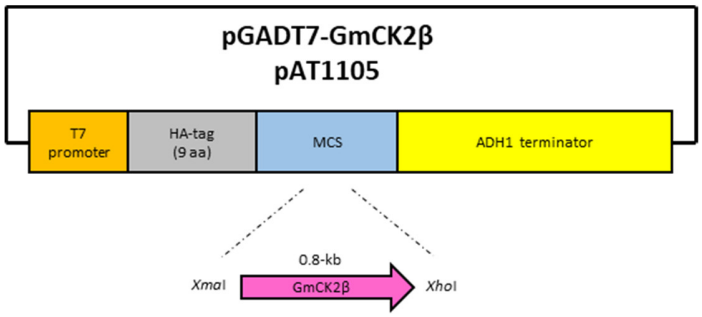
BamHI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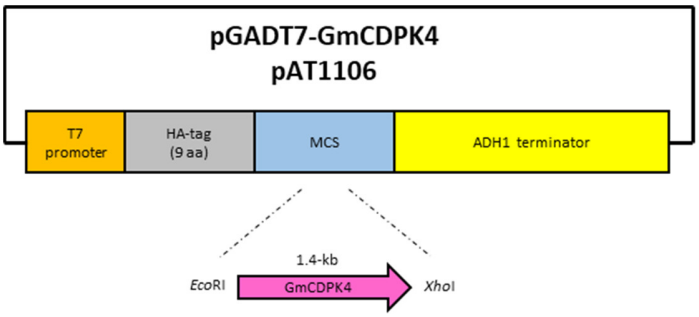
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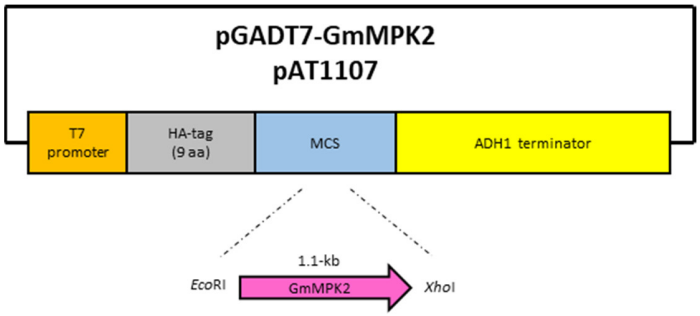
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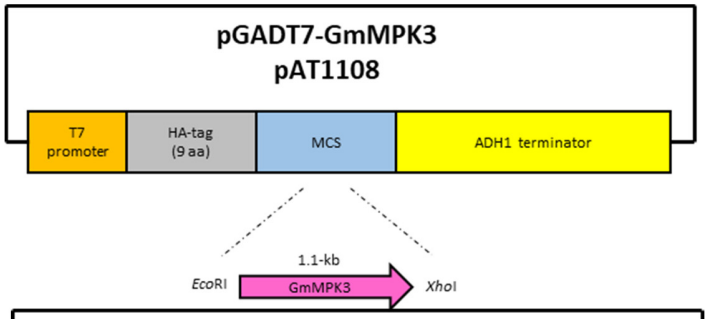
XhoI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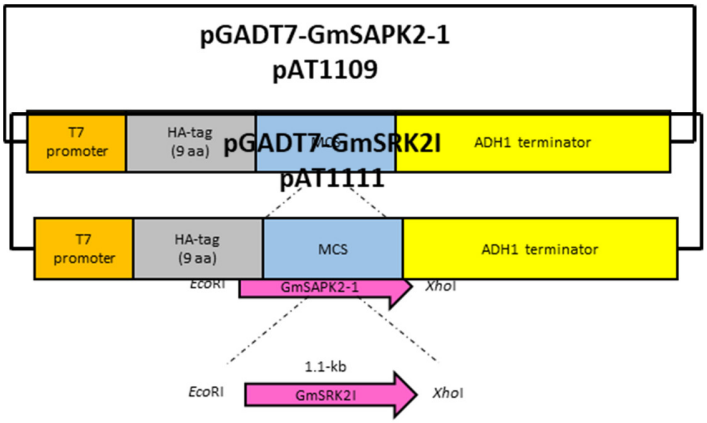
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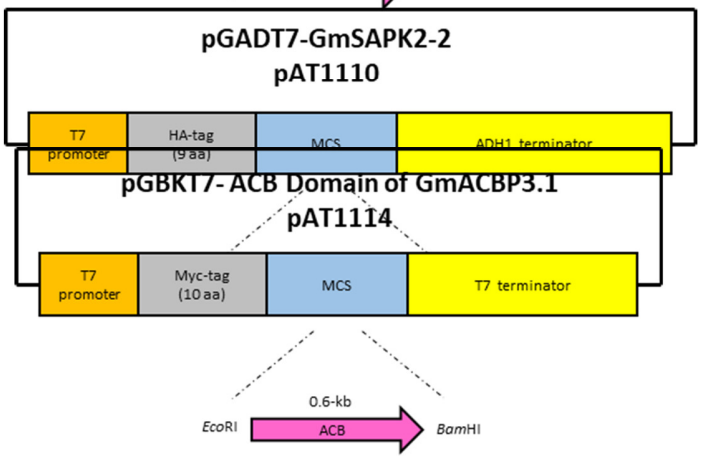
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ADH1 terminator
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T7 promoter
HA-tag (9 aa)
MCS
ADH1 terminator
EcoRI
XhoI
1.1-kb
EcoRI
GmSRK2I
XhoI
pGBKT7- ACB Domain of GmACBP3.1
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Myc-tag (10 aa)
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ACB
BamHI

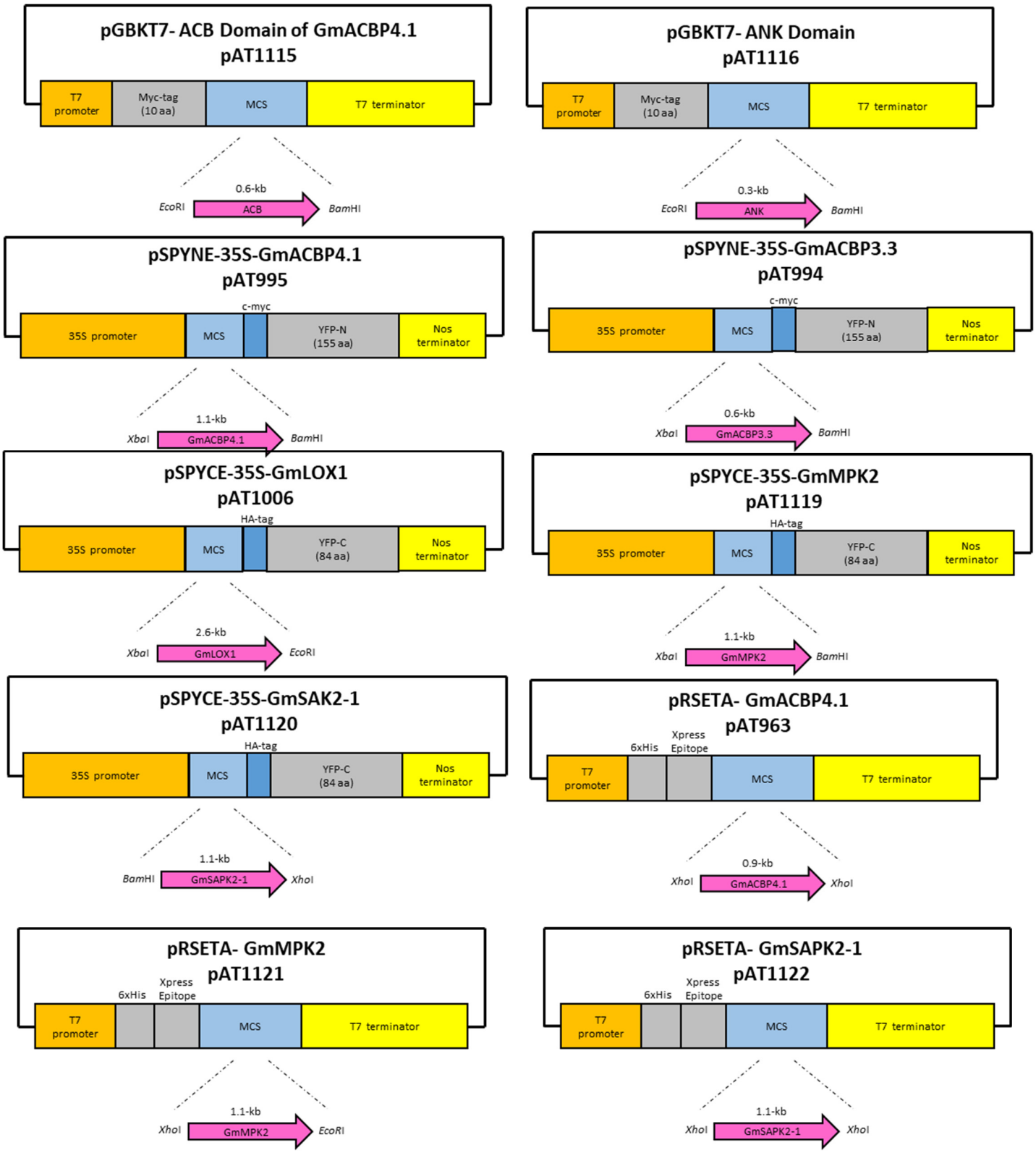

Figure S1. This figure represents all constructs used in this study, including Y2H, BiFC and *in vitro* kinase assays.