

Supplementary Fig. 1 Identification of upstream regulators of *Bsr-d1* derived from *M. oryzae*.

a Expression level of *Bsr-d1* 2 hr post chitin treatment. *OsUbg5* was used as an internal control. Values are mean \pm SD, n=3 biologically independent samples (Student's two-sided *t*-test, n.s. indicates no significance). Source data are provided as a Source Data file.

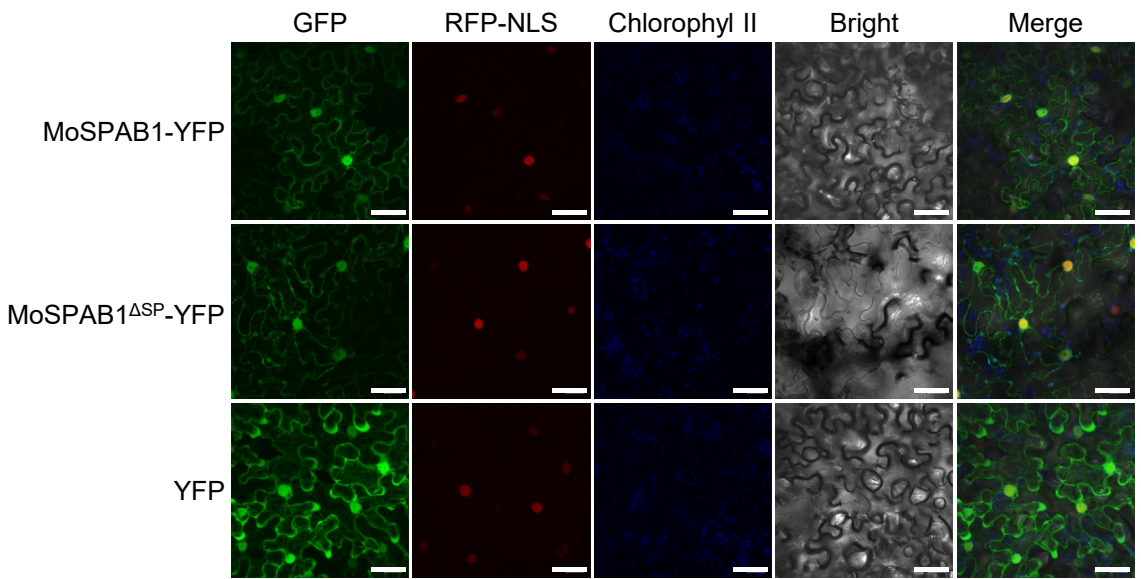
b Determination of MoSPAB2^{ΔSP} binding to the *Bsr-d1* promoter in a yeast one-hybrid assay. The *Bsr-d1* promoter was fused to the HIS2 reporter and MoSPAB2^{ΔSP} to GAL4 AD. Yeast cells transformed with the reporter and an effector construct with or without MoSPAB2^{ΔSP}. The SD/-Leu/-Trp/-His medium with 60 mM 3-amino-1,2,4-triazole (3-AT) was used to test for HIS2 expression.

c Activation of the *Bsr-d1* promoter by MoSPAB2 in luciferase assay using *N. benthamiana*. Luciferase signals were imaged (left panel) and measured (right panel) using a dual-LUC assay 48 hr after infiltration. The positive control contains transcription factor EAT1 and *OsLTPL94* promoter driving reporter. EV contains 35S:YFP as the negative control. LUC activities were normalized to REN. Values are mean \pm SD, n = 3 samples (one-way ANOVA with Dunnett T3's test, *P* values are shown in the Source Data file). Different letters indicate significant differences (*P* < 0.05). Source data are provided as a Source Data file. Similar results are obtained from three independent biological experiments.

d A schematic diagram of the DNA fragments and probes used for DAP-qPCR and EMSA. The DNA fragments (F1-F9) for DAP-qPCR are indicated by blue lines. The five probes located in F9 used for EMSA are indicated by red lines.

e Binding of MoSPAB1^{ΔSP} to probe 1 to probe 5 in EMSA. Locations of the probes are as indicated in (D); sequences of the five probes are listed in supplementary table 2. Each probe was labeled with biotin at the 5' end. 6×His was used as a negative control. Similar results are obtained from two independent biological experiments.

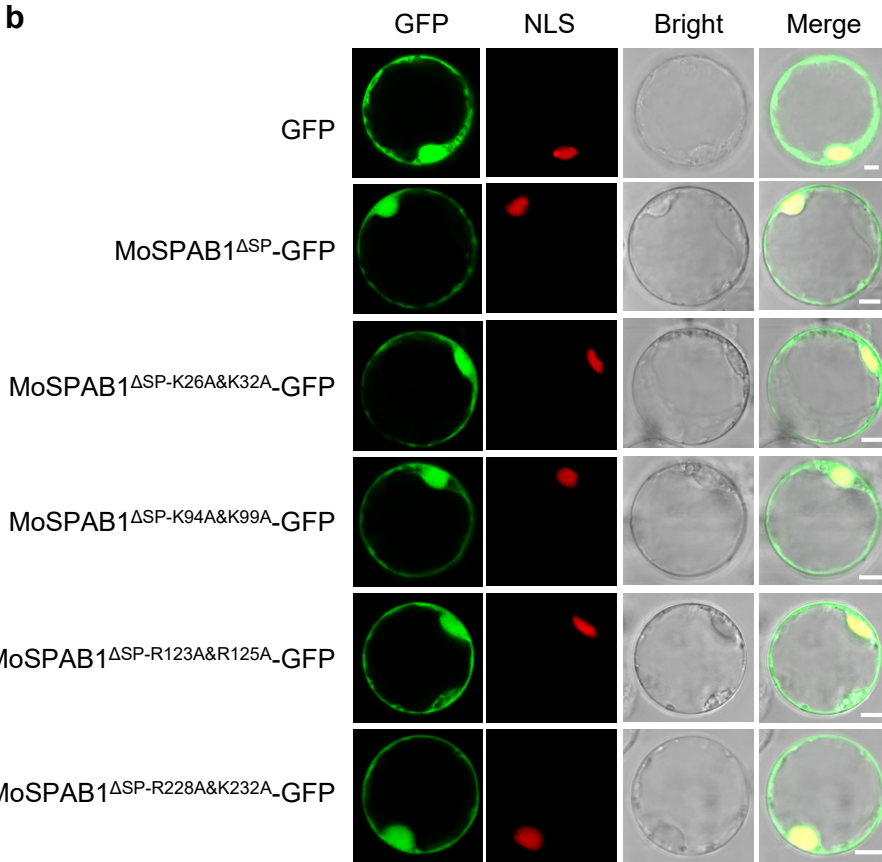
f A conserved motif deduced from the probes bound by MoSPAB1 using the MEME suite version 5.4.1. The conserved bases are displayed in colors. M: A/C, Y: C/T.



Supplementary Fig. 2 Localization of MoSPAB1-YFP and MoSPAB1^{ASP}-YFP in mesophyll cells of *N. benthamiana* leaves. The 35S:MoSPAB1-YFP, 35S:MoSPAB1^{ASP}-YFP, and 35S:YFP constructs were used to infiltrate *N. benthamiana* leaves mediated by *Agrobacterium*. Fluorescence images were observed using confocal microscopy 48 hours post inoculation. RFP-NLS serves as a nuclear marker. Chloroplasts are visualized by chlorophyll II, which is represented by blue pseudocolor. Scale bars, 20 μ m. Similar results are obtained from two independent biological experiments.

a

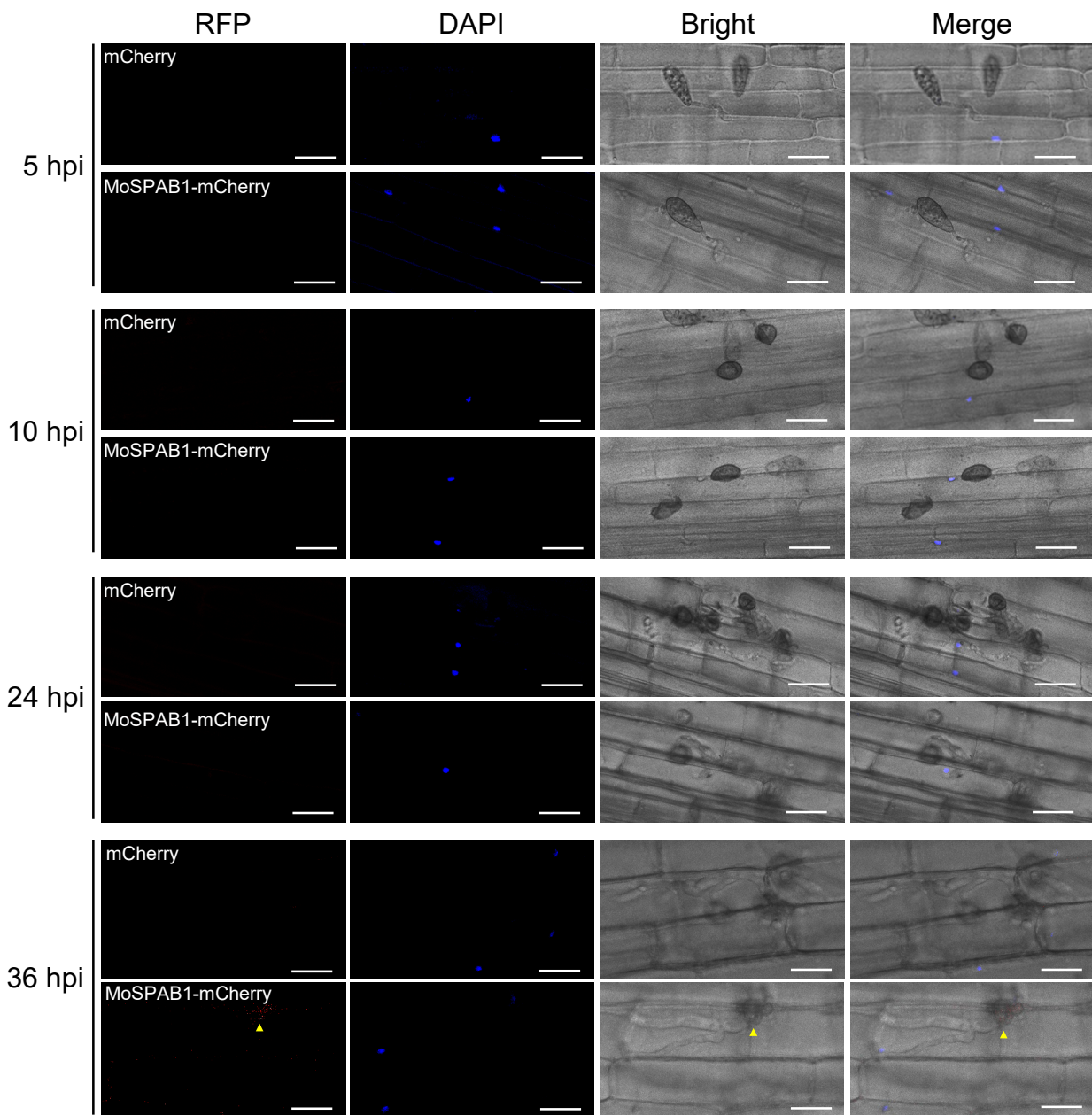
MLFTPIRSL	ASLLALASCA	VAQNV <u>K</u> AIYL	<u>F</u> KDVMQSDTH	ALKTSGFDTV	50
LLFRIGILPN	ADLVYYSTGS	DGNPVDWPVV	TNGSYVGGQA	LTD <u>K</u> ITSL <u>K</u> T	100
APTLIERVEV	SLVSHDTTFQ	<u>V</u> IRDRIAADG	TGASTPLYRA	FDVLKQTWEL	150
DAFNNDDES	YHVPSTVDF	QMLGLMGYKY	STAPYTNMNF	WADVQNRINA	200
SVPGLLDRQY	LQVYDGGGAN	NPGTWQTR <u>L</u> G	<u>M</u> KIVPLLWVN	NDYKPDHGNT	250
PAQAQTRFAN	WNSQYNLAGG	GYWNDYDIEK	LNSSYEGYGG	ALTSVFGQ	298



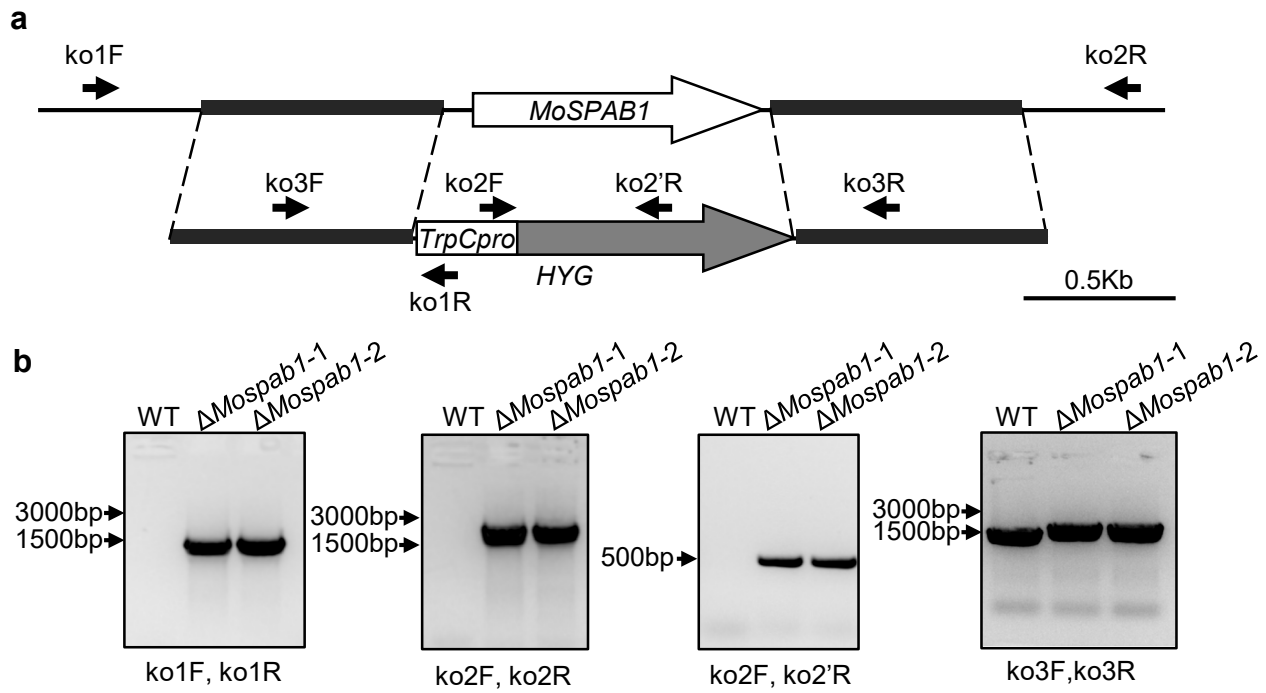
Supplementary Fig. 3 Analysis of nuclear localization signals of MoSPAB1 and localization of mutant MoSPAB1 in rice protoplasts.

a Analysis of nuclear localization signals of MoSPAB1. The underlined amino acids potentially serve as nuclear localization signals. Key amino acids K and R are highlighted in bold.

b Localization of mutant MoSPAB1 in rice protoplasts. The underlined amino acids in bold were changed into alanine (A), individually. MoSPAB1^{ΔSP}-GFP, MoSPAB1^{K26A&K32A}-GFP, MoSPAB1^{K94A&K99A}-GFP, MoSPAB1^{R123A&R125A}-GFP, and MoSPAB1^{R228A&K232A}-GFP were individually expressed transiently in rice protoplasts for 16 hours. Rice protoplasts were examined under a confocal microscope. NLS in PBI221-H2B-mCherry serves as a nuclear marker. Scale bars, 5 μm. Similar results are obtained from two independent biological experiments.



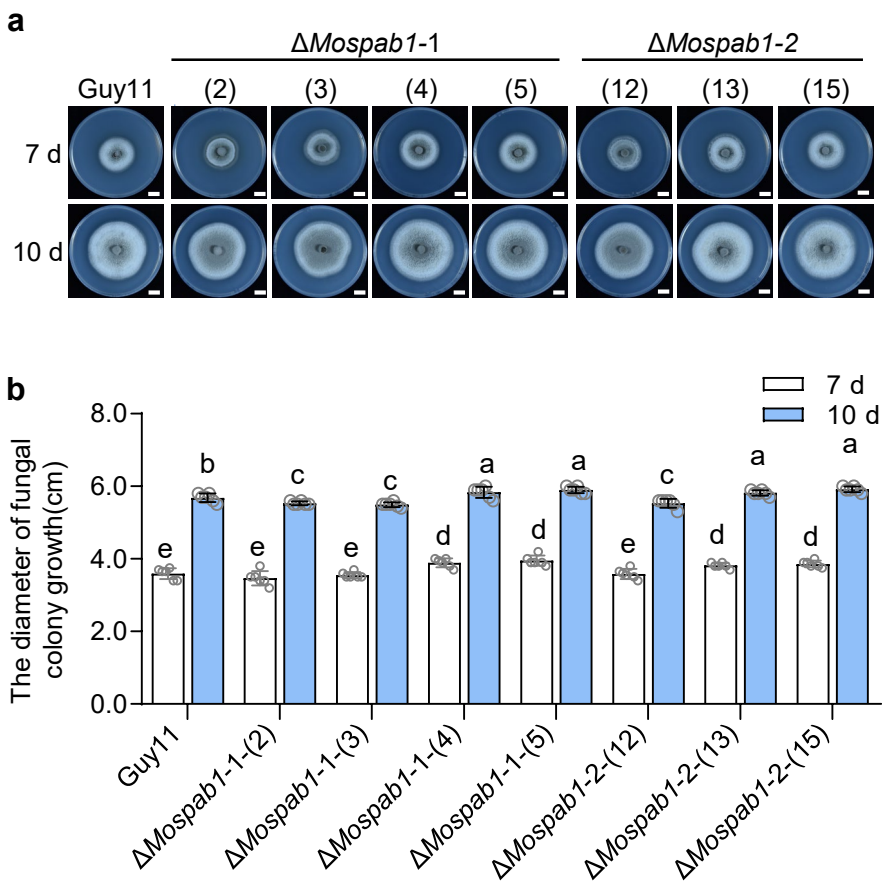
Supplementary Fig. 4 Development of the *MoSPAB1:MoSPAB1-mCherry* strain on rice leaf sheath. Rice leaf sheath was inoculated with conidial suspensions of the *MoSPAB1:MoSPAB1-mCherry* (labeled *MoSPAB1-mCherry*) strain and images taken at 5, 10, 24, and 36 hours post inoculation. *MoSPAB1:mCherry* (labeled mCherry) strain is the negative control. Yellow triangles indicate the *MoSPAB1-mCherry* in invasion hyphae. Scale bars, 20 μ m. Similar results are obtained from two independent biological experiments.



Supplementary Fig. 5 Generation of the Δ *Mospab1* mutant.

a A schematic diagram of targeted deletion of *MoSPAB1* in *M. oryzae*.

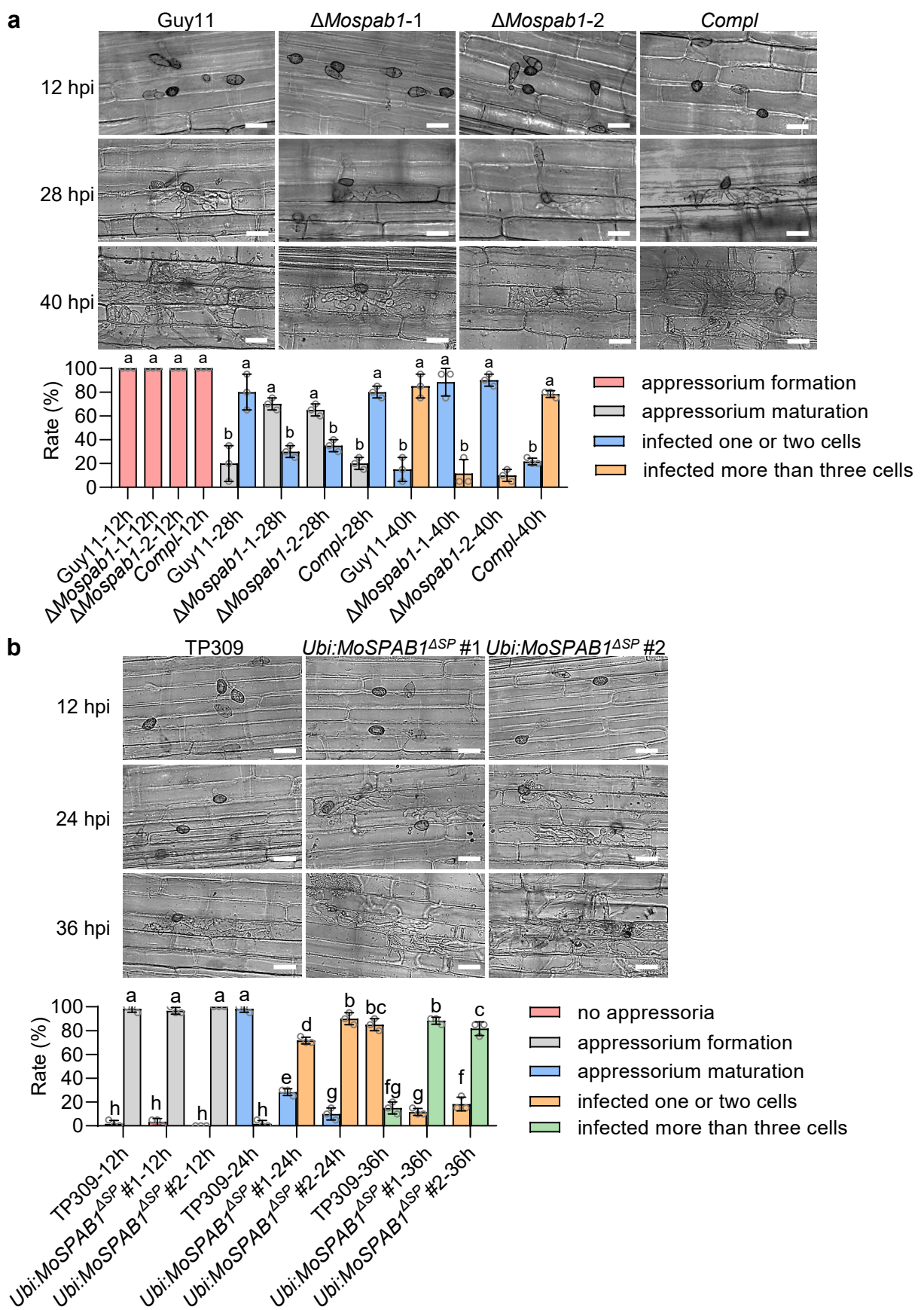
b DNA gel blot analysis of the Δ *Mospab1* mutants. Genomic DNA was analyzed by PCR with primer pairs in (a).



Supplementary Fig. 6 Mycelial growth of Guy11 and the Δ Mospab1 mutants on complete medium (CM).

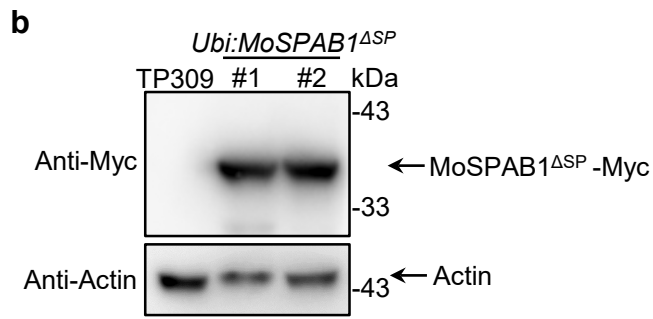
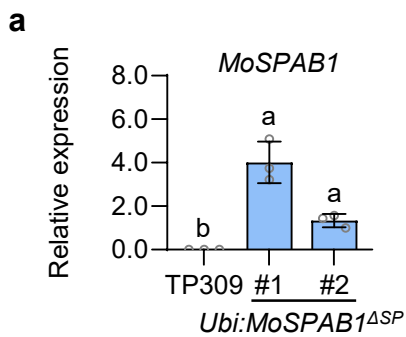
a Colonies of Guy11 and the Δ Mospab1 mutants grown on CM plates for 7 and 10 days. Similar results are obtained from two independent biological experiments.

b Quantified diameters of colonies in (A). Bars represent mean \pm SD, n = 6 biologically independent samples (one-way ANOVA with two-sided least significant difference (LSD) test, P values are shown in the Source Data file). Different letters indicate significant differences ($P < 0.05$). Source data are provided as a Source Data file.



Supplementary Fig. 7 Representative laser-scanning microscopic images of rice sheath cells infected by *M. oryzae*.

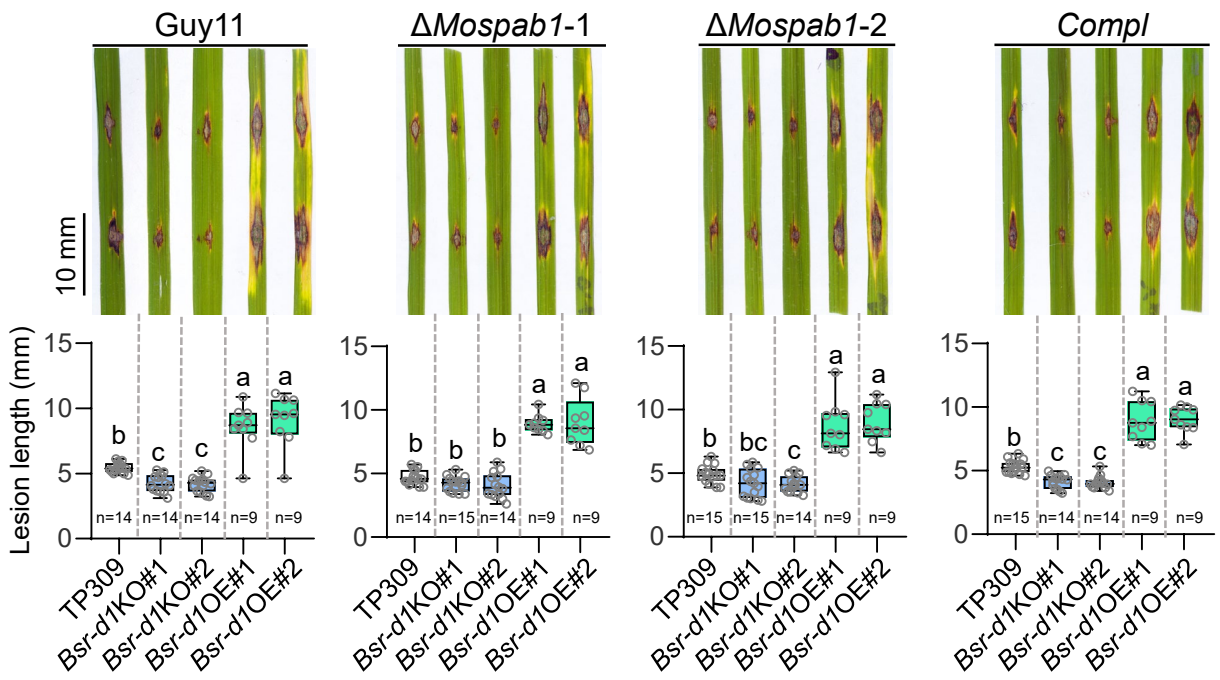
a Representative laser-scanning microscopic images of TP309 sheath cells infected by Guy11, Δ Mospab1, and a complemented strain individually (upper panel) and distribution of fungal infection progressing at 12, 28, and 40 hpi (lower panel). Scale bars, 20 μ m. **b** Representative laser scanning microscopic images of TP309 and *Ubi:MoSPAB1^{ASP}* sheath cells infected by Guy11 (upper panel) and distribution of fungal infection progressing at 12, 24, and 36 hpi (lower panel). Scale bars, 20 μ m. In a and b, a total of 100 spores are counted. n= 3 independent experiments (one-way ANOVA with two-sided least significant difference (LSD) test, *P* values are shown in the Source Data file). Different letters indicate significant differences (*P* < 0.05). Source data are provided as a Source Data file.



Supplementary Fig. 8 Heterologous *MoSPAB1 Δ SP* expression in TP309 rice plants and detection of MoSPAB1 protein.

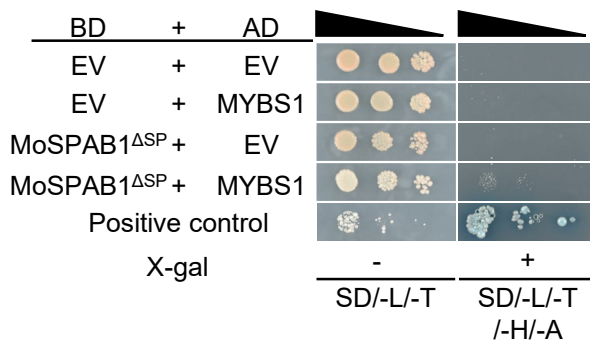
a *MoSPAB1 Δ SP* RNA levels were measured by RT-qPCR. Bars represent mean \pm SD ($n = 3$ biologically independent samples) and analyzed by one-way ANOVA with Dunnett T3's test. P values are shown in the Source Data file. Different letters indicate significant differences at $P < 0.05$. Source data are provided as a Source Data file.

b *MoSPAB1 Δ SP*-Myc fusion protein was detected by immunoblotting using an antibody against Myc. Actin was used as a loading control.



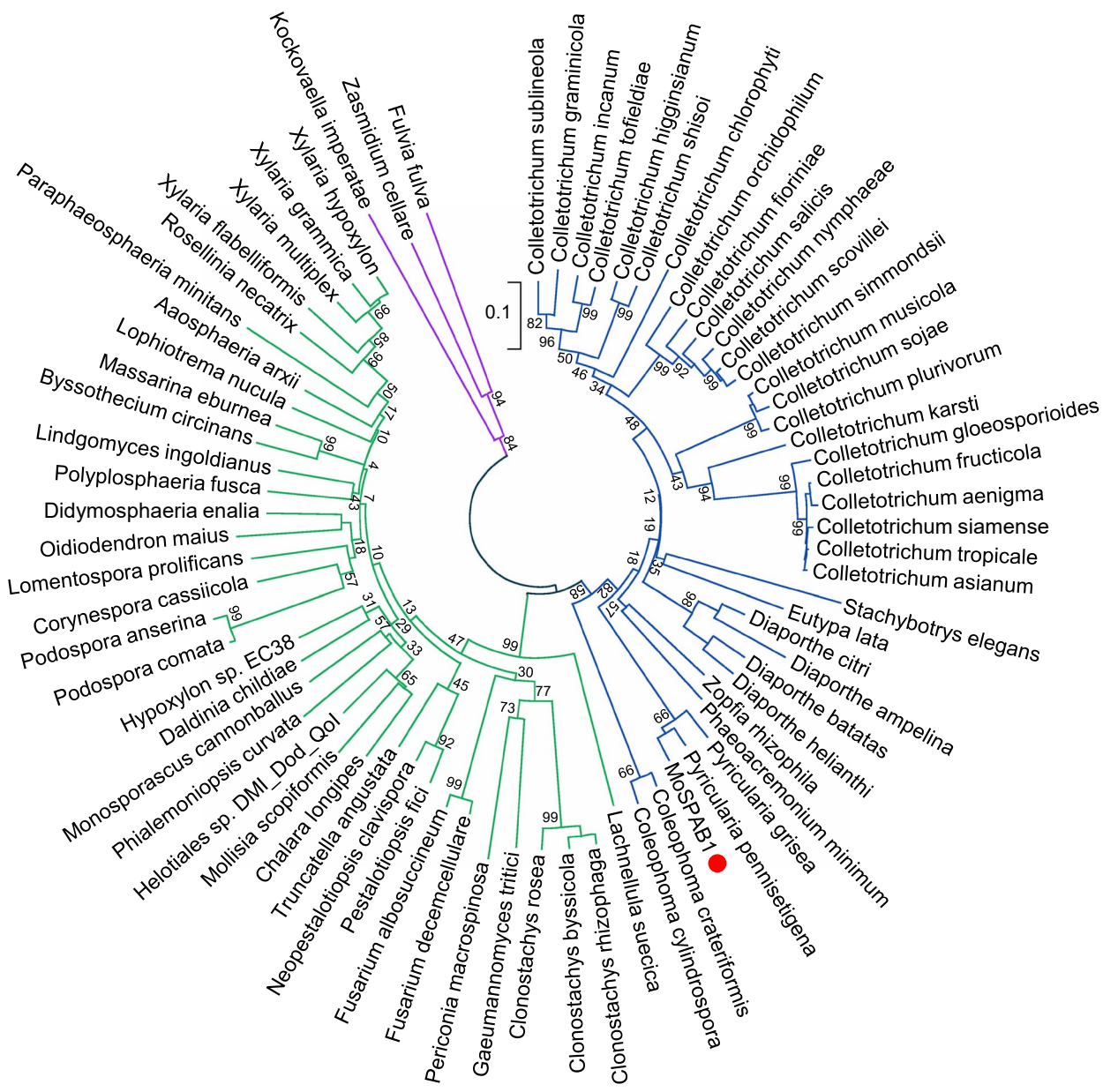
Supplementary Fig. 9 Pathogenicity of *Guy11*, two $\Delta Mospab1$ mutants, and a complemented strain on *Bsr-d1* transgenic lines in punch inoculation.

Different *M. oryzae* strains were used to inoculate three-week-old leaves of *Bsr-d1KO* lines, *Bsr-d1OE* lines, and TP309. Photos of leaves with lesions were taken (upper panel) and lesion length quantified (lower panel) 6 dpi. This experiment was done three times. Different letters indicate significant differences at $P < 0.05$. Dunnett T3's multiple-comparison test with one-way ANOVA (mean \pm SD; $n = 9\sim 15$ samples, n is shown in this figure). P values are shown in the Source Data file. Similar results are obtained from three independent biological experiments. Source data are provided as a Source Data file.



Supplementary Fig. 10 Determination of the MoSPAB1-MYBS1 interaction using the yeast two-hybrid.

Yeast cells containing two plasmids were diluted to 1×, 10×, and 100× with water and inoculated on SD/-L/-T and SD/-L/-T/-H/-A plates with X-gal added and grown at 28 °C for 2-4 days. SD/-L/-T represents a medium without leucine and tryptophan. SD/-L/-T/-H/-A represents a medium without leucine, tryptophan, histidine, and adenine. pGBKT7-53 and pGADT7-T were used as the positive control. Similar results are obtained from three independent biological experiments.



Supplementary Fig. 11 Phylogenetic relationship of MoSPAB1 homologous proteins from fungi. MEGA-X was used to construct the phylogenetic tree. Bootstrap values from 1,000 replicates were used to assess the robustness of the tree.

20 40 60 80 100

27th-47th

MoSPAB1 -----MLFTPIRS---GLASLLALAS---CAVAQNVKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 72

Y34 -----MLFTPIRS---GLASLLALAS---CAVAQNVKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 72

PoMZ -----MLFTPIRS---GLASLLALAS---CAVAQNVKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 72

PspL5 -----MLFTPIRS---GLASLLALAS---CAVAQDVKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 72

PpBr36 -----MLFTSTRS---GLASLLALAS---CAVAQNVKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 72

PgN1 -----MLFTPIRA---GLASLLALAS---CAVAQNVKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 72

CFIO01 -----MGASKEISLCLTIVWVLL---LFVN---TAVAAGVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILPNADLVYVSTGSDG 76

CSUB01 -----MNNWTLNRLAIYVVFALLLHG-SLLVYA---AAAANTVKSIFLFDKVLQSDTTHAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 80

HER10 -----MMGVYKRTGLCLTITWVLLS---LFAN---AAAAAGVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 77

JM77 -----MGYKRTGLCLTITWVLLS---LFAN---AAAAAGVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 77

CSIM01 -----MMGVFKRTGLCLTITWVLLS---LFAN---AAAAAGVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 77

CORC01 -----MMGGFKRFGLYTLAWTLTICIHVPFILAY---AAADTVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 82

CkaCkLH20 -----MYALRNLRTRVATQALLTLFISTTVF---AQTNQNVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 81

CSAL01 -----MGVFGIGLCLTITWVLLS---LFAD---AAAAAGVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 76

CNYM01 -----MMGVSKGTGLCLTITWVLLS---LFAN---AAAAAGVKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 77

CGCTS75 -----MRDSVKATVYARIYVVFALILAPLLAS---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

C1238 -----MKRWTNLFATIVVLLLHG-SRIVY---ATADTNKSIYLFKDVLSNTTAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 79

CGSCA4 -----MRDSVNETLARIYVVFALILAPLLAS---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

CGG54 -----MRDSVKATVARIYVVFALIFSPLLAS---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

CGCSA5 -----MRDSVKATVARIYVVFALILAPLLAS---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

CGCS363 -----MRDLVKATVARIYVVFALILAPLQAL---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

Q607 -----MPDSVKATVARIYVVFALILAPLLAS---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

CT0861 -----MKRWANLFLAITVLLLHG-PLFVY---AAANTVKSIFLFDKVLQSDTTHAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 79

K469DRAFT -----MPFKMGGVYALACALLFAP---FIPG---IFFKDVMSDTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 67

CGLO -----MRDSVKATVARIYVVFALIFAPLLAS---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

CGMCC -----MRDFVKATVARIYVVFALILAPLQAL---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

UCRPA7 -----MGSHVIIRAILLTLFICHPWAT---IAESEKSIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 75

CGCA056 -----MRDFVKATVARIYVVFALILAPLKA---CQSDGNVKSIIYLFKDVLSNTSALKTAGFTLLRFRIILVLENGDLVYVSTGGAG 81

CH63R -----MKRWINLN---RLVLAALVYG-PLIWA---AADTNKSIYLFKDVLSNTTAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 76

CH35J -----MKRWINLN---RLVLAALVYG-PLIWA---AADTNKSIYLFKDVLSNTTAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 76

GLRG -----MYWTLNRLAVALLVYVALLYG-SLLIHW---AADTVKSIYLFKDVLSNTTAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 78

CHSISOI -----MKRWTSLN---CLVLTLYYG-PLIWA---AADTNKSIYLFKDVLSNTTAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 76

CCHL11 MPTPTFVLFTAHLFANMKNLMNVG-FRALAALFLFS-PFLGLPFAHAANTVKSIFLFDKVLQSDTTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 98

INS49 -----MLWYGLAHTLSSLLFS---VNAATTAIFLFDKVLQSDTTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 72

KVR01 -----MLWRDFVAHSSTLLFAAFS---PVAS-TVIFLFDKVLQSDTTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 72

DHEL01 -----MLWPKFAYTLLSTLLFVASS---NPVSASTVIFLFDKVLQSDTTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 75

CPUI01 -----SFLPLCLLQFQAAL---GQTAANVKSIIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 72

B0135DRAFT -----MQLFPKLGRTLLGLLATSLEYIT---TVAADYSKAIYLFKDVMSDTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 77

CMUS01 -----MR-----SFLPLCLLQFQAAL---GQAANVKSIIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 72

CSOJ01 -----MR-----RFLSLLCLLQFQAAL---GQAANVKSIIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 72

UCREL1 -----MWLKSPLSGILLASVAEA---AAEATSVRSIFLFDKVLQSDTTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 74

BP5796 -----MHLLSKTLKAVLWSSLFLS---SVFASDGLKPIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 74

BP6252 -----MYLLSKALQAVLWSSLFLS---SVFASDGLKPIYLFKDVLSNTTAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 74

UCDDA912 -----MLWHGWHALLPTLLFAVSN---FVNAASTTAIFLFDKVLQSDTTHAKTSGFDTVLLRFRIILVLENGDLVYVSTGGAG 74

LSUE1 -----MKSYTLAALGLLPHCASAP---SATTSGIRSIYLFKDVLSNTTAKTSGFDSLVIRFRIILVLENGDLVYVSTGGAG 74

120 140 160 180 200

103rd-123rd 137th-191st

MoSPAB1 NPVDWPVVTNGSYVGGQALTDKITSKLTAP---TLIRRVBVSLSVSHDITFQVIRDRIAADG-FGASTHLYRAFVDVLRKQTELDLDAFNNDDESYYVHPSTV 167

Y34 NPVDWPVVTNGSYVGGQALTDKITSKLTAP---TLIRRVBVSLSVSHDITFQVIRDRIAADG-FGASTHLYRAFVDVLRKQTELDLDAFNNDDESYYVHPSTV 167

PoMZ NPVDWPVVTNGSYVGGQALTDKITSKLTAP---TLIRRVBVSLSVSHDITFQVIRDRIAADG-FGASTHLYRAFVDVLRKQTELDLDAFNNDDESYYVHPSTV 167

PspL5 NPVDWPVVTNGSYVGGQALTDKIIISKLTAP---TLIRRVBVSLSVSHDITFQVIRDRIAADG-FGASTHLYRAFVDVLRKQTELDLDAFNNDDESYYVHPSTV 167

PpBr36 NPVDWPVVTNGSYVGGQALTDKIIISKLTAP---TLIRRVBVSLSVSHDITFQVIRDRIAADG-FGASTHLYRAFVDVLRKQTELDLDAFNNDDESYYVHPSTV 167

PgN1 NPVDWPVVTNGSYVGGQALTDKIILYKLTAP---TLIRRVBVSLSVSHDITFQVIRDRIAADG-FGASTHLYRAFVDVLRKQTELDLDAFNNDDESYYVHPSTV 167

CFIO01 EAVDAPVVTNGSYVGGTALAEKVKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 171

CSUB01 EAVDAPVVTNGSYVGGTALAEKVKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 175

HER10 EAVDAPVVTNGSYVGGTALAEKVKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 172

JM77 EAVDAPVVTNGSYVGGTALAEKVKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 171

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CSAL01 EAVDAPVVTNGSYVGGTALAEKIKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 171

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CGCTS75 EAVDAPVVTAGSYVGGEALSEKIRSFKTKT---THINIRVBVSLSVSHDITFQVIRSLINSNG-FGSDSYLYRNFELKTEADLDAFNNDDESYYVDVSTV 176

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CGLO EAVDAPVVTAGSYVGGEALSEKIRSFKTKT---THINIRVBVSLSVSHDITFQVIRSLINSNG-FGSDSYLYRNFELKTEADLDAFNNDDESYYVDVSTV 176

CGMCC EAVDAPVVTAGSYVGGEALSEKIRSFKTKT---THINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 176

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CGCA056 EAVDAPVVTAGSYVGGEALSEKIRSFKTKT---THINIRVBVSLSVSHDITFQVIRSLINSNG-FGSDSYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 176

CH63R EAVDAPVVTNGSYVGGVALADKIKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 171

CH35J EAVDAPVVTNGSYVGGVALADKIKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 171

GLRG EAVDAPVVTNGSYVGGVALADKIKFSKTKT---TYINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDEGYYVDVSTV 173

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CCHL11 EAVDAPVVTNGSYVGGTALAEKIKFSKTKT---TINIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 193

INS49 EAVDAPVVTAGSYVGGVALADKIKFSKTKT---TLIRRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 167

KVR01 EAVDAPVVTAGSYVGGVALADKIKFSKTKT---TLIRRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 167

DHEL01 EAVDAPVVTAGSYVGGVALADKIKFSKTKT---TLIRRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 170

CPUI01 EPVDAPVVTAGSYVGGDALAEKIKFSKTKT---TDVDRVBVSLSVSHDITFQVIRALVAARS-T---VLRDGFALAKTEADLDAFNNDDESYYVDVSTV 163

B0135DRAFT EPVDAPVVTAGSYVGGDALAEKIKFSKTKT---TLVBRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 172

CMUS01 EPVDAPVVTAGSYVGGDALAEKIKFSKTKT---TDVDRVBVSLSVSHDITFQVIRALVADGGS-T---VLRDGFALAKTEADLDAFNNDDESYYVDVSTV 163

CSOJ01 EPVDAPVVTAGSYVGGDALAEKIKFSKTKT---TDVDRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 163

UCREL1 EAVDAPVVTAGSYVGGVALADKIKFSKTKTGGAT---TLIRRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 174

BP5796 QAVTITAVSNAGSYVGGVALADKIKFSKTKT---TIVNIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 169

BP6252 QAVTITAVSNAGSYVGGVALADKIKFSKTKT---TIVNIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 169

UCDDA912 DAVDAPVVTAGSYVGGVALADKIKFSKTKT---TLIRRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 152

LSUE1 -SSDVLTIASNSYVGGVALADKIKFSKTKT---TGIRNIRVBVSLSVSHDITFQVIRDLINADG-FGSDTYLYRNFELKTEADLDAFNNDDESYYVDVSTV 163

Supplementary Figure 12

137th-191st

207th-271st

220

240

260

280

300

MoSPAB1	DFAQMLGLMGVRYSTAPYTNMNFADVQNRINASVPGLLDRHYLYOYDGGAAANNFGTWTOTRLG-MKIVFLVWVNDYKPDHGNTPAQAQTRBANNSQYN	266
Y34	DFAQMLGLMGVRYSTAPYTNMNFADVQNRINASVPGLLDRHYLYOYDGGAAANNFGTWTOTRLG-MKIVFLVWVNDYKPDHGNTPAQAQTRBANNSQYN	266
PoMZ	DFAQMLGLMGVRYSTAPYTNMNFADVQNRINAAVPGLLDRHYLYOYDGGAAANNFGTWTOTRLG-MKIVFLVWVNDYKPDHGNTPAQAQTRBANNSQYN	266
PspLS	DFAQMLGLMGVRYSTAPYTNMNFADVQNRINAAVPGLLDRHYLYOYDGGAAANNFGTWTOTRLG-MKIVFLVWVNDYKPDHGNTPAQAQTRBANNSQYN	266
PpBr36	EFAQMLGLMGVRYSTAPYTNVSWFADVQNRINAAVPGLLDRHYLYOYDGGAAANNFGTWTOTRLG-MKIVFLVWVNDYKPDHGNTPAQAQTRBANNSQYN	266
PgNI	EFAKMLGLMGVRYSTAPYTNMNFADVQNRINAAVPGLLDRHYLYOYDGGAAANNFGTWTOTRLG-MKIVFLVWVNDYKPDHGNTPAQAQTRBANNSQYN	266
CFIO01	SFAHMLGEMGVQYSIAPYTNNSGFWANVRTQVESAKPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	270
CSUB01	GFAQLGALGVRYSTAPYTNNSRFWATVKSQIDAAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	274
HER10	SFAQMLGKMGVQYSIAPYTNNSGFWANVRTQVESANPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKIVFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	271
JMJ77	SFAQMLGKMGVQYSIAPYTNNSGFWANVRTQVESTNPGFLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKIVFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	270
CSIM01	SFAQMLGKMGVQYSIAPYTNNSGFWANVRTQVESANPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKIVFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	271
CORC01	SFAQMLGEMGVQYSIAPYTNNSGFWANVKAQIDASAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-TKVIIFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	276
CkaCkLH20	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIEAASAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKVIIFLVWVNDYKPSOGVTPQAQEARBAGADTYE	275
CSAL01	SFAQMLGEMGVQYSIAPYTNNSGFWANVRTQVESANPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKIVFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	270
CNYM01	SFAQMLGKMGVQYSIAPYTNNSGFWANVRSQIEAASAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKVIIFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	271
CGCTS75	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-AKVIIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CI238	MFAQLLGTIGVRYSTAPYTKSRFWANVRSQIDATVPGFLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	273
CGCSCA4	SFARLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-AKVIIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CG654	SFAHLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CGCSCA5	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-AKVIIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CGCS363	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
GQ607	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-AKVIIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CT0861	KFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGTTAAQAQRRESFSSQYA	271
K469DRAFT	SFAKMLGEMGVQYSITPVTNLNFWANVQDQINTAVPGLLDRHYLYOYDGGAGNNFGTWTOTRLG-IPVIFLVWVNDYKPSOGVTPAARAREBEGASEQYG	263
CGLO	SFAHLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-AKVIIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CGMCC	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
UCRPA7	SFATMLGTIGVRYSTAPYTNINFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKISIFLVWVNDYKPSOGTTAAQAQTKSGVYTYA	269
CGCA056	SFAQLLGTIGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGVTPDQAQGRSTEQQYD	275
CH63R	AFARLLGVLGVQYSIAPYTNIEFWANVQDQINTAVPGLLDRHYLYOYDGGAGNNFGTWTOTRLG-IPVIFLVWVNDYKPSOGVTPAARAREBEGASEQYG	272
CH35J	AFARLLGVLGVQYSIAPYTNIEFWANVQDQINTAVPGLLDRHYLYOYDGGAGNNFGTWTOTRLG-IPVIFLVWVNDYKPSOGVTPAARAREBEGASEQYG	272
GLRG	AFARLLGALGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IKVIFLVWVNDYKPSOGVTPAQAQRRESFSSQYA	270
CSHISOI	AFARLLGALGVRYSTAPYTNNSGFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-IPVIFLVWVNDYKPSOGVTPAARAREBEGASEQYG	270
CCHL11	SFAQLLGGDGVQYSIAPYTNNSNFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-ISVIFLVWVNDYKPSOGTTNPAQAQRRESFSSQYA	292
INS49	SFAQLLGGDGVRYSTAPYTNNSNFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-ISVIFLVWVNDYKPSOGTTNPAQAQRRESFSSQYA	262
KVR01	TFAKLLGEGVQYSIAPYTNIAFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-LKVTIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	262
DHEL01	TFAKLLGEGVQYSIAPYTNIAFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-LKVTIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	265
CPLU01	AFAEILGEGVQYSIAPYTNIAFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKVIIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	262
BOI35DRAFT	DFALMLGEMGVQYSIAPYTNNSNFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKIVIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	262
MUS01	AFAEILGEGVQYSIAPYTNIAFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKVIIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	262
CSOJ01	AFAEILGEGVQYSIAPYTNIAFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKVIIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	262
UCREL1	AFAGMLGEGVQYSIAPYTNIAFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-LKVTIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	274
BP5796	KFAEMLGNIGVRYSTAPYTNLDFWASIGSSLNETNPGYLRALYLCVGGENNDPGEQDVLDM-KVIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	268
BP6252	KFAEMLGNIGVRYSTAPYTNLDFWASIGSSLNETNPGYLRALYLCVGGENNDPGEQDVLDM-KVIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	268
UCDDA912	SFAKLLGGDGVRYSTAPYTNNSNFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-LKVTIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	247
LSUE1	AFAKMLGEGVRYSTAPYTNNSNFWANVRSQIDAEAPGLFDRVYLYOYDGGAGNNFGTWTOTRLG-MKVIIFLVWVNDYKPSOGVTPQAQAKBANNTQYA	258

320

340

360

380

400

MoSPAB1	LAGGGWVNDYDIEKLNSSYEYGGALTS-----VFQG-----	298
Y34	LAGGGWVNDYDIEKLNSSYEYGGALTS-----VFQG-----	298
PoMZ	LAGGGWVNDYDIEKLNSSYEYGGALTS-----VFQG-----	298
PspLS	LAGGGWVNDYDIEKLNSSYEYGGALTSHPETGLEPNNVRLSKSNLPYYNTSNTTSRWEPPGTDTEKLGKQYMGKYSALLPSPSQAGQIRAAHL	366
PpBr36	LAGGGWVNDYDIEKLNSSYEYGGALTS-----VFQG-----	297
PgNI	LAGGGWVNDYDIEKLNSSYEYGGALTS-----VFQG-----	298
CFIO01	VAGGGWVNDYDIEKMSSYTDYGALTS-----VF-----	300
CSUB01	VAGGGWVNDYDIEKMSSYAEYAAALTS-----VFQ-----	305
HER10	VAGGGWVNDYDIEKMSSYTDYGALTS-----VF-----	301
JMJ77	VAGGGWVNDYDIEKMSSYTDYGALTS-----VF-----	300
CSIM01	VAGGGWVNDYDIEKMSSYTDYGALTS-----VF-----	301
CORC01	VAGGGWVNDYDIEKMSSYSDYGALTS-----VF-----	306
CkaCkLH20	VAGGGWVNDYDIEKMSSYVEYAAALTD-----VFA-----	306
CSAL01	VAGGGWVNDYDIEKMSSYVDYGALTS-----IF-----	300
CNYM01	VVAGGGWVNDYDIEKMSSYTDYGALTS-----VF-----	301
CGCTS75	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
CI238	VAGGGWVNDYDIEKMSSYTEYGTALTS-----VFR-----	304
CGCSCA4	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
CG654	VAGGGWVNDYDIEKMSSYDEYGDALLT-----VFQ-----	306
CGCSCA5	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
CGCS363	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
GQ607	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
CT0861	VAGGGWVNDYDIEKMSSYTEYGTALTS-----VFQ-----	304
K469DRAFT	VAGGGWVNDYDIEKMSSYTSYSGSLTS-----VFQEKTEGESPPVSM-----	303
CGLO	VAGGGWVNDYDIEKMSSYDEYGDALLT-----VFQ-----	306
CGMCC	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
UCRPA7	VAGGGWVNDYDIEKMSSYVEYGGVLT-----VFQ-----	300
CGCA056	VAGGGWVNDYDIEKMSSYEYGDALLT-----VFQ-----	306
CH63R	VAGGGWVNDYDIEKMSSYVEYAAALTD-----VFQ-----	301
CH35J	VAGGGWVNDYDIEKMSSYVEYAAALTD-----VFQ-----	301
GLRG	VAGGGWVNDYDIEKMSSYADYAAALAG-----VFQ-----	303
CSHISOI	VAGGGWVNDYDIEKMSSYVEYAAALTD-----VFQ-----	301
CCHL11	VAGGGWVNDYDIEKLGASDEYGGALTS-----VFQ-----	323
INS49	VDEGGWVNDYDIEKMSSYTSYQAALTS-----VFQE-----	294
KVR01	VDEGGWVNDYDIEKMSSYTAAYQAITN-----VFPA-----	294
DHEL01	VDEGGWVNDYDIEKMSSYASAYQAALTN-----VFPA-----	297
CPLU01	VAGGGWVNDYDIEKMSSYDEYAGALVS-----VFQ-----	293
BOI35DRAFT	LDVAGWVNDYDIEKMSSYDDYAGVLS-----IFG-----	302
MUS01	VAGGGWVNDYDIEKMSSYDEYAGALVS-----VFQ-----	293
CSOJ01	VAGGGWVNDYDIEKMSSYDEYAGALVR-----VFQ-----	293
UCREL1	VAGGGWVNDYDIEKMSSYDAYGGVLT-----IFQ-----	305
BP5796	VAGGGWVNDYDIEKMSSYTYADALLD-----VFQ-----	299
BP6252	VAGGGWVNDYDIEKMSSYTYADALLD-----VFQ-----	299
UCDDA912	VDEGGWVNDYDIEKSSYVSLPVTLYK-----RSQ-----	267
LSUE1	LAGGGWVNDYDIEKLGSSYIAPSENLSPPCCRRASIVQR-----TFLANVQLKHESGLIILE-----	317

Supplementary Figure 12 continued

Supplementary Fig. 12 Sequence alignment of MoSPAB1 and homologous proteins.

Regions of amino acids 27-47, 103-123, 137-191, and 207-271 were labeled with red boxes. Shades from dark to light indicate similarity degrees of 100%, 80%, 60%, and less than 60%. Y34, the OOU_Y34scaffold01081g from *Pyricularia oryzae* Y34; PoMZ, the PoMZ_02865 from *Pyricularia oryzae*; PspLS, the PspLS_09416 from *Pyricularia* sp. CBS 133598; PpBr36, the PpBr36_02267 from *Pyricularia pennisetigena*; PgNI, the PgNI_02481 from *Pyricularia grisea*; CFIO01, the CFIO01_08786 from *Colletotrichum fiorinae* PJ7; CSUB01, the CSUB01_11810 from *Colletotrichum sublineola*; HER10, the HER10_EVM0008022 from *Colletotrichum scovillei*; JMJ77, the JMJ77_0014689 from *Colletotrichum scovillei*; CSIM01, the CSIM01_07887 from *Colletotrichum simmondsii*; CORC01, the CORC01_09639 from *Colletotrichum orchidophilum*; CkaCkLH20, the CkaCkLH20_04340 from *Colletotrichum karsti*; CSAL01, the CSAL01_01070 from *Colletotrichum salicis*; CNYM01, the CNYM01_12775 from *Colletotrichum nymphaeae* SA-01; CGCTS75, the CGCTS75_v014773 from *Colletotrichum tropicale*; Cl238, the Cl238_02416 from *Colletotrichum incanum*; CGCSCA4, the CGCSCA4_v013087 from *Colletotrichum siamense*; GCG54, the GCG54_00014612 from *Colletotrichum gloeosporioides*; CGCSCA5, the CGCSCA5_v015001 from *Colletotrichum siamense*; CGCS363, the CGCS363_v013914 from *Colletotrichum siamense*; GQ607, the GQ607_014599 from *Colletotrichum asianum*; CT0861, the CT0861_02089 from *Colletotrichum tofieldiae*; K469DRAFT, the K469DRAFT_741528 from *Zopfia rhizophila* CBS 207.26; CGLO, the CGLO_05580 from *Colletotrichum gloeosporioides* Cg-14; CGMCC, the CGMCC3_g17995 from *Colletotrichum fructicola*; UCRPA7, the UCRPA7_3110 from *Phaeoacremonium minimum* UCRPA7; CGCA056, the CGCA056_v014942 from *Colletotrichum aenigma*; CH63R, the CH63R_12215 from *Colletotrichum higginsianum* IMI 349063; CH35J, the CH35J_009866 from *Colletotrichum higginsianum*; GLRG, the GLRG_09307 from *Colletotrichum graminicola* M1.001; CSHISOI, the CSHISOI_06683 from *Colletotrichum shisoi*; CCHL11, the CCHL11_07208 from *Colletotrichum chlorophyte*; INS49, the INS49_011234 from *Diaporthe citri*; KVR01, the KVR01_009678 from *Diaporthe batatas*; DHEL01, the DHEL01_v204942 from *Diapeliathinanthi*; CPLU01, the CPLU01_12574 from *Colletotrichum plurivorum*; B0I35DRAFT, the B0I35DRAFT_347999 from *Stachybotrys elegans*; CMUS01, the CMUS01_16400 from *Colletotrichum musica*; CSOJ01, the CSOJ01_1383 from *Colletotrichum sojae*; UCREL1, the UCREL1_11766 from *Eutypa lata* UCREL1; BP5796, the BP5796_12446 from *Coleophoma crateriformis*; BP6252, the BP6252_13955 from *Coleophoma cylindrospora*; UCDDA912, the UCDDA912_g02556 from *Diaporthe ampelina*; LSUE1, the LSUE1_G003910 from *Lachnellula suecica*.

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Bsr-d1 (+) -82 AATCATCCAC CGCTCGCT GCTGCTGCTA -55
              | | | | | | | | | |
SbBsr-d1 (+) -809 TGCACACAGT AGCTCGCT CGCGCACCTT -782

Bsr-d1 (+) -82 AATCATCCAC CGCTCGC-TGCTGCTGCTA -55
              | | | | | | | | | |
AcBsr-d1 (-) -159 GCTACATGAA TGCTTGTA CACTACATAT- -186

Motif          (C/A)(G/C)(C/G)T(T/C)G(C/A)(T/C)

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Supplementary Fig. 13 Conserved cis-motif (C/A)(G/C)(C/G)T(T/C)G(C/A)T bound by MoSPAB1 was found in *SbBsr-d1* and *AcBsr-d1* promoters.
 '+' and '-' behind the gene represent the sense and antisense strand, respectively.