

Figure S1. Septation phenotypes of *S. japonicus pmk1Δ* cells. Exponentially growing *S. japonicus* wild type and *pmk1Δ* strains were incubated for 10 h in YES medium plus 5 μ g/ml calcofluor white, 5 mM Caffeine or 1M sorbitol, and the percentage of unseptated, septated and multiseptated cells (represented as mean \pm SD from biological triplicates; number of total cells ≥ 200) was determined by fluorescence microscopy after calcofluor white staining.

Pmk1

Gly-rich

S. japonicus MDRRHRVYRVFHQEMFVEPNFKVKVELGQGAYGITVCAARNMASKEQEGVAIKKITNIFSK
S. pombe MDRRHRVYRVFNQEMYVEPNFKVKVELGQGAYGITVCAARNVASKDQEAVALKKITNVFSK
*****.*:*:*****.*:*:*:*:*:*:*:*:*:*:

IV V (Hinge)

S. japonicus PILTKRALRLIKLLIHLNRHR-----NMEADLNAIKSGQP
S. pombe SILTKRALRLIKLLIHFRNHRNITCIYDLDIINPYNFNEVYIYEELMADLNAIKSGQP
.*****.*:*:*****.

S. japonicus LTAHFQSFYIQILCGLKYIHSANVIHRDLKPGNLLVNADCELKICDFGLARGFSDNPDE
S. pombe LTAHFQSFYIQILCGLKYIHSANVIHRDLKPGNLLVNADCELKICDFGLARGCSENPEE
*****.*:*:*:

Act. Loop

S. japonicus NAGFMTEYVATRWYRAPEIMLSFSSYHKGDIDVWSVGCILAELLGGRPFFKGKDYVHQNLN
S. pombe NPGFMTEYVATRWYRAPEIMLSFSSYHKGDIDVWSVGCILAELLGGTPLFKGKDFVHQNLN
*.*****.*:*:*:*:*:*:*:*:*:*:

S. japonicus ILHYLGTPDEETLRSISRERAYNYIRSFPPKKPIPFETIPFYANPLALDLLSRMLTFDPA
S. pombe ILHQLGTPDEETLSHISSRAQEYVRSLPKQRPIPFETNFPPKANPLALDLLAKLAFDPN
*** *****.*:

CD domain

S. japonicus KRISVTEALEHPYLAVWHDPADEPECPIPFDFSFEAINDMNELRDLIQREVLAFRRNVRR
S. pombe RRISSVDDALEHPYLAVWHDPSDEPVCDVSFDDFSFEYIEDANELRRVILDEVLFNRQKVR
:*:

S. japonicus SPNPSPHLPHIQINSQLSRASAMHSQHSGHVS NHLRSSMPTSNQTQNESNDLSPRPHSP
S. pombe RSHPTNPTVN-----IPQPAQTVPNSDNGS FNVSSSSSQTSNKKRHDSYNETAAID
.:*: *: : ..*.:*:..*.. ** ***.:...: . .

S. japonicus RLIDANDLEAELSKY
S. pombe HKSDDNRNH-----
.:...: . .

B

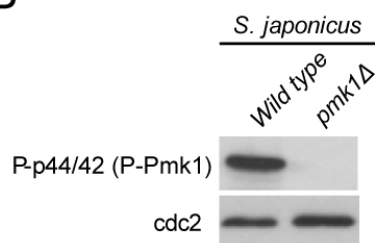


Figure S2. Conserved structural features of Pmk1 MAPKs in *S. pombe* and *S. japonicus*. (A) ClustalW analysis (<https://www.genome.jp/tools-bin/clustalw>) of amino-acids sequences of Pmk1 MAPKs in *S. pombe* and *S. japonicus*. '*': identical amino acid; ':': conserved substitution, '·': semi-conserved substitution. Conserved residues/motifs involved in ATP binding are shaded in yellow. The gate-keeper residue is shaded in blue. Putative common docking (CD) sites are shaded in purple. The phosphorylatable amino acids at the conserved -TEY- activation loop are shaded in green. (B) *S. japonicus* wild type and *pmk1Δ* strains were grown in YES medium to mid-log phase, and activated Pmk1 was detected with anti-phospho-p44/42 antibody, whereas anti-Cdc2 was used as a loading control.

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Chaetothyriales DV737_g786      MSDLSGRKVFVKVFNQDFIVDERYTVTKELGQGAYGIVCAATNTNTG--EG
Chaetothyriales DV736_g4926    MSDLSGRKVFVKVFNQDFIVDDRYTVTKELGQGAYGIVCAATNTQTG--EG
O. camponoti CP532_1836        MAGLQGRKVFVKVFNQDFIVDERYTVTKELGQGAYGIVCAAVNNQTT--EG
S. japonicus Pmk1              --MDRRHRVYRVFVHQEMFVEPNFKVVKELGQGAYGIVCAAKNMAKQEG
S. pombe Pmk1                  --MDRRHRVYRVFVHQEMYVEPNFKVVKELGQGAYGIVCAARNVASKDQEA
                                :*:::*:::*: :. :.*.***** * : *.
                                IV
Chaetothyriales DV737_g786      VAIKKVTNVFSKKILAKRALREIKLLQHFRGHRN-----
Chaetothyriales DV736_g4926    VAIKKVTNVFSKKILAKRALREIKLLQHFRGHR-----
O. camponoti CP532_1836        VAIKKVTNIFSKKILAKRALREIKLMQHFRGHR-----
S. japonicus Pmk1              VAIKKITNIFSKPILTKRALREIKLLIHLRNHR-----
S. pombe Pmk1                  VAIKKITNVFSKSIITKRALREIKLLIHFRNHRNITCIYDLDIINPYNFN
                                *****:***:*** **:*****: *:*.**
                                V (Hinge)
Chaetothyriales DV737_g786      -----ELMECDLAAIIRSGQPLTDAHFQSFIYQILCGLKYIHSANVLHR
Chaetothyriales DV736_g4926    -----NLMECDLAAIIRSGQPLTDAHFQSFIYQILCGLKYIHSANVLHR
O. camponoti CP532_1836        -----NLMECDLAAIIRSGQALTDHFQSFIYQILCGLKYIHSANVLHR
S. japonicus Pmk1              -----NMEADLNAAIKSGQPLTDAHFQSFIYQILCGLKYIHSANVIHR
S. pombe Pmk1                  EVYIYEELMEADLNAAIKSGQPLTDAHFQSFIYQILCGLKYIHSANVIHR
                                **.* **.* **.*:***.*****:***:***

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Figure S3. Conserved sequences surrounding the N-lobe subdomains IV and V in several fungal CIP MAPKs. MAPKs ClustalW analysis (<https://www.genome.jp/tools-bin/clustalw>) of sequences surrounding the N-lobe subdomains IV and V in of Pmk1 MAPKs in *S. pombe* and *S. japonicus*, and putative MAPKs from *Chaetothyriales* (Gen Pep: DV737_g786 and DV736_g4926), and *Ophiocordyceps camponoti* (Gen Pep: CP532_1836). '*': identical amino acid; ':': conserved substitution, '!': semi-conserved substitution.

Pck1

		HR1
<i>S. japonicus</i>	MYSIEAADDVQKKIDREKSLIQGAKAMVDSTGNSEVKQRIEKKIREASSNIDYLTNRIN	
<i>S. pombe</i>	MVQLD DALQDAYKKVEREESLILGAKAMVASTKNPEVKRRLESNIIVSNNIKYLRERID	
	* : : *	
	SLMIEKN---APSLRGIQKAFDEKSVSSSSMSKVVNGKSAFDILLKAPINEEIIIMTK	
	ALKVESGSEERESQSDKSSKKYSDSAKSTNSDDHLLSYNRSAFDLFNSKPLSPKEKISTM	
	: * : * : : * : : * : : : * : * : : : * : * : : * : * : * : * : * : * : *	
	HR1	
	MKFTQMRLVVEEQCLAGVDKIVNLYSKESKNTEEAQAQREEILQKTRLLKSALKRYKELY	
	LQHLQMRLSIBQQCVSGIEKIMSLYSKEQKDKTDVTIKLKEGKQKVNLLKRSLSKRYNELH	
	: : : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	C2	
	LPSDEPNSTASETS-----IAKNLFKPLTGTVKLTIHAIKNVHDHTDANEQSHGAHDTFLN	
	LPEDISTPSSEKQQAAGLNFRLGAKPISGTLKVTIHSLRNIEHTSFLQTHSFTMPSYAV	
	* * : : : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	C2	
	IVVDNRVCKSRVTQHDWTNEAFVFEMNKARECEVVYDRKPKDSLPIALLWVPSALILD	
	LYVDDAQVAKSRISQTDTWDETFFDVHRAKEFQIIIEKKKDFDIPALILIPITTLIAE	
	: : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	C2	
	DSRRKRNQLQELSEIDWKMNDSMLPLKHSSTRTN--ASVSTDVASNAGAAPPQGDTRKL	
	ELRRKRNIQEMSETSWKPSIAESASRSDEKSGKSDPINAPNSSSISTNSPLAFTAYYKL	
	: * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	Ps	
	LSQVWLSLEPAGQICVSLEFTKKVPNSKVISDNGLGRGQATROKKEVISDFLGHSPFLR	
	LSKSWLSLEPVGQICISLSFSKRTTKRQFP-ETELGRGQATROKKEQVVASQVGHQFVQR	
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	C1	
	QFYQIMRCVAVCADFLKDGSGQLCAECSTYCHRRCLMKTINRCIAKTHSVTAPPEGGESLK	
	QFYQIMRCVAVCAELFSYSPGLQCENCSFVCHKCKVTKVLASCIQNSSEKSDPGG---LR	
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	C1	
	HHIPHRFEFYNFSANWCSHCGYFISFLKDKCYKCKECGITCHIRCSRLIPDLGMSNDM	
	YRIPHRFEFYNFSIGAQWCAHCGFFFLRRLKDCFKCCEGITCHGQCAHLIPDYCGMSNDL	
	: * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	ANHILNEIRSTKLLTSRVMSAASVSKPAAPEIKSPTPFSFRKSGGVPSISQGLLFATQ	
	KHQLLELEVSKRPKK---PELPNQENKTTNEKVYRKPLSSQNTPTDPTLPTISQGLLAATQ	
	: : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	QLAGSLPEAPPPRP-----AIPAHSPSPSIAETLLKPEVPDVKQCSSP-----SSIASK	
	PVTSVLNTSPLEKTPKDRSLNVTSPSSSTPTPASVLAPPSSASLSSSKDANRSVPESPRR	
	: : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	KGKPRIGLDDPTFLAVLGKGNFGKVMIAEYKHNKRLYAIKVLKDSILKNNELKSEKSEK	
	EKKNRVTLDPTFLAVLGKGNFGKVMIAEYKVNKKFYAIKVLKKEAILKNEELKSEKTEK	
	: * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	RVFMTANKEKHPFLNLNLFASFQIGTRVYFVMEYIDGGDLMLHIQREQFSLKRAQFYAAEV	
	HVFEVANKEKHPFLNLNLFASFQIGTRVYFVMEYILGGDLMVHIQREQFSVKKARFYGAEV	
	: * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	Activation Loop	
	CLGLKYFHENHIYRDLKLDNILLSDGHIKIADYGLCKENMTEGKFTSTFCGTPEFMAP	
	CLALKYFHENGIAIYRDLKLDNILLCPDGHIRIADYGLCKENMLLGNITSTFCGTPEFMAP	
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	EILLDQQYNRAVDWNAFQVLLYQMLLGQSPFKGDEDEEIFEAILNDEPMFPIHMPGEAVD	
	EILLEQQYSKVDWNAFQVLLYQMLLGQSPFKGDEDEEIPDAILNDEPLFPIHMPGEAVS	
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	IMQKLLTRDIDKRLGGGPRDALDVMEHPFFRGVDWDMIFKKQIEPTYKPRITGAYDINN	
	LLRGLLTRDPNORLGGGPKDANEVMAHPFFASIVWDDLYNKLYEPSYKPLINDPRLNNE	
	: : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
	Turn motif	Hydrophobic motif
	DVEFTREPRVLTVPVNSILSKTEQESFRGFSSFAGSED	
	DEEFTSACPTLTVPVNTVLTQQQECFRGFSSFATE--	
	* * * * * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	

Figure S4. Conserved structural features of Pck1 orthologs in *S. pombe* and *S. japonicus*. Conserved domain structure of Pck1 orthologs from *S. pombe* and *S. japonicus* obtained after protein sequence alignment by CLUSTALW (<https://www.genome.jp/tools-bin/clustalw>). '*': identical amino acid; ':': conserved substitution, ':': semi-conserved substitution. Labels: HR1 (red), putative rho-binding repeat; C2 (yellow), putative Ca(2+)-binding motif; Ps (green), putative pseudosubstrate motif; C1 (blue), putative diacylglycerol binding motif. Amino acid sequence alignment of Pck1 and Pck2 is also shown. Conserved canonical phosphorylated residues at the activation loop (AL), turn motif (TM), and hydrophobic motif (HM) within the catalytic domain (gray) are marked in red.

Pck2

HR1

<i>S. japonicus</i>	MTINDAI	TEVERKIGRERSMTHGARAMEQLTRNQVHQQLRANIKAEARNIAYLEERIQ
<i>S. pombe</i>	MDMIDEAI	TEVVVKIERERSVTHGALSMLRLTQNTVHQQLHSNTEESKKSITYLEERIE

* : * : * * * * * * * * * * : * : * : * : * : * : * : * : * : * : *

KLRLRQAGVHSKSSSTSVSG---LSTGNGQDSEDKSKETNSQPPLTNLDIIKYDTPITIAK
 KLKLRFNGVRKSNSEKPSVGIEKNPSFSTTKSAKSFSTSSNIDSNLDLNYDTPITISK
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

HR1

ISVMIQQLEFKLTLEKQFREGIDRMALYQREGDKRSIFEAETKRVESAQRKILQQALM
 ISFLQQLEFKLSVEEQYRKGIKMAKLYEREHRRSIAEAEGKYVESAQRITLLKQALM
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

C2

RYHDLHIEIDDDLTNTGTQLIAPNIRRPQSGTLTICIGSLRNVNHSSTISITRTTETVAVI
 RYHDLHIEIDEDVPSTESRGNLNARRPQSGLLKITVGSRLNVTHSAG-ISKQTEMIVAI
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

C2

KIEDVERSTRPFRNDKFNFAFDIDVEKANEVEIVVYDKND-KTIPIALLWIRLSDLVE
 RAEDLERARTPFRSRTDRFNETFEIDLEKTNEVEIVVYKNEKLLLPVGLLWIRLSDLVE
 : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

QLRRKKEQEISDSGWVSADKMDTDFLSKSTGNRRSLLVPIKNETSHGSSSTTSVSPFV
 KQRRKKEQEISDSGWVSADKMDTDFLSKSTGNRRSLLVPIKNETSHGSSSTTSVSPFV
 : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Ps

SAWFSMEPVGQIYLSLNFVKHNLKRPFDAELGRQGAIRARKITIEVFHGKFEVQQQFYQ
 SAWFSLEPMGQINLTMTNFTKHNRKRPMDAGLGRQGAIRARKITIEVFHGKFEVQQQFYQ
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

C1

IMRCALCGEFLKNAAGMOCIDCHYTKHKKCYPKVVKCISKPSDGTENEYEKINHRIPHH
 IMRCALCGEFLKNAAGMOCIDCHYTKHKKCYPKVVKCISKPSDGTENEYEKINHRIPHH
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

C1

FEAHTNIGANWCCHGYILPLGKVKARKCTECGVTAHVQCMHLPDFCGMSMEMANRILY
 FESHTNIGANWCCHGYILPLGKVKARKCTECGVTAHVQCMHLPDFCGMSMEMANRILY
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

ELRTTKPRKTPATRSASIPSTPVSKLTSKSEANHAKDSVSTTSLISPLAPTQSSPPP
 EIRTTIYKAQQHKQKSSHHKHHHKKSSSSSKHKENDKASVITTTTPTSPADPVP
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

VSTFVSVPVIEISSPPLTPAPSIKRPPIPGDNEQPLSPYSIPQAEATPKQDVTIVDS
 TSPKPLAIEPVKRPVHAGNLEVTSVSDNKLGAIVQVVEQVDDKADALTKPPSLDAVKE
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

VGRPVQATDANLAKTLVEPSKVVLDSFNFIISVLGKGNFGKVMLESKKTKNLFKVLK
 PIPVPSVETSVAQDLTHKAKRIGLEDFTFLSVLKGKNGFKVMAELKSEKQLYAIKVLK
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

KSFLENDEIESIKSEKRVFLVANREKHPFLNLHSCFQTETRIFFVMDYVSGGDLMLHI
 KEFLENDEVESTKSEKRVFLVANREKHPFLNLHSCFQTETRIFFVMDYVSGGDLMLHI
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

QQEQFYPRRAQFYAAEVCLALKYFHDNGIYRDLKLDNILLSPDGHKLADYGLCKENMW
 QQEQFSRRRAQFYAAEVCLALKYFHDNGIYRDLKLDNILLSPDGHKLVADYGLCKEDMW
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Activation Loop

DKNTIVTCGTPEFMAPEILLEQKYTRAVDWWAFGLIYQMLLGQSPFRGDEEEIFDAI
 HDNTATTCGTPEFMAPEILLEQKYTRAVDWWAFGLIYQMLLGQSPFRGDEEEIFDAI
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

LTDEPLYPIHMPRDSVFILQQLTRAPEKRLGSGPNDVMAHFFFSNINWDDIYHKRI
 LSDEPLYPIHMPRDSVFILQQLTRAPEKRLGSGPNDVMAHFFFSNINWDDIYHKRI
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Turn motif

QPPFVVKLEGGPKTKYFDEEFTSELPILTIQSTLSPERMHFEFGSYISDFDTPLGN--
 QPPYIPSLNSPTDTKYFDEEFTRELPLTPVNSILTKEMQHFEGFSYSCEDDKPSTTDNA
 * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Hydrophobic motif

Figure S5. Conserved structural features of Pck2 orthologs in *S. pombe* and *S. japonicus*. Conserved domain structure of Pck2 orthologs from *S. pombe* and *S. japonicus* obtained after protein sequence alignment by CLUSTALW (<https://www.genome.jp/tools-bin/clustalw>). '*': identical amino acid; ' ': conserved substitution, ' ': semi-conserved substitution. Labels: HR1 (red), putative rho-binding repeat; C2 (yellow), putative Ca(2+)-binding motif; Ps (green), putative pseudosubstrate motif; C1 (blue), putative diacylglycerol binding motif. Amino acid sequence alignment of Pck1 and Pck2 is also shown. Conserved canonical phosphorylated residues at the activation loop (AL), turn motif (TM), and hydrophobic motif (HM) within the catalytic domain (gray) are marked in red.

Table S1. *S. japonicus* and *S. pombe* strains used in this work.

<i>S. japonicus</i> strains	Genotype	Source
NIG2028	<i>h⁻ prototroph</i>	Furuya & Niki 2009
NIG5091	<i>h⁻ ura4-D3</i>	Furuya & Niki 2009
EGJ4	<i>h⁻ pmk1::ura4⁺ ura4-D3</i>	This work
EGJ108	<i>h⁺ pck1::NatMX6</i>	This work
EGJ73	<i>h⁻ pck2::ura4⁺ ura4-D3</i>	This work
EGJ128	<i>h⁺ pck1::NatMX6 pmk1::ura4⁺</i>	This work
EGJ83	<i>h⁻ pmk1::NatMX6 ura4-D3</i>	This work
PH6	<i>h⁻ pmk1^{Sj}-GFP::NatMX6</i>	This work
EGJ140	<i>h⁻ sty1::ura4⁺ pmk1^{Sj}-GFP::NatMX6</i>	This work
EGJ99	<i>h⁻ pmk1^{Sj}-HA::ura4⁺ pmk1::NatMX6 ura4-D3</i>	This work
EGJ132	<i>h⁻ pmk1^{Sj}(ins 82-105)-HA::ura4⁺ pmk1::NatMX6 ura4-D3</i>	This work
EGJ96	<i>h⁻ pmk1^{Sp}-HA::ura4⁺ pmk1::NatMX6 ura4-D3</i>	This work
EGJ102	<i>h⁻ pmk1^{Sp}(Δ 82-105)-HA::ura4⁺ pmk1::NatMX6 ura4-D3</i>	This work
<i>S. pombe</i> strains	Genotype	Source
MM1	<i>h⁺</i>	Lab stock
MI102	<i>h⁺ pmk1::KanMX6</i>	Madrid <i>et al.</i> (2007)
MM1904	<i>h⁻ pmk1::NatMX6</i>	Madrid <i>et al.</i> (2017)
BV829	<i>h⁻ pck1::ura4⁺</i>	Dr Takashi Toda
MM1197	<i>h⁺ pck2::NatMX6</i>	This work
LS111	<i>h⁺ pmk1^{Sp}-GFP::leu1⁺ pmk1::KanMX6</i>	Sánchez-Mir <i>et al.</i> (2012)
EG685	<i>h⁻ pmk1^{Sj}-HA::leu1⁺ pmk1::NatMX6</i>	This work
EG686	<i>h⁻ pmk1^{Sj}(ins 82-105)-HA::leu1⁺ pmk1::NatMX6</i>	This work
EG682	<i>h⁻ pmk1^{Sp}-HA::leu1⁺ pmk1::NatMX6</i>	This work
EG684	<i>h⁻ pmk1^{Sp}(Δ 82-105)-HA::leu1⁺ pmk1::NatMX6</i>	This work

All *S. pombe* strains are *ade6-M216 leu1-32 ura4D-18*.

Table S2. Oligonucleotides used in this work.

OLIGONUCLEOTIDE	SEQUENCE 5'-3'	Use
Pmk1Djp-W	CCGCGTTTAATTACGATCATTACACC	<i>pmk1</i> ⁺ deletion
Pmk1Djp-X (Ura4)	GAGCGGAAGAACGGAATCGTGGCGGCCGATGGTATTCCTTGCACT CGAGAC	<i>pmk1</i> ⁺ deletion (<i>Ura4</i> ⁺)
Pmk1Djp-Y (Ura4)	GCAGTGCGGTATCGTATAATTAGTGTCTAAGCAAGATACTGAAAGC TGCC	<i>pmk1</i> ⁺ deletion (<i>Ura4</i> ⁺)
Pmk1Djp-X (NatR)	GGGGATCCGTCGACCTGCAGCGTACGAGATGGTATTCCTTGCACT TCGAGAC	<i>pmk1</i> ⁺ deletion (<i>NatR</i>)
Pmk1Djp-Y (NatR)	GTTTAAACGAGCTCGAATTCATCGATCTAAGCAAGATACTGAAAG CTGGC	<i>pmk1</i> ⁺ deletion (<i>NatR</i>)
Pmk1Djp-Z	ACTACCACTTCTCACTACATTCTG	<i>pmk1</i> ⁺ deletion
Pmk1Djp-Comp2-5'	CGCGTTCACCTCACATTTCTTCGTG	Confirmation of <i>pmk1</i> ⁺ deletion.
Pck1Djp-W	CACGCAGTTCTGTGTATTCCGGTTTT	<i>pck1</i> ⁺ deletion
Pck1Djp-X (NatR)	GCGCGCCTTAATTAACCCGGGGATCCGTCGCGCGACTAAATTTAGC AATGCTTAG	<i>pck1</i> ⁺ deletion (<i>NatR</i>)
Pck1Djp-Y (NatR)	CCATCCAGTTTAAACGAGCTCGAATTCATCGTGTTCCTCGTGCGCG CTTACGAACA	<i>pck1</i> ⁺ deletion (<i>NatR</i>)
Pck1Djp-Z	AGCAGCGAATTAAGCGTCAATTCC	<i>pck1</i> ⁺ deletion
Pck1Djp-Comp-5'	TTCTTCAACTGGAGGATTCTGTAAC	Confirmation of <i>pck1</i> ⁺ deletion.
NatR-Comp-R	TTATTGTCAGTACTGATTAGGGGCA	Confirmation of <i>NatR</i> deletions.
Pck2Djp-W	CTTCGTATGCTCCATTCTTGATTGT	<i>pck2</i> ⁺ deletion
Pck2Djp-X (Ura4)	GAGCGGAAGAACGGAATCGTGGCGGCCTTCTTTAAGGGAAACCGT GAGGTAC	<i>pck2</i> ⁺ deletion (<i>Ura4</i> ⁺)
Pck2Djp-Y (Ura4)	GCAGTGCGGTATCGTATAATTAGTGTCTCATTAAAGCATTTCACGG CGATC	<i>pck2</i> ⁺ deletion (<i>Ura4</i> ⁺)
Pck2Djp-Z	GTTCTACGGTCTTGATCTGCTGAAC	<i>pck2</i> ⁺ deletion
Pck2Djp-Comp-5'	TTCTTCAACTGGAGGATTCTGTAAC	Confirmation of <i>pck2</i> ⁺ deletion.
Ura4Sj-Comp-R	CTTCTTGGCGACTGCATTAGGATGC	Confirmation of <i>Ura4</i> ⁺ deletion.
Pmk1Sj:GFP-SalI-5'	ATAATGTGCGACGTATGGCAACCATGTGGTAGAC	<i>pmk1</i> ⁺ C-terminal tagging
Pmk1Sj:GFP-PacI-3'	ATAATGTTAATTAAGTACTTGGACAGTTCTGCCTC	<i>pmk1</i> ⁺ C-terminal tagging
GFP-Comp-5'	CTGCCCTTTCCAAAGATCCCAACG	Confirmation of C-terminal tagging
Sty1Djp-W	GCATGGGCGCGTTCGGTCTTGATG	<i>sty1</i> ⁺ deletion
Sty1Djp-X (URA4)	GAGCGGAAGAACGGAATCGTGGCGGCCACACCAGCACTGTGGACGT ACTTC	<i>sty1</i> ⁺ deletion (<i>Ura4</i> ⁺)
Sty1Djp-Y (URA4)	GCAGTGCGGTATCGTATAATTAGTGTGACGATCTGCAGCAAGAATAC ATTG	<i>sty1</i> ⁺ deletion (<i>Ura4</i> ⁺)
Sty1Djp-Z	TGCTTGACCTCACTATCCACATTATG	<i>sty1</i> ⁺ deletion
Sty1jp-COMP5'	ATGGCTGAATTTGTTTCGTACACAGAT	Confirmation of <i>sty1</i> ⁺ deletion.
PromPmk1Jp-NoII-5'	ACTTAGCGGCCGCCGCGTTTAATTACGATCATTACACC	<i>pmk1</i> ⁺ ^{Sj} ORF Cloning and C-terminal tagging
Pmk1Jp:HA-BamHI-3'	ACTTAGGATCCTTAGCCCGCATAGTCAGGAACATCGTATGGGTAGC CGTACTTGACAGTTCTGCCTCGAGATC	<i>pmk1</i> ⁺ ^{Sj} ORF Cloning and C-terminal tagging
Pmk1Jp-Exon-5'	ACTTGCAATTTACGATCTCGACATTATAAATCCATACAATTTTAATGAA GTTTACATTTACGAAGAGATGGAAGCAGATTTAAATGCCATT	<i>pmk1</i> ⁺ ^{Sj} ORF Cloning and <i>pmk1</i> ⁺ ^{Sp} Exon2 insertion
Pmk1Jp-Exon-3'	AATGTCGAGATCGTAAATGCAAGTAATTCCTGTGATTCCGAAGAT GAATC	<i>pmk1</i> ⁺ ^{Sj} ORF Cloning and <i>pmk1</i> ⁺ ^{Sp} Exon2 insertion
PromPmk1Sp-XbaI-5'	ACTTATCTAGATTTCTCATTGCCGCTTCTG	<i>pmk1</i> ⁺ ^{Sp} ORF Cloning and C-terminal tagging
Pmk1Sp-HA-SmaI-3'	CCTTACCCGGGTAGTGGTGATGATGGTGATGTGCATAGTCCGG GACGTCATAGGGATAGCCCGCATAGTCAGGAACATCGTATGGGT AGGATCCGTTATGGCGATTATCATCAGAC	<i>pmk1</i> ⁺ ^{Sp} ORF Cloning and C-terminal tagging
Pmk1Sp-Δ Exon-5'	CATTTTCGTAATCATCGTAACATGGAGGCCGATTGAATG	<i>pmk1</i> ⁺ ^{Sp} ORF Cloning and Exon2 deletion.
Pmk1Sp-Δ Exon-3'	CATTCAAATCGGCCTCCATGTTACGATGATTACGAAATG	<i>pmk1</i> ⁺ ^{Sp} ORF Cloning and Exon2 deletion.
Pck2-Del-F	CACATTAATATTAATAAACGGAAGCGAAAAATTGCAGATAAGAAGTTA AGCGGAAAAATCAGGATTAGGCCATTTAAAGTACGGATCCCCGGG TTAATTAA	<i>pck2</i> ⁺ deletion (<i>NatR</i>)
Pck2-Del-R	AAAAAGTCGAAATTAGAATAATTTATCAATGCAATGAAAGATTAAGA AAATGAGAGTAACTTTATGCTCAATTTAAGGTGGAATTCGAGCTCG TTTAAAC	<i>pck2</i> ⁺ deletion (<i>NatR</i>)