

1   **Supplementary materials**

2   **Supplementary Figure 1.**

3   Phylogenetic analysis of Pmt proteins in filamentous fungi and yeasts. Genetyx  
4   software with an UPGMA method was used for constructing the phylogenetic tree.  
5   UniProt database accession numbers for the proteins are as follows. *CnPmt1*,Q5KIZ1;  
6   *CnPmt2*,Q5KAF1;                   *CnPmt4*,A3E242;                   *SpOma1*/Ogm1,O13898;  
7   *SpOma2*/Ogm2,Q9C100; *SpOma4*/Ogm4,O42933; *ScPmt1*,P33775; *ScPmt2*,P31382;  
8   *ScPmt3*,P47190; *ScPmt4*,P46971; *ScPmt5*,P52867; *ScPmt6*,P42934; *CaPmt1*,O74189;  
9   *CaPmt2*,Q5ADM9;    *CaPmt4*,Q59X23;    *CaPmt5*,Q5ACU3;    *CaPmt6*,Q5A688;  
10   *AfPmt1*,B0XYZ3;    *AfPmt2*,B0XPY7;    *AfPmt4*,B0YA13;    *AnPmtA*,Q96WN5;  
11   *AnPmtB*,Q5B3W9;    *AnPmtC*,Q5BDC1;    *AaPmtA*,Q96VV1;    *NcPmt1*,Q7SH94;  
12   *NcPmt2*,Q1K4Z4; *NcPmt4*,Q7SD53. *Cryptococcus neoformans*, *Schizosaccharomyces*  
13   *pombe*, *Saccharomyces cerevisiae*, *Candida albicans*, *Aspergillus fumigatus*, *A.*  
14   *nidulans*, *A. awamori*, and *Neurospora crassa* are abbreviated as *Cn*, *Sp*, *Sc*, *Ca*, *Af*,  
15   *An*, *Aa*, and *Nc*, respectively.

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17   **Supplementary Figure 2.**

18   Disruption of *Anpmt* genes. Schematic representation of the disruptions of *AnpmtB*  
19   (A), *AnpmtC* (B), and *AnpmtApmtB* (C) and recombination of *AnpmtB* (D) and  
20   *AnpmtC* (E). Southern blot analysis of total DNA isolated from strain AKU89 (lanes 1  
21   and 3) or from the respective disruptants (lanes 2 and 4) are shown in the panels on the  
22   right (A, B, C). Probes were derived from retained regions of *AnpmtA* (A and C) and  
23   *AnpmtB* (B and C) as indicated. PCR using total DNA isolated from strain AKU89  
24   (lane 2), from the *ΔAnpmt* (lane 2), or the recomplemented strains (lane 4) are shown  
25   in the panels on the right (D, E).  $\lambda$  DNA digested with *Hind*III was used as a size

1 marker (lane1).

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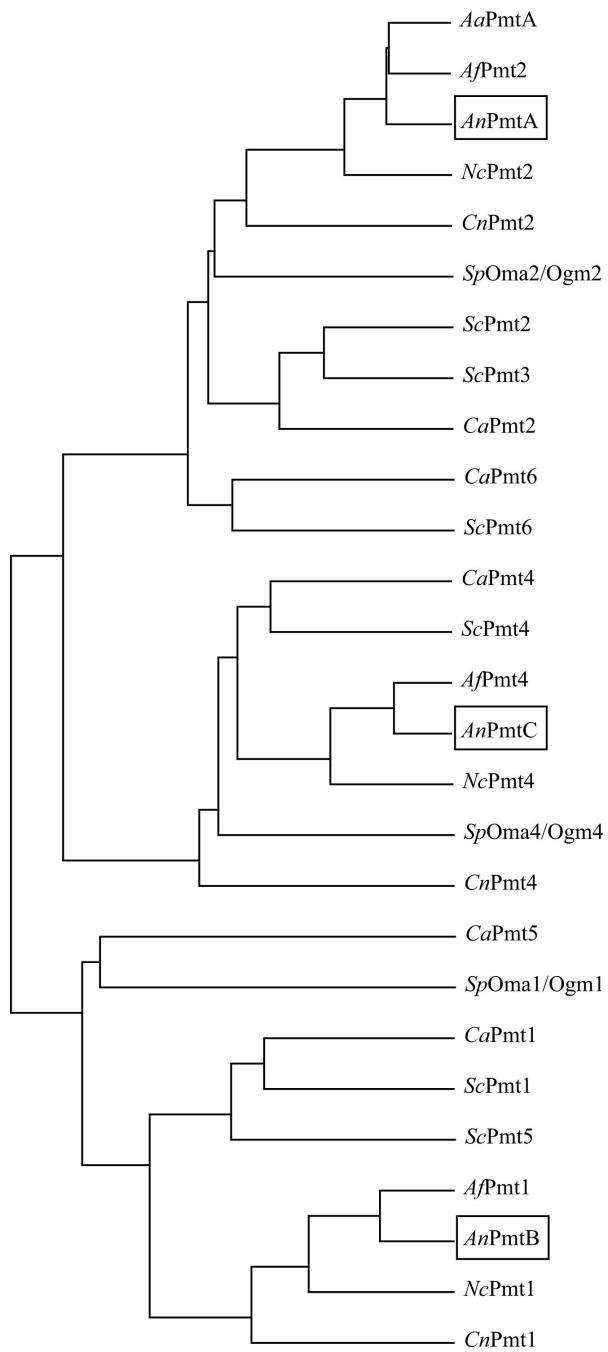
### 3 Supplemental Table. Oligonucleotides used in this study

Oligonucleotide primers	Sequence	Restriction site (underlined)
pmtB-F	5'-ATTYWTIGAYGTICAYCCICC-3',	
pmtB-R	5'-AGGRAARTARTGRTGIARRAA-3'	
pmtC-F	5'-TTYGAYTNCAACCCICCTT-3'	
pmtC-R	5'-TANCCNGTIACYTGYTGICC-3'	
An-pmtB-RT-F	5'-ATGGCGAAGGACACCCCTGGA-3'	
An-pmtB-RT-R	5'-TTCATTGAGACCGGGAATCGGAGT-3'	
An-pmtC-RT-F	5'-ATGGGATTATCGGCTGGCATTACCAT-3'	
An-pmtC-RT-R	5'-TTTCGCGAAGTCAAGTCATAGCCAAG-3'	
F1-PnkuB	5'- <u>GATATCGGACCTTCTGACTGGACC</u> -3' <i>EcoRV</i>	
R1-PnkuB	5'-CGCAGAGGTGACCGAAGTCGATATGTGTGAGACGCAAACA-3'	
F2-aur	5'-TGTGCGCTCACACATATCGACTTCGGTCACCTCTGCG-3'	
R2-aur	5'-CTCCTTAGAACATTACTCCTCAAGGGCTGAAAGTATGCC-3'	
F3-TnkuB	5'-GGCATACTTCAGCCCTTGAAGGAGTAATGTTCTAAGGAG-3',	
R3-TnkuB	5'-CGATATCAGTGCCTTCCC-3' <i>EcoRV</i>	
pmtB-around-F	5'-AATCTAGAAGGCCTAGGACCGTAGGTGTATTCCC-3'	
pmtB-around-R	5'-AAAAAAACAGCTGAATTCTCCCTAAATTCG-3'	
ptrA-KpnI-F	5'-AAAGGTACCGGGGTGACGATGAGCCGCTC-3' <i>KpnI</i>	
ptrA-KpnI-R	5'-TGGTACCGGCATTGATTACGGGATCC-3' <i>KpnI</i>	
pmtB-pr-F	5'-GGTTTCCCTGGCGATGAAA-3'	
pmtB-pr-R	5'-TGAATTCTTATTCAATTGAGACCGGGAATC-3'	
F2-AnpmtB	5'-TTAAG <u>TCGACATGACACCTTCCGGAGCGTG</u> -3' <i>SalI</i>	
R2-AnpmtB	5'-CACCG <u>TCGACGTATGACTTTAGATAGTGT</u> CAG-3' <i>SalI</i>	
F1-AnpGpB	5'-GGATTGATGTAATGTAGTCGACATGACACCTCCG-3'	
R1-AnpGpB	5'-CGGAAGGTGTCACTGCGACTACATTACATCAAATCC-3'	
F2-AnpGpB	5'-TCTAAAAGTCATCGTCGACGAGTGGAAATGTGTAACGG-3'	
R2-AnpGpB	5'-CCGTTACACATTCCACTCGCGACGTATGACTTTAGA-3'	
F-AnpmtBPr	5'-CCGAGATCACCGTCAGGTT-3'	
R-AnpmtBPr	5'-CGGGGAAATAGTGGTGTAA-3'	
pmtC-around-F	5'-AATCTAGAAGGCCTACCGTGCTTACCGGAAT-3'	
pmtC-around-R	5'-TTTCGCGAAGTCAAGTCATAGCCAAG-3'	
pmtC-pr-F	5'-ATAAAGCTCCATCACTATGCGCAC-3'	
pmtC-pr-R	5'-TTTCGCGAAGTCAAGTCATAGCCAAG-3'	
F1-AnpyrG	5'-CAC <u>CATGATTGGTATGTTCCCTCGGA</u> -3' <i>NsiI</i>	
R1-AnpyrG	5'-TAGGG <u>CATGTTCCCTCTAGCGCAAACAAAGTTC</u> -3' <i>SphI</i>	
F3-AnpmtC	5'-CACAGTCGACGTCTCACTTGGTGGAGATATA-3' <i>SalI</i>	
R3-AnpmtC	5'-CCAAGTCGACATTGGGGCCTATATCAGG-3' <i>SalI</i>	
F-AnpmtCPr	5'-ATGTCTTCATGCCCTCTCTG-3'	
R-AnpmtCPr	5'-ATGGCGAAGCTGGACGATATC-3'	
F1-PglaA	5'-AAG <u>CTTGTCAAGGGACAGCAAGTAT</u> -3' <i>HindIII</i>	
R1-PglaA	5'-GGTAC <u>CTCGCTTCTTTGAGGGAC</u> -3' <i>KpnI</i>	
argB-ApaI-F	5'-GGGCCCGCATGCAATAATTGAGCAA-3' <i>ApaI</i>	
argB-ApaI-R	5'-GGGCCCGTCGACCTACAGCCATTGCG-3' <i>ApaI</i>	
F2I-TglaA	5'- <u>GATATCAGATCTTAGACTATTCACTTCTATTGAT</u> -3' <i>EcoRV</i> <i>BgIII (double)</i>	
R2I-PglaA	5'-GAATT <u>CGGGCCGCTGGGGAGTAACGATGTTGA</u> -3' <i>EcoRI</i> <i>NotI (double)</i>	
F1-5660.2-exp	5'-AAGACCATGGGGTCGTTCACGCTATCCAC-3' <i>NcoI</i>	
R1-5660.2-exp	5'-ACAAG <u>TCGACGTGCCGGTCAGGATT</u> CGT-3' <i>SalI</i>	
F1-3HA	5'-TTGACCATGG <u>TCGACGCTAGCTACCCATACGATGTT</u> -3' <i>SalI</i>	

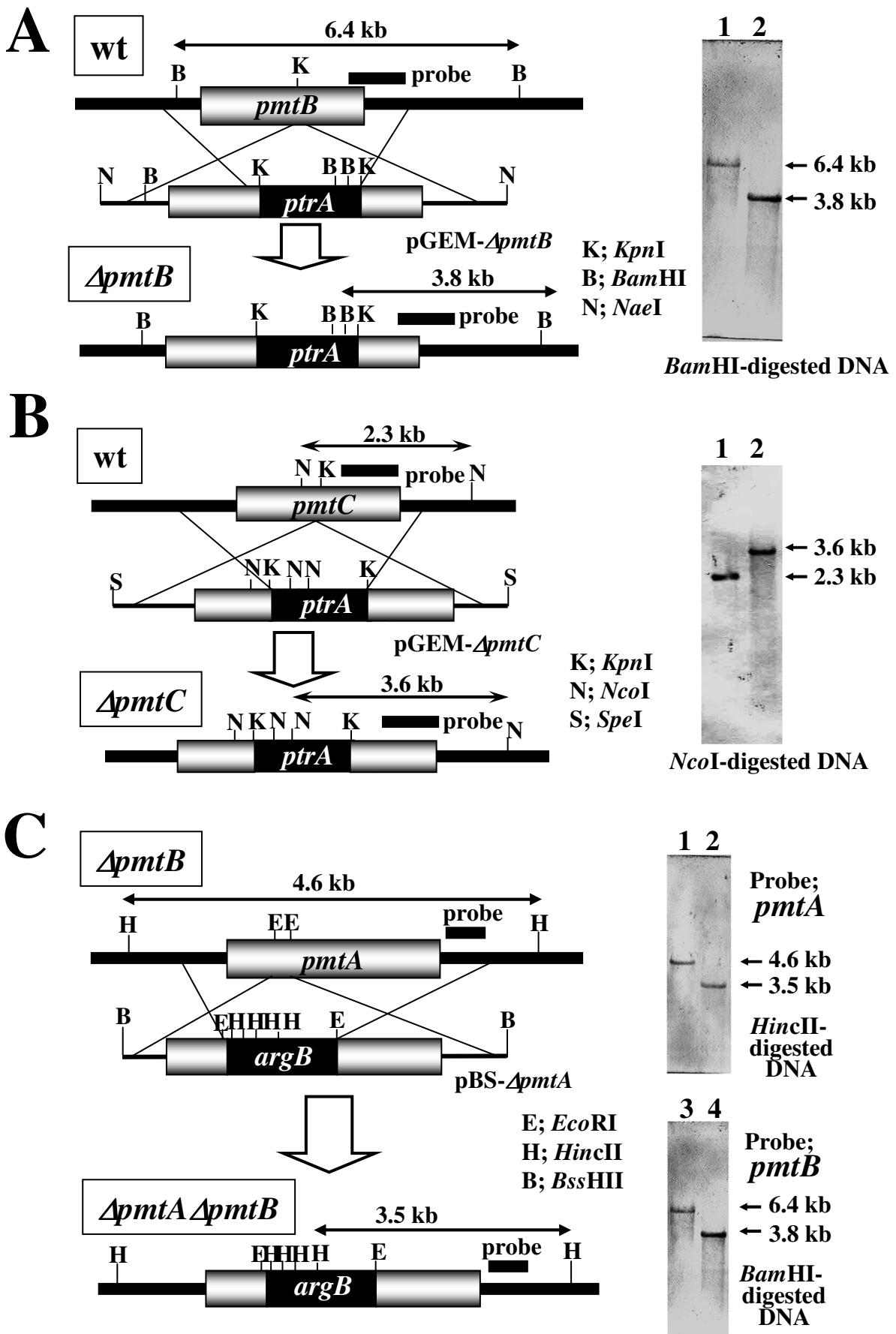
R1-3HA	5'-GATTCTGCAGCTAACCGTAATCCGGTACATCGTAT-3'	<i>PstI</i>
NotI-wscA-F	5'-AAAAGCGGCCGCATGAGGTGTTACCG-3'	<i>NotI</i>
BglII-3HA-R	5'-AAAAAGATCTCTAACCGTAATCCGG-3'	<i>BglII</i>

1 I, Y, W, R, and N indicates Inosine, C or T, A or T, A or G, and A, C, T, or G, respectively.

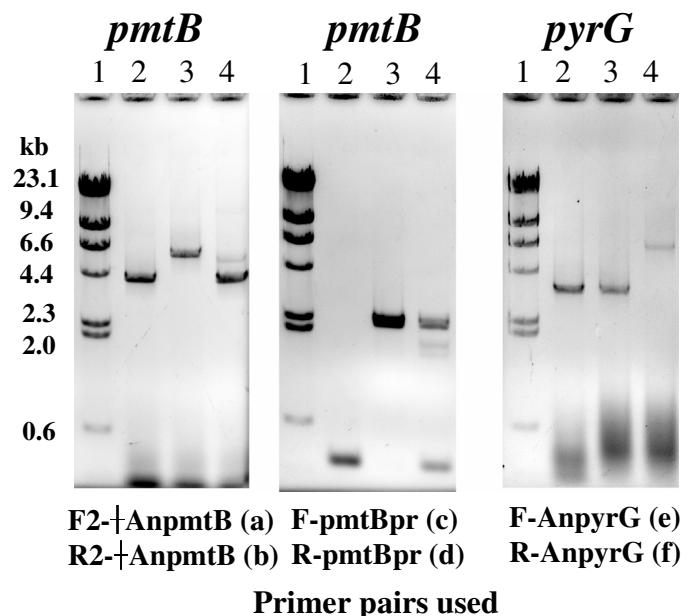
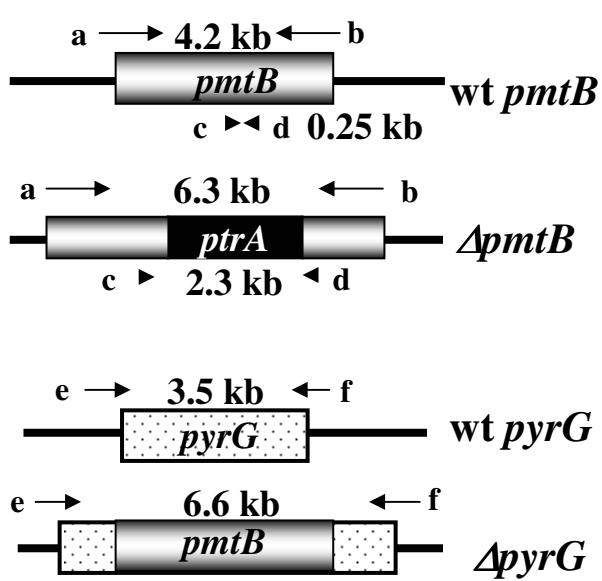
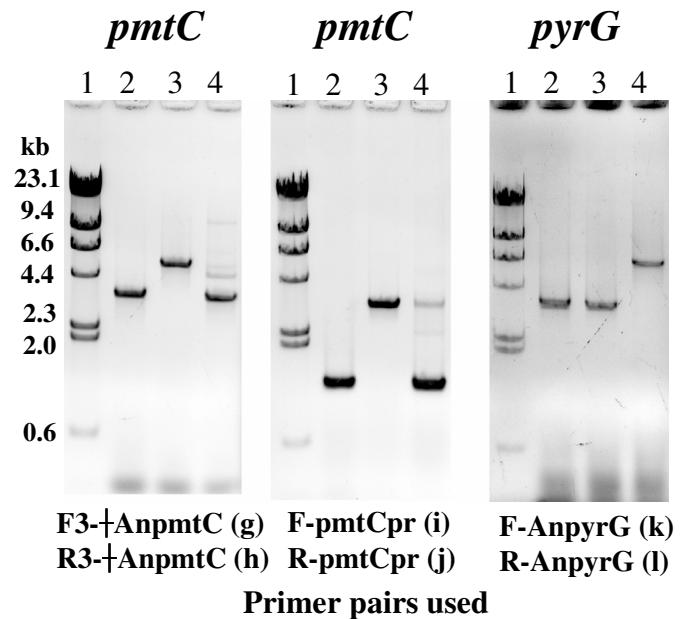
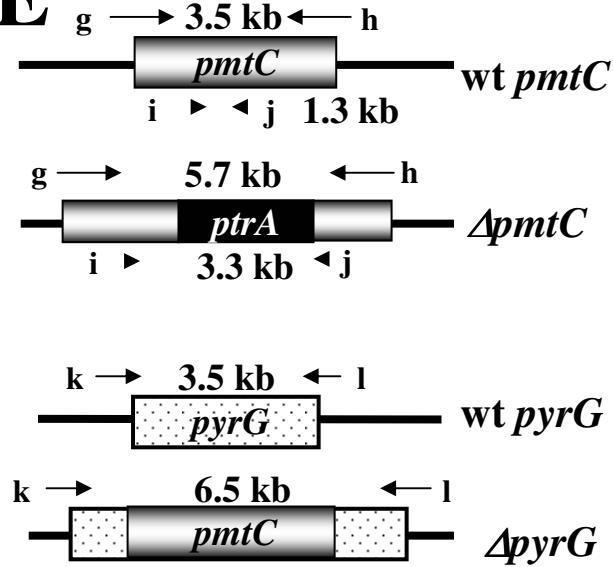
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Supplementary Figure 1. Goto, M. et al.



Supplementary Figure 2. Goto, M., et al.

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Supplementary Figure 2. Goto, M., et al.