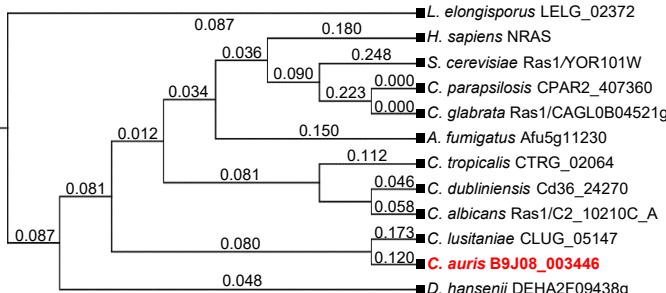


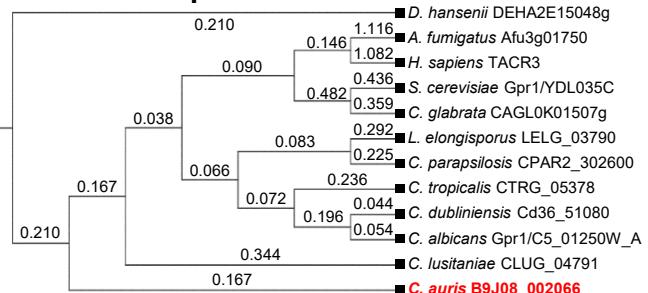
Figure S1 (Kim et al.)

(A)

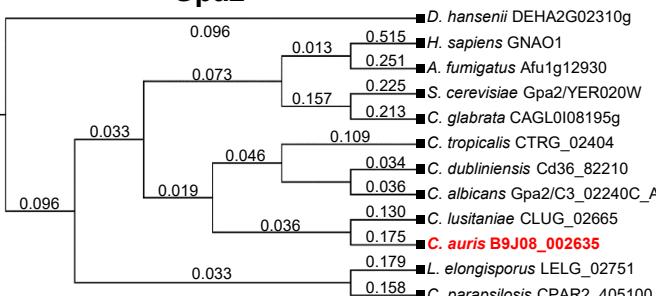
Ras1



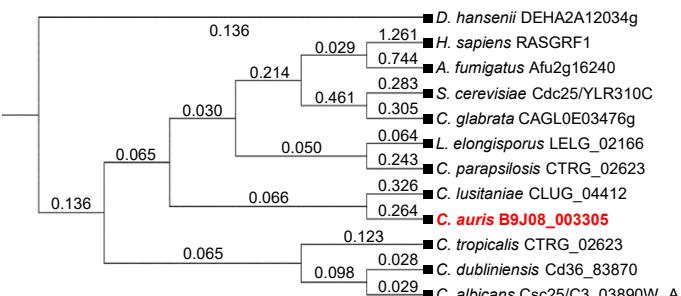
Gpr1



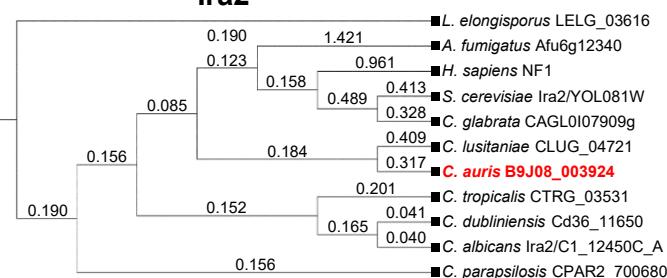
Gpa2



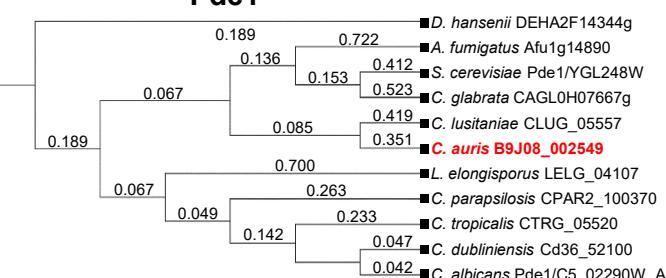
Cdc25



Ira2



Pde1



Pde2

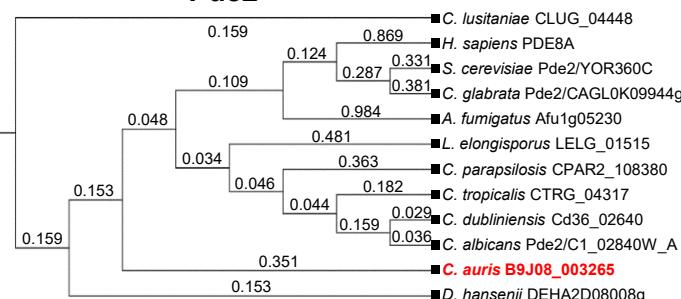


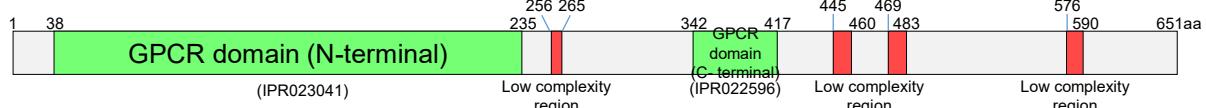
Figure S1 (Kim et al.)

(B)

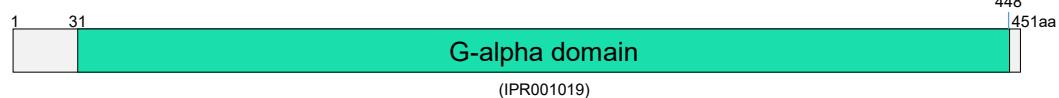
Ras1 (B9J08_003446)



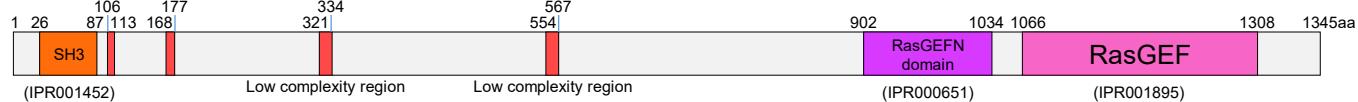
Gpr1 (B9J08_002066)



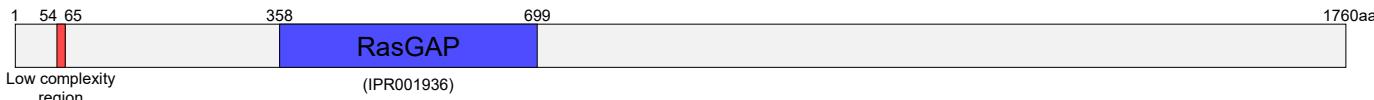
Gpa2 (B9J08_002635)



Cdc25 (B9J08_003305)



Ira2 (B9J08_003924)



Pde1 (B9J08_002549)



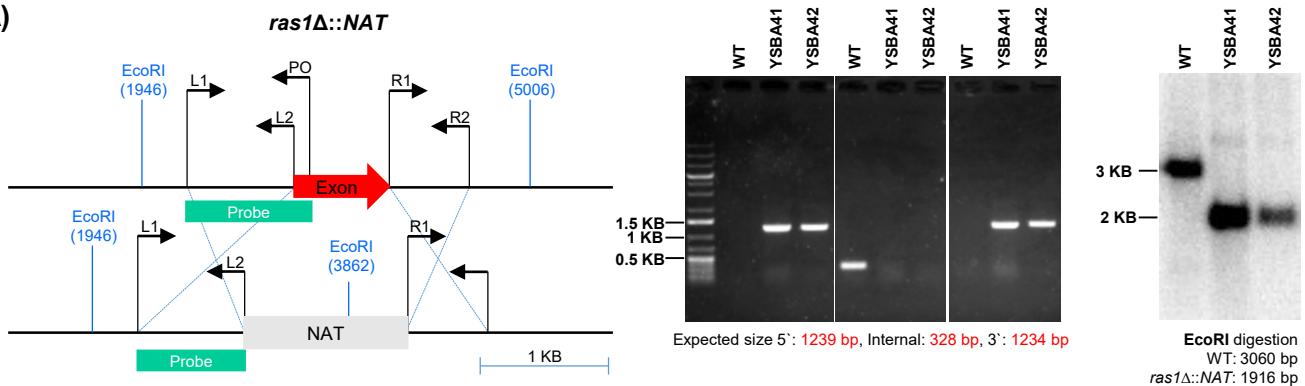
Pde2 (B9J08_003265)



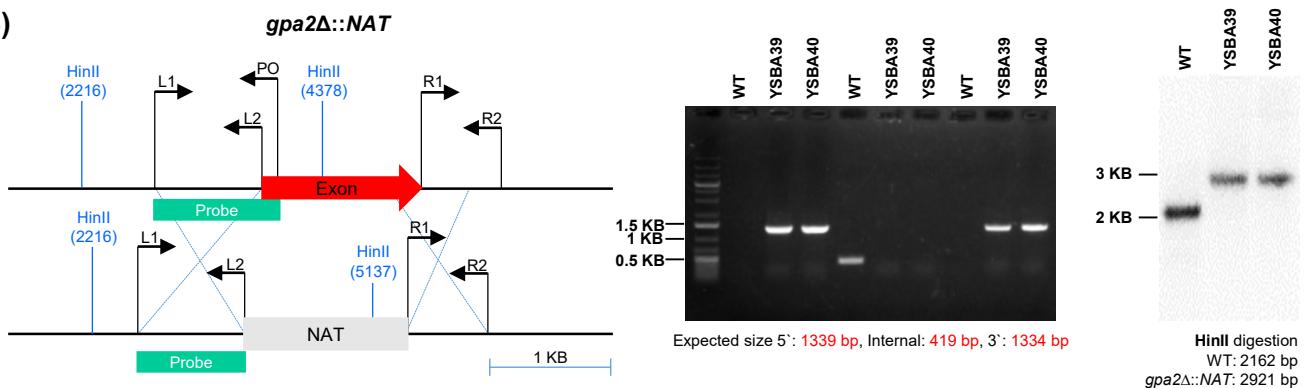
Figure S1. Evolutionary relationships and protein domains of Ras/cAMP/PKA signaling pathway genes. (A) A cladogram was constructed using the amino acid sequences of Ras1, Gpr1, Gpa2, Cdc25, Ira2, Pde1, and Pde2 from *Candida* species, related species, and humans. The analysis was performed using the CLC Sequence Viewer 8.0 software. (B) The protein domains of Ras/cAMP/PKA genes were analyzed using available domain information on InterPro (<https://www.ebi.ac.uk/interpro/>).

Figure S2 (Kim et al.)

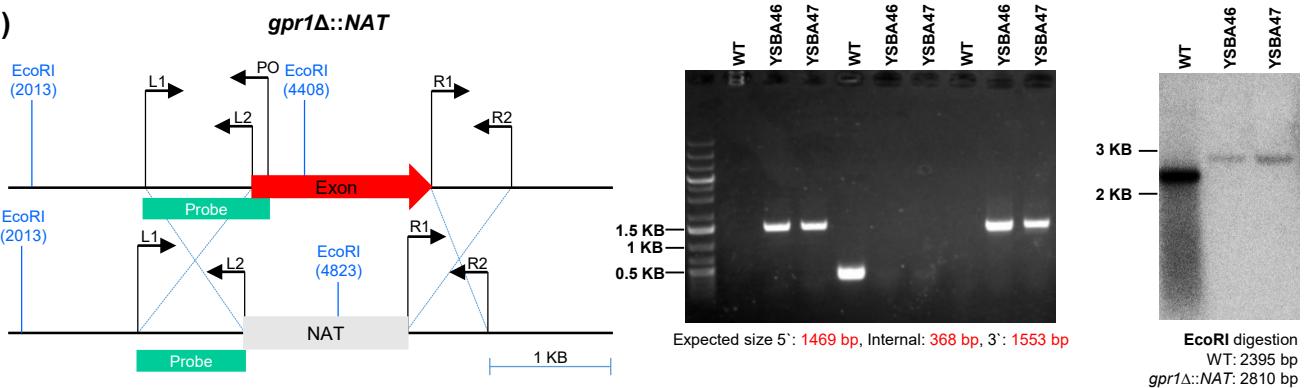
(A)



(B)



(C)



(D)

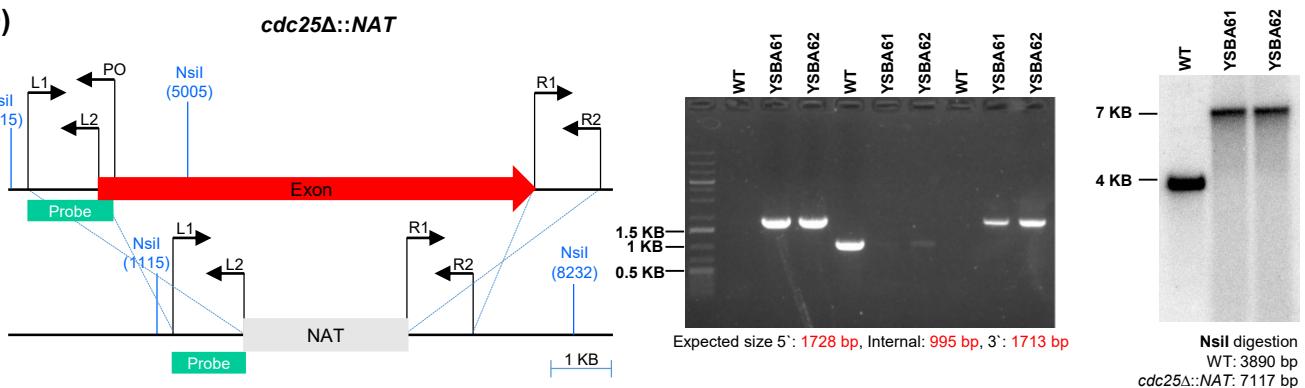
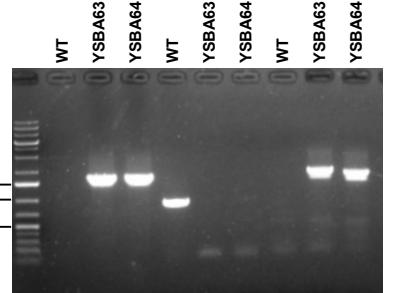
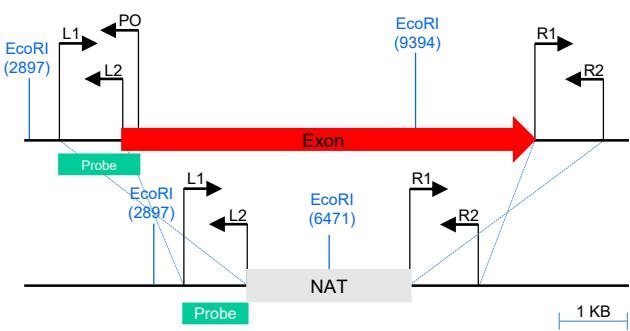


Figure S2 (Kim et al.)

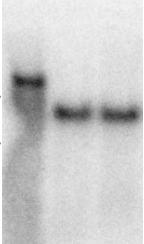
(E)

ira2Δ::NAT



Expected size 5': 1635 bp, Internal: 880 bp, 3': 1655 bp

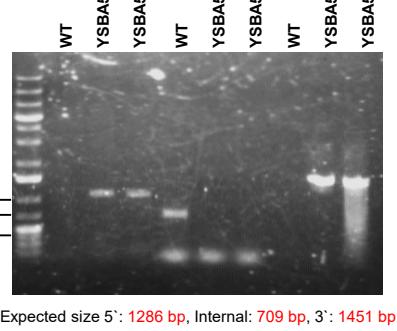
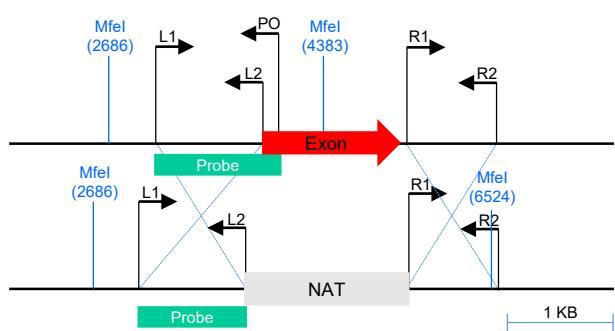
WT
YSBA63
YSBA64



EcoRI digestion
WT: 6497 bp
ira2Δ::NAT: 3574 bp

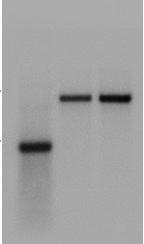
(F)

pde1Δ::NAT



Expected size 5': 1286 bp, Internal: 709 bp, 3': 1451 bp

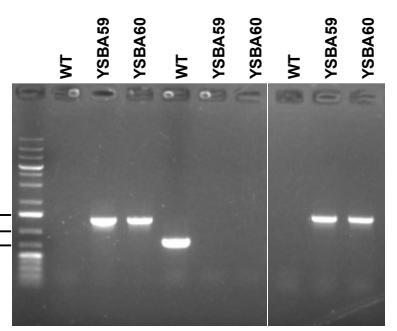
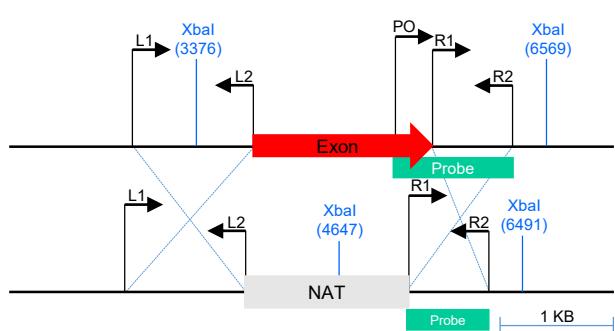
WT
YSBA55
YSBA56



Mfel digestion
WT: 1697 bp
pde1Δ::NAT: 3838 bp

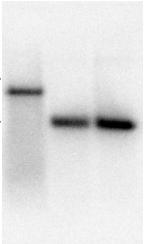
(G)

pde2Δ::NAT



Expected size 5': 1329 bp, Internal: 758 bp, 3': 1400 bp

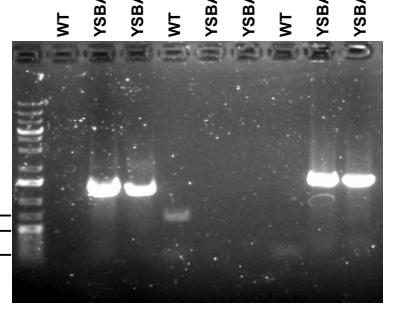
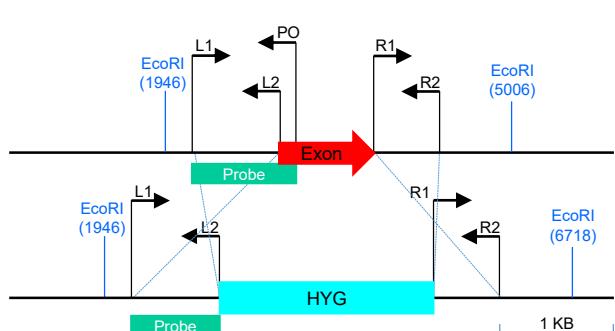
WT
YSBA59
YSBA60



XbaI digestion
WT: 3193 bp
pde2Δ::NAT: 1884 bp

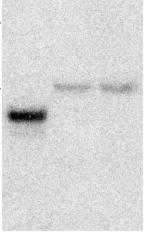
(H)

ras1Δ::HYG



Expected size 5': 1143 bp, Internal: 600 bp, 3': 1175 bp

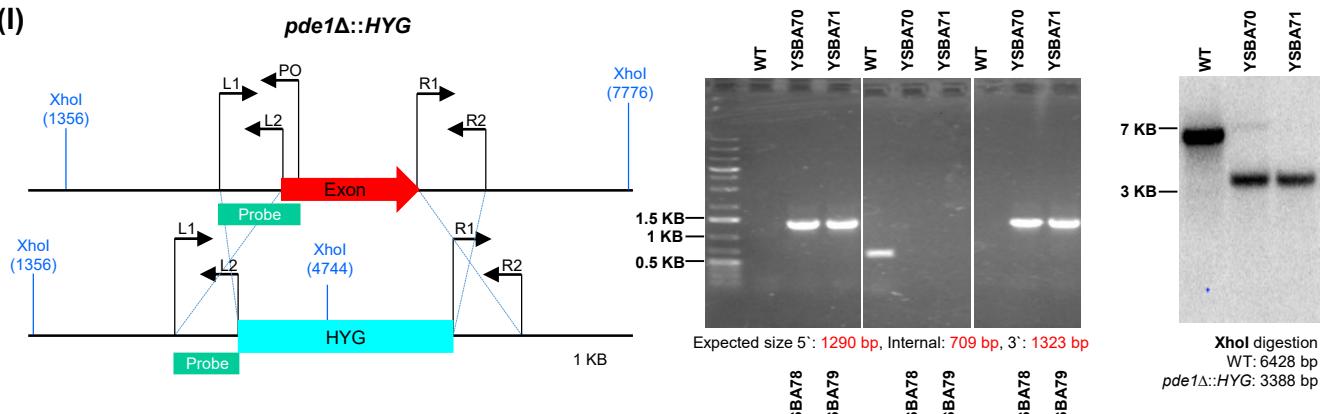
WT
YSBA68
YSBA69



EcoRI digestion
WT: 3060 bp
ras1Δ::HYG: 4772 bp

Figure S2 (Kim et al.)

(I)



(J)

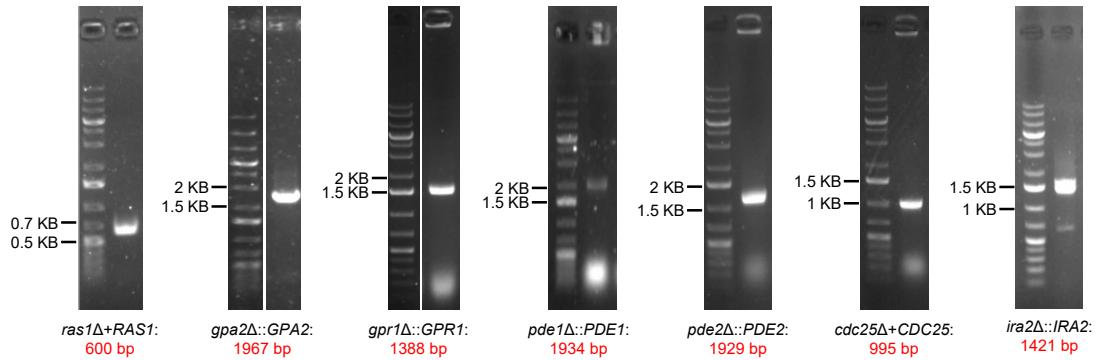


Figure S2 (Kim et al.)

(K)

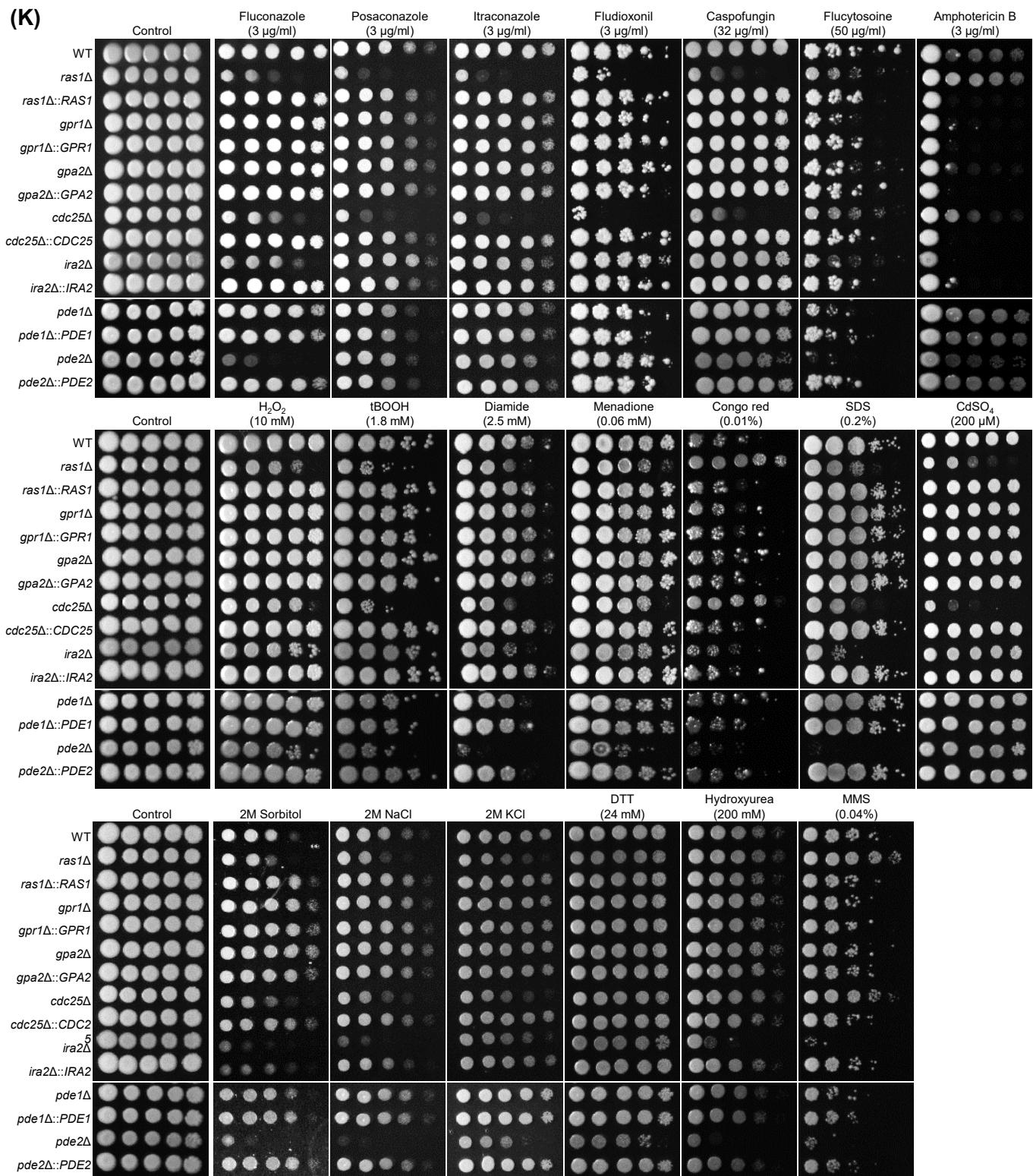
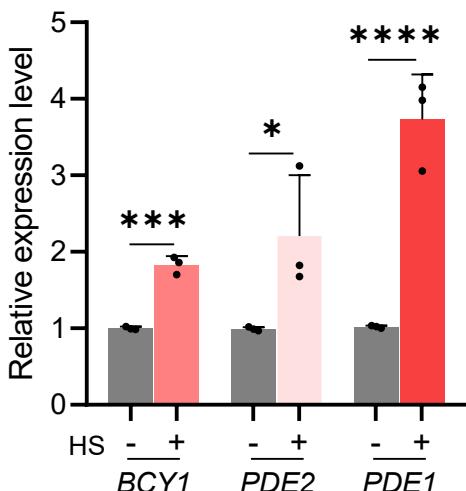


Figure S2. Construction, validation, and analysis of gene deletion mutants in *Candida auris*.

(A to I) Homologous recombination strategies between the wild-type gene and the deletion cassette are illustrated graphically (left panels). Transformants were confirmed by diagnostic PCR (center panels) and Southern blot analysis (right panels). (J) Validation of complemented strains. (K) Spot analysis of *C. auris* wild-type and mutants under stress-inducing conditions.

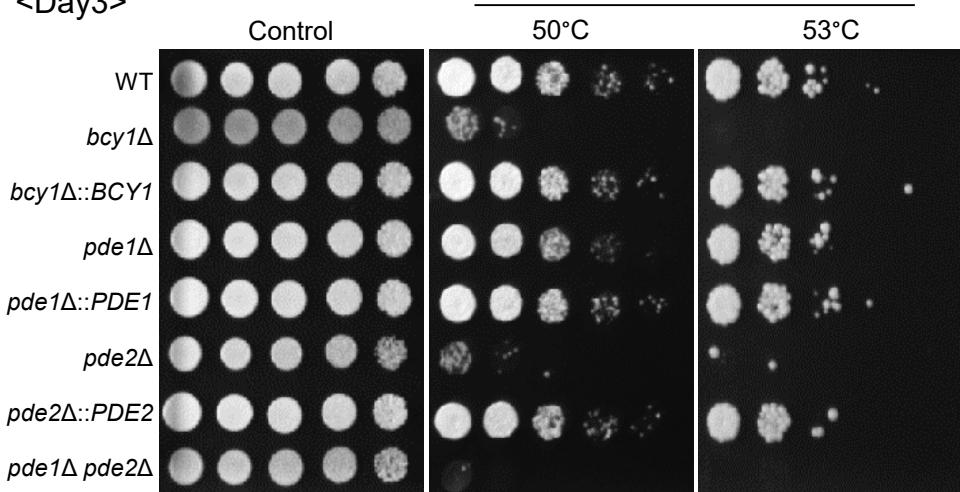
Figure S3 (Kim et al.)

(A)



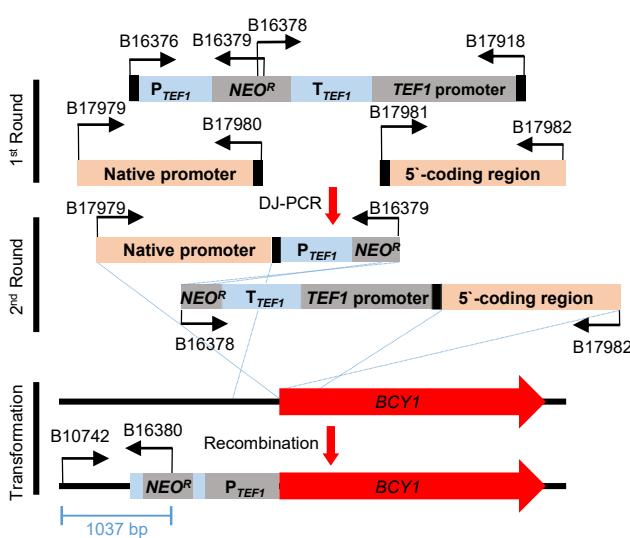
(B)

<Day3> Heat shock (10 min)



(C)

$P_{TEF1}:BCY1$



(D)

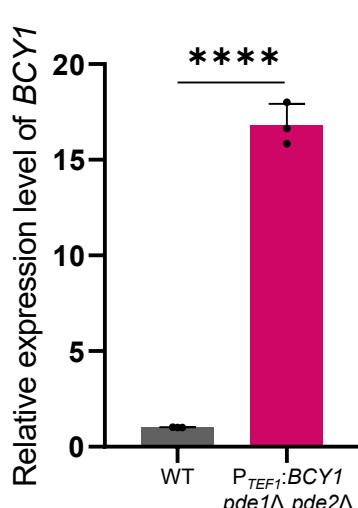
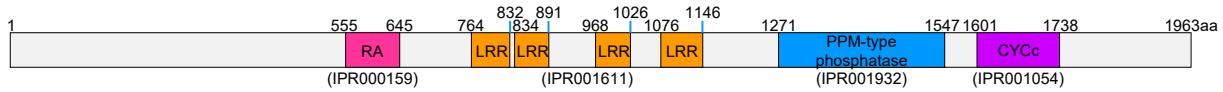


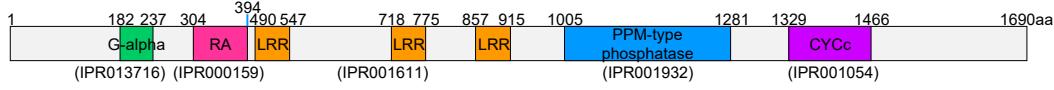
Figure S3. Validation of the roles of Pde1/2 and Bcy1 in *C. auris* thermotolerance. (A) qRT-PCR analysis of *BCY1*, *PDE1*, and *PDE2* in the wild-type strain. (B) Qualitative spot assays for measuring the thermotolerance of the wild-type and mutant strains. (C) Strategy for construction of the *BCY1* overexpression strain using the *TEF1* promoter. (D) qRT-PCR analysis of *BCY1* in the wild-type and *BCY1^{oe}* *pde1Δ pde2Δ* strains. (A and D) Statistical analysis was performed using Student's t test (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$).

Figure S4 (Kim et al.)

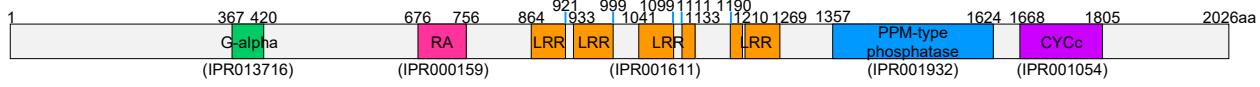
C. auris Cyr1 (B9J08_004540)



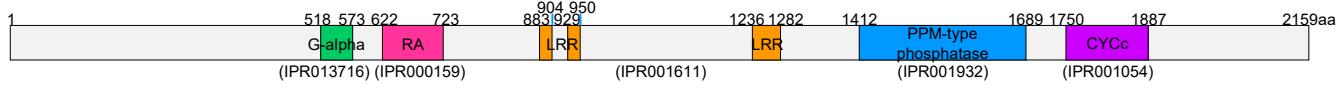
C. albicans Cyr1 (C7_03070C_A)



S. cerevisiae Cyr1 (YJL005W)



A. fumigatus Cyr1 (Q4WMW1)



C. neoformans Cac1 (CNAG_03202)

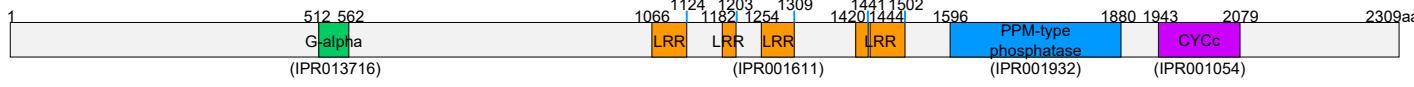


Figure S4. Protein domain analysis of adenylate cyclase in fungal species. The available domain information on InterPro (<https://www.ebi.ac.uk/interpro/>) was used to perform a protein domain analysis of adenylate cyclase in fungal species, such as *C. auris*, *C. albicans*, *S. cerevisiae*, *A. fumigatus*, and *C. neoformans*. (G-alpha: G-alpha binding domain, RA: Ras-associating domain, LRR: Leucine-rich repeat, CYCc: Adenylyl cyclase class-3/4/guanylyl cyclase domain).