

Table S1. Strains used in this study

Strain	Genotype	Parent	Reference
H99	MAT α		[1]
YSB64	MAT α <i>hog1Δ::NAT-STM#177</i>	H99	[2]
YSB42	MAT α <i>cac1Δ::NAT-STM#159</i>	H99	[3]
YSB53	MAT α <i>ras1Δ::NAT-STM#150</i>	H99	[3]
KK1	MAT α <i>cna1Δ::NAT-STM#117</i>	H99	[4]
KK2	MAT α <i>cnb1Δ::NAT-STM#117</i>	H99	[4]
KK3	MAT α <i>mpk1Δ::NAT-STM#150</i>	H99	[4]
YSB552	MAT α <i>ire1Δ::NAT-STM#224</i>	H99	[5]
YSB723	MAT α <i>hx1Δ::NAT-STM#295</i>	H99	[5]
YSB3785	MAT α <i>rad53Δ::NAT-STM#184</i>	H99	[6]
YSB1263	MAT α <i>crz1Δ::NAT-STM#231</i>	H99	[7]
KW308	MAT α <i>ire1Δ::NAT-STM#224 hx1Δ::NEO</i>	YSB552	[8]
KW309	MAT α <i>ire1Δ::NAT-STM#224 hx1Δ::NEO</i>	YSB552	[8]
KW610	MAT α <i>cna1Δ::NAT-STM#117 ire1Δ::NEO</i>	KK1	This study
KW611	MAT α <i>cna1Δ::NAT-STM#117 ire1Δ::NEO</i>	KK1	This study
KW614	MAT α <i>cnb1Δ::NAT-STM#117 ire1Δ::NEO</i>	KK2	This study
KW615	MAT α <i>cnb1Δ::NAT-STM#117 ire1Δ::NEO</i>	KK2	This study
KW629	MAT α <i>cna1Δ::NAT-STM#117 hog1Δ::NEO</i>	KK1	This study
KW632	MAT α <i>cna1Δ::NAT-STM#117 hog1Δ::NEO</i>	KK1	This study
KW630	MAT α <i>cnb1Δ::NAT-STM#117 hog1Δ::NEO</i>	KK2	This study
KW637	MAT α <i>cnb1Δ::NAT-STM#117 hog1Δ::NEO</i>	KK2	This study
KW638	MAT α <i>cnb1Δ::NAT-STM#117 hog1Δ::NEO</i>	KK2	This study
KW986	MAT α <i>cna1Δ::NAT-STM#117 crz1Δ::NEO</i>	KK1	This study
KW1009	MAT α <i>cna1Δ::NAT-STM#117 crz1Δ::NEO</i>	KK1	This study
KW1010	MAT α <i>cna1Δ::NAT-STM#117 crz1Δ::NEO</i>	KK1	This study
KW987	MAT α <i>cnb1Δ::NAT-STM#117 crz1Δ::NEO</i>	KK2	This study
KW1011	MAT α <i>cnb1Δ::NAT-STM#117 crz1Δ::NEO</i>	KK2	This study
KW1012	MAT α <i>cnb1Δ::NAT-STM#117 crz1Δ::NEO</i>	KK2	This study
KW753	MAT α CPY-4xFLAG-NEO	H99	This study
KW754	MAT α CPY-4xFLAG-NEO	H99	This study
KW755	MAT α CPY-4xFLAG-NEO	H99	This study

Each NAT-STM# indicates the Nat^r marker with a unique signature tag.

References

- [1] J.R. Perfect, N. Katabchi, G.M. Cox, C.W. Ingram, C.L. Beiser, Karyotyping of *Cryptococcus neoformans* as an epidemiological tool, *J. Clin. Microbiol.* 31 (1993) 3305-3309.
- [2] Y.S. Bahn, K. Kojima, G.M. Cox, J. Heitman, Specialization of the HOG pathway and its impact on differentiation and virulence of *Cryptococcus neoformans*, *Mol Biol Cell* 16 (2005) 2285-2300.

- [3] Y.S. Bahn, J.K. Hicks, S.S. Giles, G.M. Cox, J. Heitman, Adenylyl cyclase-associated protein Aca1 regulates virulence and differentiation of *Cryptococcus neoformans* via the cyclic AMP-protein kinase A cascade, *Eukaryot Cell* 3 (2004) 1476-1491.
- [4] K. Kojima, Y.S. Bahn, J. Heitman, Calcineurin, Mpk1 and Hog1 MAPK pathways independently control fludioxonil antifungal sensitivity in *Cryptococcus neoformans*, *Microbiology* 152 (2006) 591-604.
- [5] S.A. Cheon, K.W. Jung, Y.L. Chen, J. Heitman, Y.S. Bahn, H.A. Kang, Unique evolution of the UPR pathway with a novel bZIP transcription factor, Hxl1, for controlling pathogenicity of *Cryptococcus neoformans*, *PLoS Pathog.* 7 (2011) e1002177.
- [6] K.T. Lee, Y.S. So, D.H. Yang, K.W. Jung, J. Choi, D.G. Lee, H. Kwon, J. Jang, L.L. Wang, S. Cha, G.L. Meyers, E. Jeong, J.H. Jin, Y. Lee, J. Hong, S. Bang, J.H. Ji, G. Park, H.J. Byun, S. Park, Y.M. Park, G. Adedoyin, T. Kim, A.K. Averette, J.S. Choi, J. Heitman, E. Cheong, Y.H. Lee, Y.S. Bahn, Systematic fungal analysis of kinases in the fungal pathogen *Cryptococcus neoformans*, *Nat Commun* 7 (2016) 12766.
- [7] K.W. Jung, D.H. Yang, S. Maeng, K.T. Lee, Y.S. So, J. Hong, J. Choi, H.J. Byun, H. Kim, S. Bang, M.H. Song, J.W. Lee, M.S. Kim, S.Y. Kim, J.H. Ji, G. Park, H. Kwon, S. Cha, G.L. Meyers, L.L. Wang, J. Jang, G. Janbon, G. Adedoyin, T. Kim, A.K. Averette, J. Heitman, E. Cheong, Y.H. Lee, Y.W. Lee, Y.S. Bahn, Systematic functional profiling of transcription factor networks in *Cryptococcus neoformans*, *Nat Commun* 6 (2015) 6757.
- [8] K.W. Jung, Y.S. So, Y.S. Bahn, Unique roles of the unfolded protein response pathway in fungal development and differentiation, *Sci Rep* 6 (2016) 33413.