

Table S1

Name	Species	JGI Protein ID	FungiDB Gene ID	EnsemblFungi Gene ID
Erg3	<i>Candida albicans</i> SC5314	59490	C1_04770C_A	C1_04770C_A
Erg3	<i>Choanephora cucurbitarum</i> NRRL2744	516289		
Erg3	<i>Cunninghamella echinulata</i> NRRL1382	185651		
Erg3	<i>Cryptococcus neoformans</i> H99	446	CNAG_00519	CNAG_00519
Erg3a	<i>Lichtheimia corymbifera</i> JMRC:FSU:9682	10330	LCOR_09389.1	LCOR_09389.1
Erg3b	<i>Lichtheimia corymbifera</i> JMRC:FSU:9682	4998	LCOR_04579.1	LCOR_04579.1
Erg3a	<i>Lichtheimia ramosa</i> JMRC:FSU:6197	7192		LRAMOSA02887
Erg3b	<i>Lichtheimia ramosa</i> JMRC:FSU:6197	11099		LRAMOSA06288
Erg3	<i>Malassezia pachydermatis</i> CBS1879	2056	Malapachy_0912	Malapachy_0912
Erg3	<i>Mucor circinelloides</i> 1006PhL	6367	HMPREF1544_06438	HMPREF1544_06438
Erg3	<i>Mucor lusitanicus</i> MU402	1381623		
Erg3	<i>Mucor lusitanicus</i> CBS277.49 v2.0	156917	QYA_156917	MUCCIDRAFT_156917
Erg3	<i>Mucor racemosus</i> UBOCC-A-109155	3973		
Erg3	<i>Phycomyces blakesleeanus</i> NRRL1555	178901	PHYBL_178901	
Erg3a	<i>Rhizopus azygosporus</i> CBS357.93			CU097_003763
Erg3b	<i>Rhizopus azygosporus</i> CBS357.93			CU097_010180
Erg3a	<i>Rhizopus delemar</i> 99-880	4689	RO3G_07367	RO3G_07367
Erg3b	<i>Rhizopus delemar</i> 99-880	7668	RO3G_13407	RO3G_13407
Erg3	<i>Rhizopus microsporus</i> var. <i>microsporus</i> ATCC52813	213209		RHIMIDRAFT_213209
Erg3	<i>Saccharomyces cerevisiae</i> S288C	4075	YLR056W	YLR056W
Erg31	<i>Schizosaccharomyces pombe</i> 972h-	372	SPAC1687.16c	SPAC1687.16c
Erg32	<i>Schizosaccharomyces pombe</i> 972h-	2860	SPBC27B12.03c	SPBC27B12.03c
Erg3	<i>Spizellomyces punctatus</i> DAOM BR117	5830	SPPG_02338	SPPG_02338
Erg3	<i>Syncephalastrum racemosum</i> NRRL2496	499858		
Erg3a	<i>Sporodiniella umbellata</i> MES 1446	444990		
Erg3b	<i>Sporodiniella umbellata</i> MES 1446	496186		
Erg3	<i>Ustilago maydis</i> 521	10884	UMAG_03593	UMAG_03593

Table S1. Erg3 amino acid sequences obtained from the genomes of listed fungal species. Identification numbers from different databases [Joint Genome Institute MycoCosm (JGI, <https://mycocosm.jgi.doe.gov>), Fungi Database (FungiDB, <https://fungidb.org>) and Ensembl Fungi (<https://fungi.ensembl.org>)] are indicated to facilitate accessibility and reproducibility.

Table S2

Name	Species	JGI Protein ID	FungiDB Gene ID	EnsemblFungi Gene ID
Erg6	<i>Candida albicans</i> SC5314	57503	C3_02150C_A	C3_02150C_A
Erg6a	<i>Choanephora cucurbitarum</i> NRRL2744	208609		
Erg6b	<i>Choanephora cucurbitarum</i> NRRL2744	449520		
Erg6a	<i>Cunninghamella echinulata</i> NRRL1382	280554		
Erg6	<i>Cryptococcus neoformans</i> H99	3420	CNAG_03819	CNAG_03819
Erg6a	<i>Lichtheimia corymbifera</i> JMRC:FSU:9682	1250	LCOR_01192.1	LCOR_01192.1
Erg6b	<i>Lichtheimia corymbifera</i> JMRC:FSU:9682	3633	LCOR_03386.1	LCOR_03386.1
Erg6d	<i>Lichtheimia corymbifera</i> JMRC:FSU:9682	3987	LCOR_03695.1	LCOR_03695.1
Erg6a	<i>Lichtheimia ramosa</i> JMRC:FSU:6197	1343		LRAMOSAA06893
Erg6b	<i>Lichtheimia ramosa</i> JMRC:FSU:6197	536		LRAMOSAA00533
Erg6d	<i>Lichtheimia ramosa</i> JMRC:FSU:6197	2430		LRAMOSAA07977
Erg6	<i>Malassezia pachydermatis</i> CBS1879	2313	Malapachy_1146	Malapachy_1146
Erg6a	<i>Mucor circinelloides</i> 1006PhL	10718	HMPREF1544_10842	HMPREF1544_10842
Erg6b	<i>Mucor circinelloides</i> 1006PhL	8587	HMPREF1544_08689	HMPREF1544_08689
Erg6c	<i>Mucor circinelloides</i> 1006PhL	9624	HMPREF1544_09736	HMPREF1544_09736
Erg6a	<i>Mucor lusitanicus</i> MU402	1319648		
Erg6b	<i>Mucor lusitanicus</i> MU402	1325190		
Erg6c	<i>Mucor lusitanicus</i> MU402	1448211		
Erg6a	<i>Mucor lusitanicus</i> CBS277.49 v2.0	155859	QYA_155859	MUCCIDRAFT_155859
Erg6b	<i>Mucor lusitanicus</i> CBS277.49 v2.0	151310	QYA_151310	MUCCIDRAFT_151310
Erg6c	<i>Mucor lusitanicus</i> CBS277.49 v2.0	74496	QYA_74496	MUCCIDRAFT_74496
Erg6a	<i>Mucor racemosus</i> UBOCC-A-109155	9296		
Erg6b	<i>Mucor racemosus</i> UBOCC-A-109155	5625		
Erg6c	<i>Mucor racemosus</i> UBOCC-A-109155	11127		
Erg6a	<i>Phycomyces blakesleeanus</i> NRRL1555	128748	PHYBL_128748	
Erg6b	<i>Phycomyces blakesleeanus</i> NRRL1555	114967	PHYBL_114967	
Erg6a	<i>Rhizopus azygosporus</i> CBS357.93			CU097_001869
Erg6a	<i>Rhizopus delemar</i> 99-880	9579	RO3G_15767	RO3G_15767
Erg6e	<i>Rhizopus delemar</i> 99-880	1008	RO3G_16049	RO3G_16049
Erg6a	<i>Rhizophagus irregularis</i> DAOM 197198	1517096		
Erg6b	<i>Rhizophagus irregularis</i> DAOM 197198	1668347		
Erg6a	<i>Rhizopus microsporus</i> var. <i>microsporus</i> ATCC52813	203690		RHIMIDRAFT_203690
Erg6	<i>Saccharomyces cerevisiae</i> S288C	4664	YML008C	YML008C
Erg6	<i>Schizosaccharomyces pombe</i> 972h-	3100	SPBC16E9.05	SPBC16E9.05
Erg6	<i>Spizellomyces punctatus</i> DAOM BR117	8734	SPPG_05059	SPPG_05059
Erg6a	<i>Syncephalastrum racemosum</i> NRRL2496	499603		
Erg6b	<i>Syncephalastrum racemosum</i> NRRL2496	466111		
Erg6a	<i>Sporodiniella umbellata</i> MES 1446	459696		
Erg6e	<i>Sporodiniella umbellata</i> MES 1446	469068		
Erg6	<i>Ustilago maydis</i> 521	10455	UMAG_03182	UMAG_03182

Table S2. Erg6 amino acid sequences obtained from the genomes of listed fungal species. Identification numbers from different databases [Joint Genome Institute MycoCosm (JGI, <https://mycocosm.jgi.doe.gov>), Fungi Database (FungiDB, <https://fungidb.org>) and Ensembl Fungi (<https://fungi.ensembl.org>)] are indicated to facilitate accessibility and reproducibility.

Table S3

Strain	Species	Genotype	Reference
MU402	<i>M. lusitanicus</i>	<i>pyrG⁻ leuA⁻</i>	(75)
MU636	<i>M. lusitanicus</i>	<i>pyrG⁻::pyrG⁺ leuA⁻</i>	(35)
MIN11	<i>M. lusitanicus</i>	<i>erg3::pyrG leuA⁻</i>	This study
MIN12	<i>M. lusitanicus</i>	<i>erg3::pyrG leuA⁻</i>	This study
MIN13	<i>M. lusitanicus</i>	<i>erg6a::pyrG leuA⁻</i>	This study
MIN14	<i>M. lusitanicus</i>	<i>erg6a::pyrG leuA⁻</i>	This study
1006PhL	<i>M. circinelloides</i>	wildtype	(39)
MIN6	<i>M. circinelloides</i>	<i>pyrF-59Δ</i>	This study
CPA6	<i>M. circinelloides</i>	<i>pyrF-59Δ::pyrF⁺</i>	This study
MIN15	<i>M. circinelloides</i>	<i>erg3::pyrF</i>	This study
MIN16	<i>M. circinelloides</i>	<i>erg3::pyrF</i>	This study
MIN17	<i>M. circinelloides</i>	<i>erg6a::pyrF</i>	This study
MIN18	<i>M. circinelloides</i>	<i>erg6a::pyrF</i>	This study

Table S3. Strains used in this study, showing from which species they derive, genotype, and references.

Table S4

Name	Species	Sequence (5' → 3')	Description
JOHE51488	<i>Mlu</i>	TGCCTCAGCATTGGTACTTG	<i>pyrG</i> PCR
JOHE51489	<i>Mlu</i>	GTACACTGGCCATGCTATCG	<i>pyrG</i> PCR
JOHE51528	<i>Mlu</i>	CGATAGCATGGCCAGTGTACTAGAGTTTACGATGCAGGCCAGT	<i>erg3</i> deletion, overlap with <i>pyrG</i>
JOHE51539	<i>Mlu</i>	CAAGTACCAATGCTGAGGCAATTTCTGTGTGTCAGTCCGCAC	<i>erg3</i> deletion, overlap with <i>pyrG</i>
JOHE51529	<i>Mlu</i>	ATTAGAACAGAAGGGCAGTCGG	<i>erg3</i> deletion
JOHE51538	<i>Mlu</i>	CGATCATGCTTACGGTGGTTGAGT	<i>erg3</i> deletion
JOHE51540	<i>Mlu</i>	CGATAGCATGGCCAGTGTACGTGTGCCAAGTGTAGATGTTGTG	<i>erg6a</i> deletion, overlap with <i>pyrG</i>
JOHE51552	<i>Mlu</i>	CAAGTACCAATGCTGAGGCACATCTGTCTCAATATCCGTCGTC	<i>erg6a</i> deletion, overlap with <i>pyrG</i>
JOHE51541	<i>Mlu</i>	ATTTGCCCCGCTGTAGATGATAC	<i>erg6a</i> deletion
JOHE51551	<i>Mlu</i>	AGTGTAGCAAAAGTTGCCCTTG	<i>erg6a</i> deletion
JOHE51511	<i>Mlu</i>	ACCTTGAGCACACAAACAAAGG	<i>pyrG</i> , 5' junction PCR
JOHE51510	<i>Mlu</i>	CCTTTGTTTGTGTGCTCAAGGT	<i>pyrG</i> , 3' junction PCR
JOHE51533	<i>Mlu</i>	ACAGGAAGTGAGTACAACGGACA	<i>erg3</i> , 5' junction PCR
JOHE51534	<i>Mlu</i>	CATCGCCTCATACTACTCAAAGC	<i>erg3</i> , 3' junction PCR
JOHE51531	<i>Mlu</i>	TGTGGTATCTACTGGTTCCATCG	<i>erg3</i> , WT allele PCR
JOHE51536	<i>Mlu</i>	ATGTTGTGTGTCGAGTAGCACC	<i>erg3</i> , WT allele PCR
JOHE51545	<i>Mlu</i>	GTCTATGTGGCGCTCAATTCTAC	<i>erg6a</i> , 5' junction PCR
JOHE51546	<i>Mlu</i>	GCGTCCTCTCCATTCTACTAC	<i>erg6a</i> , 3' junction PCR
JOHE51543	<i>Mlu</i>	GCTGGTGATATTACGAGTCTGC	<i>erg6a</i> , WT allele PCR
JOHE51549	<i>Mlu</i>	GGAGAGATTTGATGGTGGTGT	<i>erg6a</i> , WT allele PCR
JOHE51498	<i>Mci</i>	AGAATGCCAGACCTGAATTTTTGG	<i>pyrF</i> PCR
JOHE51499	<i>Mci</i>	AATAGTAATACCTCTGCCAACGG	<i>pyrF</i> PCR
JOHE51623	<i>Mci</i>	CCGTTGGCAGAGGGTATTACTATTGATATGGTAGCGAACCCGATG	<i>erg3</i> deletion, overlap with <i>pyrF</i>
JOHE51628	<i>Mci</i>	CCAAAAATTCAGGTCTGGCATTCTAATTTCTGTGTGTCAGTCCGCAC	<i>erg3</i> deletion, overlap with <i>pyrF</i>
JOHE51624	<i>Mci</i>	GGATGAGTCTTCAGGTGCAGTAA	<i>erg3</i> deletion
JOHE51627	<i>Mci</i>	AATCCGAGAATGATGTGTAATACC	<i>erg3</i> deletion
JOHE51630	<i>Mci</i>	CCGTTGGCAGAGGGTATTACTATTCAACATCAAATCTCTCCCCTTC	<i>erg6a</i> deletion, overlap with <i>pyrF</i>
JOHE51634	<i>Mci</i>	CCAAAAATTCAGGTCTGGCATTCTCTCAATATCCGTCTTCCCCTTAC	<i>erg6a</i> deletion, overlap with <i>pyrF</i>
JOHE51629	<i>Mci</i>	AAGATTGGAGCACCTCAAGAGAC	<i>erg6a</i> deletion
JOHE51633	<i>Mci</i>	AGTCGTGCAGCAGGTAGTTTTAG	<i>erg6a</i> deletion
JOHE51503	<i>Mci</i>	GAGCAGCAGCATAGAAAGTACCA	<i>pyrF</i> , 5' junction PCR
JOHE51504	<i>Mci</i>	TATCAAGAAGGACTAGGCTTGCC	<i>pyrF</i> , 3' junction PCR
JOHE51625	<i>Mci</i>	TGTCACCTACACGAATCTTACCC	<i>erg3</i> , 5' junction PCR
JOHE51626	<i>Mci</i>	AGAGAATATGGCGCTTCAGAGAC	<i>erg3</i> , 3' junction PCR
JOHE51625	<i>Mci</i>	TGTCACCTACACGAATCTTACCC	<i>erg3</i> , WT allele PCR
JOHE51637	<i>Mci</i>	TGTTTCATCGGTGGGTTGACG	<i>erg3</i> , WT allele PCR
JOHE51631	<i>Mci</i>	CTGATTTACAGTACGCCTGAGT	<i>erg6a</i> , 5' junction PCR
JOHE51632	<i>Mci</i>	GGTAAAGAATATGGGCACAGGTC	<i>erg6a</i> , 3' junction PCR
JOHE51631	<i>Mci</i>	CTGATTTACAGTACGCCTGAGT	<i>erg6a</i> , WT allele PCR
JOHE51641	<i>Mci</i>	GCATCACCAACATTGGCAAG	<i>erg6a</i> , WT allele PCR
JOHE51712	<i>Mci</i>	GCAAGGCGATATGGGTGTTG	<i>erg6b</i> , qPCR
JOHE51713	<i>Mci</i>	GACTGAAGAGCGAAGAAACCC	<i>erg6b</i> , qPCR
JOHE51714	<i>Mci</i>	ACTCAAGCTGGTCCGTATGC	<i>erg6c</i> , qPCR
JOHE51715	<i>Mci</i>	ACAACAGAATCGCCTGCAAC	<i>erg6c</i> , qPCR
JOHE51665	<i>Mci</i>	AGGGTCAATACACTCTTGAAG	<i>vma1</i> , qPCR
JOHE51667	<i>Mci</i>	GGAGAACGAACAGGCCAGAG	<i>vma1</i> , qPCR

Table S4. Species-specific primers [*M. lusitanicus* (*Mlu*) or *M. circinelloides* (*Mci*)] used in this study, showing systematic name, nucleotide sequence, and a brief description explaining its use.

Table S5

Species	Database	Reference
<i>Candida albicans</i> SC5314	JGI	(78)
<i>Choanephora cucurbitarum</i> NRRL2744 v1.0	JGI	(79)
<i>Cryptococcus neoformans</i> var. <i>grubii</i> H99	JGI	(80)
<i>Cunninghamella echinulata</i> NRRL1382 v1.0	JGI	(79)
<i>Lichtheimia corymbifera</i> JMRC:FSU:9682	JGI	(45)
<i>Lichtheimia ramosa</i> JMRC:FSU:6197	JGI	(81)
<i>Malassezia pachydermatis</i> CBS1879	JGI	(82)
<i>Mucor circinelloides</i> 1006PhL	JGI	(39)
<i>Mucor lusitanicus</i> MU402 v1.0	JGI	(38)
<i>Mucor racemosus</i> UBOCC-A-109155	JGI	(83)
<i>Phycomyces blakesleeanus</i> NRRL1555 v2.0	JGI	(37)
<i>Rhizophagus irregularis</i> DAOM 197198 v2.0	JGI	(84)
<i>Rhizopus azygosporus</i> CBS357.93	EnsemblFungi	(47)
<i>Rhizopus delemar</i> 99-880	JGI	(46)
<i>Rhizopus microsporus</i> var. <i>microsporus</i> ATCC52813 v1.0	JGI	(85)
<i>Saccharomyces cerevisiae</i> S288C	JGI	(86)
<i>Schizosaccharomyces pombe</i> 972h-	JGI	(87)
<i>Spizellomyces punctatus</i> DAOM BR117	JGI	(88)
<i>Sporodiniella umbellata</i> MES 1446 v1.0	JGI	(79)
<i>Syncephalastrum racemosum</i> NRRL2496 v1.0	JGI	(89)
<i>Ustilago maydis</i> 521	JGI	(90)

Table S5. Proteomes from these species were obtained from publicly available repositories either at the Joint Genome Institute MycoCosm (JGI, <https://mycocosm.jgi.doe.gov>) or, if unavailable, at the EnsemblFungi (<https://fungi.ensembl.org>) databases.