Supplementary Material

Table S1. Oligonucleotide primers designed for and used in the present study.

Primers (5' to 3')	
F_ARO10KanMX	TTATTTACAAGATAACAAAGAAACTCCCTTAAGCATGGCCGTACGCTGCAGGTCGAC
R_ARO10KanMX	TGGTAGCAGTGTTTTATAATTGCGCCCACAAGTTTCTATATCGATGAATTCGAGCTCG
F_ARO4_BamHI	ATAGGATCCATATTGACACTCTTTCATTGGGC
R_ARO4_EcoRI	ATTGAATTCCTATTTCTTGTTAACTTCTCTTCTTTGTCT
F_ARO4_OLE	TTCATGGGTGTTACTTTGCATGGTGTTGCTGCTATCACCACTA
R_ARO4_OLE	AGCAGCAACACCATGCAAAGTAACACCCATGAAATGGTGAGAA
F_PAL2_attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTAAAAAAATGTCTCAAATCGAAGCAATGTTG
R_PAL2_attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTTTAGCAAATCGGAATCGGAGCT
F_ARO1_qPCR	GCTACAGTTTCTTCTCAGTACG
R_ARO1_qPCR	CGACGTACAATTTAGAGATTGG
F_ARO2_qPCR	CCTCACGACTACTCCGACAT
R_ARO2_qPCR	CGTTTCTCTAGCAGAAGCTCT
F_ARO3_qPCR	GCTGGAAAGGGTTGATTAAC
R_ARO3_qPCR	CCAACATCTCACCAGCAAT
F_ARO4_qPCR	CGAATCTCAACTGCACAGA
R_ARO4_qPCR	GCTTGACAAGCATCCACAG
F_ARO7_qPCR	GGTTCTGTTGCCACTAGAGAT
R_ARO7_qPCR	GCTTTGTGTATAGCGGGATAT
F_ARO8_qPCR	CGACTTCCTAATTGTGGAAGAT
R_ARO8_qPCR	GCTTTGGAGAACTTTGTGC
F_ARO9_qPCR	GCTACAGGAGCAAAAGTCATC
R_ARO9_qPCR	CCAGTTGACCAATTATCGAG
F_PHA2_qPCR	GGATTGTTCTTCCACATCTG
R_PHA2_qPCR	GCTGTTTCACTAGCAATGG
F_26S_qPCR	CCTATGATTTGAGTATCTCAGC
R_26S_qPCR	CGTAATTGGAATCGTTGACTAT

Table S2. Sequencing primers designed for and used in the present study.

F1_ARO3_seq	ATGTTCATTAAAAACGATCACG
F2_ARO3_seq	GCACAGAGAATTAGCATCCG
F3_ARO3_seq	GCTGTAGAACCTGTTGTCACTT
R1_ARO3_seq	CGTTCTTAAATCCAATAGGGAA
R2_ARO3_seq	TTTTTTCAAGGCCTTTCTTCTG
R3_ARO3_seq	CCTTTGATTCTCCAGTCTTCC
F1_ARO4_seq	ATGAGTGAATCTCCAATGTTCG
F2_ARO4_seq	GCCAGAACCACCGAATCTCAAC
R1_ARO4_seq	GGCCAATTCTCTGTGCAGTT
R2_ARO4_seq	TTTCTTGTTAACTTCTCTTCTTTGT
F1_ARO7_seq	ATGGATTTCACAAAACCAGAAA
F2_ARO7_seq	CATTAATTTCGAAAAGAGATGGT
R1_ARO7_seq	CCGAAGTTATTCTTATCATCACC
R2_ARO7_seq	CTCTTCCAACCTTCTTAGCAAG
F1_GCN4_seq	ATGTCCGAATATCAGCCAAGT
F2_GCN4_seq	GCAATTGAATCCACTGAAGAAG
R1_GCN4_seq	CCAGATTGGATGGTACCAGA
R2_GCN4_seq	GCGTTCGCCAACTAATTTCT
F1_PHA2_seq	CGTACTACATCATCTGCGACA
R1_PHA2_seq	GCAGCTGTTTCACTAGCAAT
F2_PHA2_seq	GCAGGTCACCTTTATAAGATTG
R2_PHA2_seq	GCCAGGTTTAAGCATATAAAAGTG

Table S3. Common known regulators of *ARO1*, *ARO2*, *ARO3*, and *ARO8* expression.

Regulator	Association Type (if known)	Description	Reference
ACE2	Negative	Transcription factor required for septum destruction after cytokinesis; phosphorylation by Cbk1p blocks nuclear exit during M/G1 transition, causing localization to daughter cell nuclei, and also increases Ace2p activity; phosphorylation by Cdc28p and Pho85p prevents nuclear import during cell cycle phases other than cytokinesis; part of RAM network that regulates cellular polarity and morphogenesis; ACE2 has a paralog, SWI5, that arose from the whole genome duplication	[1]
BAS1		Myb-related transcription factor; involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways; also involved in regulation of meiotic recombination at specific genes	[2]
GCN4	Positive	bZIP transcriptional activator of amino acid biosynthetic genes; activator responds to amino acid starvation; expression is tightly regulated at both the transcriptional and translational levels	[3] [4] [5]
LEU3	Negative	Zinc-knuckle transcription factor, repressor and activator; regulates genes involved in branched chain amino acid biosynthesis and ammonia assimilation; acts as a repressor in leucine-replete conditions and as an activator in the presence of alpha-isopropylmalate, an intermediate in leucine biosynthesis that accumulates during leucine starvation	[6] [2]
RAD3		5' to 3' DNA helicase; involved in nucleotide excision repair and transcription; subunit of RNA polII initiation factor TFIIH and of Nucleotide Excision Repair Factor 3 (NEF3); homolog of human XPD protein; mutant has aneuploidy tolerance; protein abundance increases in response to DNA replication stress	[2]
SOK2	Positive	Nuclear protein that negatively regulates pseudohyphal differentiation; plays a regulatory role in the cyclic AMP (cAMP)-dependent protein kinase (PKA) signal transduction pathway; relocalizes to the cytosol in response to hypoxia; SOK2 has a paralog, PHD1, that arose from the whole genome duplication	[7] [8]
SSL1		Subunit of the core form of RNA polymerase transcription factor TFIIH; has both protein kinase and DNA-dependent ATPase/helicase activities; essential for transcription and nucleotide excision repair; interacts with Tfb4p	[2]
SWI3		Subunit of the SWI/SNF chromatin remodeling complex; SWI/SNF regulates transcription by remodeling chromosomes; contains SANT domain that is required for SWI/SNF assembly; is essential for displacement of histone H2A-H2B dimers during ATP-dependent remodeling; required for transcription of many genes, including ADH1, ADH2, GAL1, HO, INO1 and SUC2; relocates to the cytosol under hypoxic conditions	[2]
TAF1		TFIID subunit, involved in RNA pol II transcription initiation; possesses in vitro histone acetyltransferase activity but its role in vivo appears to be minor; involved in promoter binding and G1/S progression; relocalizes to the cytosol in response to hypoxia	[2]
VPS72		Htz1p-binding component of the SWR1 complex; exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; may function as a lock that prevents removal of H2AZ from nucleosomes; required for vacuolar protein sorting	[2]
YRM1	Not applicable	Zinc finger transcription factor involved in multidrug resistance; Zn(2)-Cys(6) zinc finger transcription factor; activates genes involved in multidrug resistance; paralog of Yrr1p, acting on an overlapping set of target genes	[9]

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