

TABLE S1**Primers used in this study**

Primer	Sequence	Purpose
OD16	tgactgggattccgtgagacggac	Delete <i>C. glabrata</i> <i>PHO4</i> with <i>KANMX6</i>
OD17	ttaattaacccgggatccgacctgttcacccatcactaacag	
OD18	ctgttagtgatgggtgaacaggtcggatccccgggtaattaa	
OD19	gtttaaacgagctcgaattctacagatactccaagacaaaac	
OD20	gtttgtcttgagtatctgtagaattcgagctcgtttaaac	
OD21	atcttgtccctccaaacagaactg	
OD25	gctcgctctccattgcctattgtag	Delete <i>C. glabrata</i> <i>PHO2</i> with <i>KANMX6</i>
OD26	ttaattaacccgggatccgccatccatttaactacaaagtggc	
OD27	gccaaactttagttaaatggatggcggatccccgggtaattaa	
OD28	gtttaaacgagctcgaattcgctacgaatattcatgtacat	
OD29	atgtacatgaatattcgtagcgaattcgagctcgtttaaac	
OD30	tccatccaatcttatccgggtgc	
O1	gacagtcaaagtgtaaaggg	Delete <i>C. glabrata</i> <i>PHO31</i> with <i>KANMX6</i>
O2	ttaattaacccgggatccgcagatattaccaaactcat	
O3	atgaagttggtaaatatctcggatccccgggtaattaa	
O4	GTTTAAACGAGCTCGAATTCgacgataaaaacctgatgctt	
O5	aagcatcaggtttttatcgtcGAATTCGAGCTCGTTTTAAAC	
O6	taatctagatcttcaaacgtc	
O7	ctgcctggcttgggtggc	
O15	caccagacatccttagtgat	Delete <i>C. glabrata</i> <i>PHO30</i> with <i>NATMX6</i>
O16	ttaattaacccgggatccgctgagcatcttggggagtc	

O17	atgactccccaagatgctcagcggatccccgggtaattaa	
O18	GTTTAAACGAGCTCGAATTCagcatatccttcatctata	
O19	tatagatgaaggatatatctGAATTCGAGCTCGTTTAAAC	
O20	cggtgaaatacacacctctg	
O21	cggtcaaaaactgattccag	
O29	ggcacttaagttaatatattc	Delete <i>C. glabrata</i> <i>MSN5</i> with <i>NATMX6</i>
O30	ttaattaaccggggatccgactggccaactctccttta	
O31	taaaggagaagttggccagtcggatccccgggtaattaa	
O32	GTTTAAACGAGCTCGAATTCctgatagcggctggcttc	
O33	gaaccagccatcgctatcagGAATTCGAGCTCGTTTAAAC	
O34	acacgagcaccataaatcca	
O35	atgaatgctggggctaatcaag	
OD18	ctgttagtgatgggtgaacaggtcggatccccgggtaattaa	Delete <i>C. glabrata</i> <i>PHO4</i> with <i>NATMX6</i> in DG3
OD20	gtttgtcttgagtatctgtagaattcgagctcgtttaaac	
DWO1	CGATCGGCGGCCGCTGCATTATTTAGATCGGAAAAAGTC	Amplify <i>S. cerevisiae</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites
DWO2	CGACACTTAATTAACGTGCTCACGTTCTGCTGTAGGTG	for cloning into pRS313-13myc
DWO7	CGATCGGCGGCCGCGATGAGCTCTTTTCATCACTTCTCG	Amplify <i>S. cerevisiae</i> <i>PHO2</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites
DWO8	CGACACTTAATTAATATCCATCTATGCTCGTCAGTTAG	for cloning into pRS313-13myc
DWO5	CGATCGGCGGCCGCGTATGCATTACCTTCTCAATTAGG	Amplify <i>C. glabrata</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites
DWO6	CGACACTTAATTAATTTCTTGTACTGCTCAAGCTCTTCG	for cloning into pRS313-13myc
DWO11	CGATCGGCGGCCGCGCAGCAACCACCTTGGCGTCTGCGC	Amplify <i>C. glabrata</i> <i>PHO2</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites
DWO12	CGACACTTAATTAATATCCAACGGTTGTCTTCGTTTAC	for cloning into pRS313-13myc

O163	CGATCGGCGGCCGCtgcattatttagatcgaaaaagtc	Amplify <i>S. cerevisiae</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon
O164	CGACACTTAATTAAtcacgtgctcagttctgctgtaggtg	
O128	CGATCGGCGGCCGCtagtgaagccagtccttcacgcca	Amplify <i>S. mikatae</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon
O161	CGACACTTAATTAAtcacgtgctccattccgtttagatga	
O174	CGATCGGCGGCCGCaggtagaggaggaggcagag	Amplify <i>S. castellii</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon
O175	CGACACTTAATTAAggaatttgcttagattcctaactg	
O167	CGATCGGCGGCCGCgtatgcattaccttctcaattagg	Amplify <i>C. glabrata</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon
O168	CGACACTTAATTAAtcatttctgtactgctcaagctcttg	
O157	CGATCGGCGGCCGCcagccatgtactcatgatactg	Amplify <i>C. albicans</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon
O158	CGACACTTAATTAAAttacttctctcttcaactctcaac	
O155	TCCTACGAACTTCCAGATGGT	Quantify <i>S. cerevisiae</i> <i>ACT1</i> with quantitative reverse-transcription PCR
O156	GGCAGATTCCAAAACCCAAAA	
O153	GCCGGTTCCAAAACGTTTA	Quantify <i>S. cerevisiae</i> <i>PHO84</i> with quantitative reverse-transcription PCR
O154	GACAGTGAAGACGGATACCCA	
O151	TGCTTGTAACATCATGTCCTGC	Quantify <i>S. cerevisiae</i> <i>PHO5</i> with quantitative reverse-transcription PCR
O152	TTGAGGTCAAGTTCAAACCCT	
O75	gaccaaactacttacaactcc	Quantify <i>C. glabrata</i> <i>ACT1</i> with quantitative reverse-transcription PCR
O76	ccactttcgctgattcttgcttg	
O78	gccttgggtactctgatcgacc	Quantify <i>C. glabrata</i> <i>PHO84</i> with quantitative reverse-transcription PCR
O79a	gtgctgctcgcgacagtaac	
O81	ggttaacgccacaccagtaagagc	Quantify <i>C. glabrata</i> <i>GIT1</i> with quantitative reverse-transcription PCR
O82	gatagtgacaattcactctctc	
