Figure S1. Induction of genes during thiamine starvation of *C. glabrata* wild-type. *C. glabrata* wild-type was grown in thiamine replete and starvation conditions for four hours . qPCR was performed on reverse-transcribed RNA from these samples to determine the fold induction in thiamine starvation relative to replete. These data confirmed induction of the most highly induced genes during thiamine starvation as determined by the RNA-seq data in Figure 1. Fold induction for *CgPMU2* is 25.6±6.22 and for *CgTHI6* is 26.7±7.28. Error bars represent the standard deviation of the average of fold induction for three independently grown biological replicates. All seven genes are considered induced based on a Student's T test, P<0.01

| Species	GeneID	GeneName	Protein length
S. cerevisiae	YBR093C	PHO5	467
S. cerevisiae	YBR092C	PHO3	467
S. cerevisiae	YHR215W	PHO12	467
S. cerevisiae	YAR071W	PHO11	467
S. cerevisiae	YDL024C	DIA3	468
S. mikatae	2.235	NA	467
S. mikatae	2.234	NA	467
S. mikatae	2.233	NA	467
K. lactis	KLLA0C19338g	NA	469
K. lactis	KLLA0B00286g	NA	476
K. lactis	KLLA0A00176g	NA	476
K. lactis	KLLA0D00258g	NA	492
K. lactis	KLLA0E24949g	NA	492
S. pombe	SPBP4G3.02	pho1	453
S. pombe	SPBC428.03c	pho4	463
S. pombe	SPBC21H7.03c	N/A	463
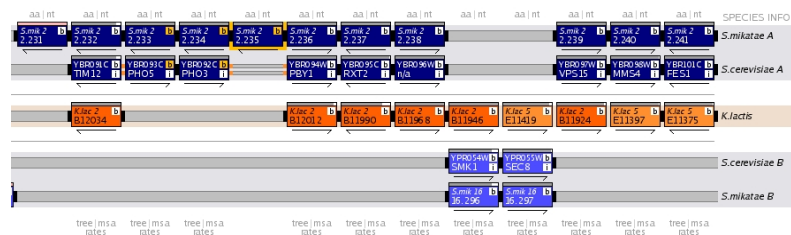
Figure S2. Syntenic relationship between *PHO5* homologs in *S. cerevisiae* and *S. mikatae*. Rows in the figure represent chromosomes and boxes represent genes. Genes are aligned in columns based on inferred syntenic relationship between species, where missing boxes indicate no syntenic homolog detected. *S. cerevisiae* and *S. mikatae* belong to a group of species whose common ancestor has experienced a whole-genome-duplication (WGD). Therefore, each species has two sets of chromosomes (A vs B) that correspond to a single set of ancestral chromosomes. *K. lactis*, as a pre-WGD species, represents the ancestral state. Other features in this figure are explained in detail on the Yeast Gene Order Browser help page (http://ygob.ucd.ie/), from which this screenshot was taken on Oct 7, 2017 (Byrne and Wolfe, 2006). This plot shows that the three *PHO5* homologs in *S. mikatae* form a single cluster, suggesting a possible origination through tandem duplication. The syntenic region in *S. cerevisiae* contains just two genes, *ScPHO5* and *ScPHO3*, which are also arranged in tandem. Note that *S. mikatae* likely experienced an additional duplication event as indicated by the yellow box around 2.235. The other three *PHO5* homologs in *S. cerevisiae* are on different chromosomes. We also looked at *K. lactis* and found that none of its five *PHO5* homologs are syntenic with those in *S. cerevisiae* or *S. mikatae*. The distantly related *S. pombe* is not included in YGOB.
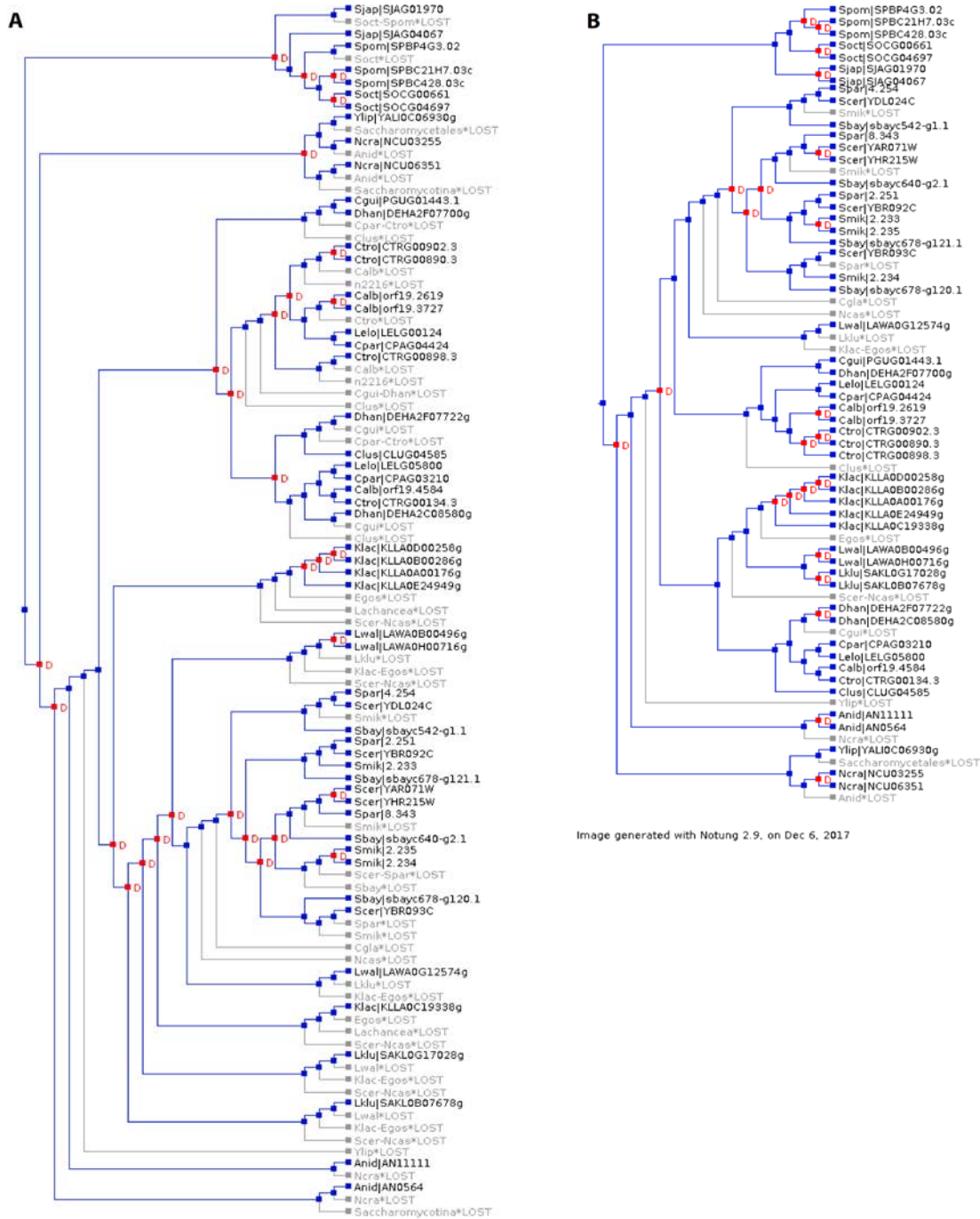
A

Image generated with Notung 2.9, on Dec 6, 2017

B

Image generated with Notung 2.9, on Dec 6, 2017

Source of sequences:
Scer|YBR093C
Scer|YDL024C
Scer|YBR092C
Scer|YHR215W
Scer|YAR071W
Smik|2.233
Smik|2.234
Smik|2.235
Spar|2.251
Spar|4.254
Spar|8.343

Figure S3. Reconciled gene tree for the *PHO5* family showing inferred duplication and loss events. (A) Reconciled tree without rearrangement. Inferred duplication events are marked with "D" in red font. Loss events are shown in gray. Species and gene names are labeled at the leaf nodes, separated by "|". (B) Reconciled and rearranged gene tree. During the rearrangement operation, Notung (v2.9) explores alternative topologies by swapping weakly supported branches with bootstrap values below 90/100 in the reconstructed gene tree. The result is a topology that minimizes the total event score (23/15 duplication/loss events compared to 29/48 before rearrangement).

Sbay|sbayc678-g120.1
Sbay|sbayc542-g1.1
Sbay|sbayc678-g121.1
Sbay|sbayc640-g2.1
Lwal|LAWA0G12574g
Lwal|LAWA0H00716g
Lwal|LAWA0B00496g
Klac|KLLA0C19338g
Klac|KLLA0B00286g
Klac|KLLA0A00176g
Klac|KLLA0D00258g
Klac|KLLA0E24949g
Lklu|SAKL0G17028g
Lklu|SAKL0B07678g
Clus|CLUG04585
Dhan|DEHA2C08580g
Dhan|DEHA2F07700g
Dhan|DEHA2F07722g
Cgui|PGUG01443.1
Ctro|CTRG00898.3
Ctro|CTRG00134.3
Ctro|CTRG00890.3
Ctro|CTRG00902.3
Calb|orf19.4584
Calb|orf19.3727
Calb|orf19.2619
Cpar|CPAG03210
Cpar|CPAG04424
Lelo|LELG00124
Lelo|LELG05800
Ylip|YALI0C06930g
Anid|AN11111
Anid|AN0564
Ncra|NCU03255
Ncra|NCU06351
Sjap|SJAG01970
Sjap|SJAG04067
Soct|SOCG04697
Soct|SOCG00661
Spom|SPBP4G3.02
Spom|SPBC21H7.03c
Spom|SPBC428.03c

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ATG ATC TTG CAT AGA TTG TTG TTG TTG TTG AAT TTG GAT TGG AAC CCA GAT AAC ACA GCT CAA GAT TTG GAT TTT AGA GCA TTG CCA GGT TAC TTC AAG G < 100
 M   I   L   H   R   L   L   L   L   L   N   L   D   W   N   P   D   N   T   A   Q   D   L   D   F   R   A   L   P   G   Y   F   K   G
         10          20          30          40          50          60          70          80          90

GT TAC ACA GTT CAA GAT ACT CCA GAT ACA AGA ATT AAT GCT ACT GAA TTG GAT TTC TTG GCA TTC GAT GAT AGA TTT TCA AAC TGG CAA CAA TTG TAC CA < 200
   Y   T   V   Q   D   T   P   D   T   R   I   N   A   T   E   L   D   F   L   A   F   D   D   R   F   S   N   W   Q   Q   L   Y   Q
           110         120         130         140         150         160         170         180         190

A GCT ATC CCA AAC GAT ACT GAA ACA CAT TCT TAC AAA TTA GTT ATT TTG GCA AGA CAT GGT CAA GGT TAT CAT AAT GCT GCT TAT GAT AGA TAC GGT GAA < 300
  A   I   P   N   D   T   E   T   H   S   Y   K   L   V   I   L   A   R   H   G   Q   G   Y   H   N   A   A   Y   D   R   Y   G   E
         210         220         230         240         250         260         270         280         290

AAA GCA TGG TAT GAT TAC TGG TCA AGA TTA GAA GGT GAC CAA TAC GGT AAT TGG TTT GAT GCA GAA TTA ACT CCA TTG GGT AAA AAG CAA GCA TTG GAA G < 400
 K   A   W   Y   D   Y   W   S   R   L   E   G   D   Q   Y   G   N   W   F   D   A   E   L   T   P   L   G   K   K   Q   A   L   E   A
         310         320         330         340         350         360         370         380         390

CA GGT CAA ACT TAT TTG ACA AAT TTG ACT GAT GGT TTG CAA AGA TTG CCT GAT AAG TTT TTC GTT TCT CCA TTA AGA AGA TGT TTG GAT ACA TGT ATC AG < 500
   G   Q   T   Y   L   T   N   L   T   D   G   L   Q   R   L   P   D   K   F   F   V   S   P   L   R   R   C   L   D   T   C   I   R
           410         420         430         440         450         460         470         480         490

A GAA TGG GAA CCA ATC TTC GCT AAG CAT AAG CCA GCA AAT TCA ACT GTT CAT GTT AAA GTT ATT GAA TAC TTA AGA GAA ACA TTG GGT ATC GAT ACT TCT < 600
  E   W   E   P   I   F   A   K   H   K   P   A   N   S   T   V   H   V   K   V   I   E   Y   L   R   E   T   L   G   I   D   T   S
         510         520         530         540         550         560         570         580         590

AAC GAA AGA GTT TCT CAT TCA CAA GCA TTG GCA GAA TAC CAA GAT CAT AGA TAC AAC ACA TCA GAT GTT ACT GTT CAT TTC GAT TAT CCT GGT GAC TAC T < 700
 N   E   R   V   S   H   S   Q   A   L   A   E   Y   Q   D   H   R   Y   N   T   S   D   V   T   V   H   F   D   Y   P   G   D   Y   S
         610         620         630         640         650         660         670         680         690

CT GAA AAA GAT CAA TTA TGG CAA CCA GAT CAT TTG GAA ACA AAA GCT GAA ATG GAT AGA AGA ACT AGA ATT GGT TTG AGA GAA ATG TTT TCT TCA GTT AA < 800
   E   K   D   Q   L   W   Q   P   D   H   L   E   T   K   A   E   M   D   R   R   T   R   I   G   L   R   E   M   F   S   S   V   N
           710         720         730         740         750         760         770         780         790

C ACT ACA GAT AAA GTT ATT TCT TTA ACA TGT CAT TCA GAT GTT ATT GAA TCT ATT TTG AGA AAC ATC AAG CAT CCA GCT ATC GAT CAT TTG CAA ACT GGT < 900
  T   T   D   K   V   I   S   L   T   C   H   S   D   V   I   E   S   I   L   R   N   I   K   H   P   A   I   D   H   L   Q   T   G
         810         820         830         840         850         860         870         880         890

AAA TTG GTT TAC ACT GTT GTT GAA TTG TCT AAG GCT CCA GCA GAT GAT CAA TCA ATG TTG GTT GTT TCT TAA
 K   L   V   Y   T   V   V   E   L   S   K   A   P   A   D   D   Q   S   M   L   V   V   S   *
         910         920         930         940         950         960         970
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Figure S4. Sequence of P*MU2/3* ancestor. *Cg*Pmu1-3 were aligned using a MUSCLE protein alignment. We identified every case where *Cg*Pmu2 and *Cg*Pmu3 had the same amino acid and it was different from *Cg*Pmu1. This identified 55 amino acids out of the 323 amino acids present in *Cg*Pmu1. We then ordered from GENEWIZ (South Plainfield, NJ) a synthetic sequence replacing codons in *CgPMU1* with a codon to put the *Cg*Pmu2/3 codon in its place.

Table S2. Stranis used in this study.

Strain number	Strain	Reference
	Yeast strains	
DG5	*C. glabrata* wild-type (*his3-*) (BG99)	Cormack and Falkow Genetics 1999
DG141	*Cgthi3::NATMX6* in DG5	Iosue et al PlosOne 2016
DG176	*C. glabrata* wild-type (*his3-ura3-*)	Iosue et al PlosOne 2016
DG2	*Cgpho4 ::KANMX6* in DG5	Kerwin and Wykoff Genetics 2009
DC3	*S. cerevisiae* wild-type K699 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3	Wykoff and O'Shea Genetics 2001
DP1	*Schizosaccharomyces pombe* wild-type 972 h-	From D. Moazed laboratory
DG29	*Cgpmu2::NATMX6* in DG5	Orkwis et al Genetics 2010
DG30	*Cgpmu3::NATMX6* in DG5	Orkwis et al Genetics 2010
DG314	*Cgpmu3::CgURA3* in DG176	This study
DG320	*CgURA3::ScPHO3* in DG314	This study
DG318	*CgURA3::ScPHO5* in DG314	This study
DG327	*CgURA3::S. mikataePHO5 g5* in DG314	This study
DG328	*CgURA3::S. mikataePHO5 g4* in DG314	This study
DG332	*CgURA3::CgPMU1* in DG314	This study
DG317	*CgURA3::CgPMU2* in DG314	This study
DG345	*CgURA3::* Ancestral *PMU2/3* in DG314	This study
DG319	*CgURA3::K. lactis KLLAO_C19338g* in DG314	This study
DG373	*CgURA3::K. lactis KLLAO_D00258g* in DG314	This study
DG326	*CgURA3:: S. kluyveriPHO5* in DG314	This study
DG331	*CgURA3::Y. lipolytica PHO5* in DG314	This study
DG329	*CgURA3::S. pombePHO1* in DG314	This study
DG330	*CgURA3::S. pombePHO4* in DG314	This study
DG338	*ScPHO5* p-*ScPHO* 3-*YFP* -pRS313 in DG29	This study
DG337	*ScPHO5* p-*ScPHO5* -*YFP* -pRS313 in DG29	This study
DG335	*ScPHO5* p-*S. mikatae PHO5 g5* -YFP-pRS313 in DG29	This study
DG336	*ScPHO5* p-*S. mikatae PHO5 g4* -YFP-pRS313 in DG29	This study
DG200	*ScPHO5* p-*CgPMU1* -*YFP* -pRS313 in DG29	Orkwis et al Genetics 2010
DG198	*ScPHO5* p-*CgPMU* 2-*YF* P-pRS313 in DG29	Orkwis et al Genetics 2010
DG199	*ScPHO5* p-*CgPMU3* -*YFP* -pRS313 in DG29	Orkwis et al Genetics 2010
DG343	*ScPHO5* p-Ancestral *PMU2/3* -*YFP* -pRS313 in DG29	This study
DG333	*ScPHO5* p-*K. lactis KLLAO_C19338g* -*YF* P-pRS313 in DG29	This study
DG367	*ScPHO5* p-*K. lactis KLLAO_D00258g* -*YFP* -pRS313 in DG29	This study
DG334	*ScPHO5* p-*S. Kluyveri PHO5* -*YFP* -pRS313 in DG29	This study
DG341	*ScPHO5* p-*Y. lipolytica PHO5* -*YFP* -pRS313 in DG29	This study
DG339	*ScPHO5* p-*S. pombe PHO1* -*YFP* -pRS313 in DG29	This study
DG340	*ScPHO5* p-*S. pombe PHO4* -*YFP* -pRS313 in DG29	This study
DG197	*ScPHO5* p-*YFP-* pRS313 in DG29	Orkwis et al Genetics 2010
	Bacterial strains	
DB346	3 Kb *CgPMU2* p-*YFP* -pRS313	Kerwin and Wykoff FEMS 2012
DB347	1 Kb *CgPMU3* p-*YFP* -pRS313	This study
DB146	*ScPHO5* p-*YFP* -pRS313	Orkwis et al Genetics 2010
DB147	*ScPHO5* p-*CgPMU2* -*YFP-* pRS313	Orkwis et al Genetics 2010
DB148	*ScPHO5* p-*CgPMU3* -*YFP* -pRS313	Orkwis et al Genetics 2010

Table S3. Primers used in this study.

Primers to Replace *CgPMU3* ORF with *CgURA3*				
DG314	*Cgpmu3::CgURA3* in DG176	O1858	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAcacaggaaacagctatgacc	
		O1859	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTgttgtaaaacgacggccagt	
		O1905	TTA CTC TTA CTA GGT ATC AAT AG	Check Primer (5')
		O1906	GGTCATAGCTGTTTCCTGTG	Check Primer (3')
Primers to Replace *CgURA3* in *Cgpmu3::CgURA3* with phosphatase ORFs				
	CgURA3::CgPMU2 in DG314	O1860	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgatccttcataaattgct	
		O1861	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTttaggatactacgatgaccg	
DG317		O1932	TTACTCAGAAAGGGACCAAC	Check Primer (5')
	CgURA3::ScPHO5 in DG314	O1862	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgtttaaatctgttgttta	
		O1863	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTctattgtctcaatagactgg	
DG318		O1933	CAACTTAACTGCCGAATAC	Check Primer (5')
	CgURA3::K. lactis KLLA0_C19338g in DG314	O1935a	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAATGAATTTATTATTACTCAC	
		O1936a	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTTTATTGTATTAGAAGTGATG	
DG319		O1937a	TAACTATCTCGCTACTGTAG	Check Primer (5')
	CgURA3::ScPHO3 in DG314	O1864	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgtttaagtctgttgttta	
		O1865	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTttattgtttttaataggggtat	
DG320		O1934	GTACGTTCCTCAAGGTGCTC	Check Primer (5')
	CgURA3:: S. kluyveriPHO5 in DG314	O1938	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAATGATTGGTTTACCATTTTT	
		O1939	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTTCAGTATGAAGCCAAGGTTA	
DG326		O1940	ATCGAAAACTACTTGGCGAC	Check Primer (5')
	CgURA3::S. mikataePHO5 g5 in DG314	O1941	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAATGTTCAAGTCTGTTGTTTA	
		O1942	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTCTATTGCTTTAGTAGAGTAC	
DG327		O1943	ACGTTCCATTCATGGGCAAC	Check Primer (5')
	CgURA3::S. mikataePHO5 g4 in DG314	O1944	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAATGTTCAATTCGATTCTTTA	
		O1945	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTCTATTGTCTCAGTAAACTG	
DG328		O1946	GGTTTGGTTGAGTTTCACCC	Check Primer (5')
	CgURA3::S. pombePHO1 in DG314	O1979	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgttcttgcaaaatttatt	
		O1980	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTttaataaggataaacagcag	
DG329		O1981	tcactgacaatactcctgag	Check Primer (5')
	CgURA3::S. pombePHO4 in DG314	O1982	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgaagttaagtggtatttc	
		O1983	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTctaagtctagtagtagacgg	
DG330		O1984	gatcgtaaggtattcttagc	Check Primer (5')
	CgURA3::Y. lipolytica PHO5 in DG314	O1985	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgagcaagtaccgaaaact	
		O1986	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTctacaactctccctcgcaca	
DG331		O1987	TAAGACCTTCCCTCTGGACC	Check Primer (5')
	CgURA3::CgPMU1 in DG314	O1988	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgatcctacatagactgct	
		O1989	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTtttatgacacaacaagcattg	
DG332		O1990	gtgcacacgtgtgatgaacg	Check Primer (5')
	CgURA3:: Ancestral PMU2/3 in DG314	O2019	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAatgATCTTGCATAGATTGTT	
		O2020	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTttaAGAAACAACCAACATTG	
DG345		O2042	CATTCAGATGTTATTGAATC	Check Primer (5')
	CgURA3::K. lactis KLLA0_D00258g in DG314	O2122	TGTCATCAGATATATCAAATATATATCCACTCTCGTTACAATGAAGCAGATCAAAAACGCAG	
		O2123	ATGTAGACGGTGATCCTATTTGATATAGATGATCGGAGTTTTACTTGTTACTAACGGGACCG	
DG373		O2124	TTCCTGTCCTATCGAGGAC	Check Primer (5')
	Primers to add homology for ntegration of phosphatase ORFs	O1947	CATATATCATCCTTAGCATTGTTCTTAGACTAAATGTTATTGTAGAAATCAAATACCCAACTGTCATCAGATATATCAAAT	
		O1948	TTTTATGCAGTGAACTTTTAGCGAATGGATGAACAAAGAAACATAGACCCGGCTACCAATGTAGACGGTGATCCTATTTG	
	Check for integration of phosphatase ORFs (3')	O1931	ATGAACAAAGAAACATAGACC	
Primers to insert phosphatase ORFs into *ScPHO5* p-*YFP*-pRS313 plasmid				
	ScPHO5 p-*K. lactis KLLA0_C19338g* -YF P-pRS313 in DG29	O2043	caaatagagcaagcaaattcgagattaccaATGAATTTATTATTACTCAC	
		O2044	accagtgaataattcttcacctttagacatTTATTGTATTAGAAGTGATG	
DG333		O1937a	TAACTATCTCGCTACTGTAG	Check Primer (5')
	ScPHO5 p-*S. Kluyveri PHO5* -YFP-pRS313 in DG29	O2045	caaatagagcaagcaaattcgagattaccaATGATTGGTTTACCATTTTT	
		O2046	accagtgaataattcttcacctttagacatTCAGTATGAAGCCAAGGTTA	
DG334		O1940	ATCGAAAACTACTTGGCGAC	Check Primer (5')
	ScPHO5 p-*S. mikatae PHO5 g5* -YFP-pRS313 in DG29	O2047	caaatagagcaagcaaattcgagattaccaATGTTCAAGTCTGTTGTTTA	
		O2048	accagtgaataattcttcacctttagacatCTATTGCTTTAGTAGAGTAC	
DG335		O1943	ACGTTCCATTCATGGGCAAC	Check Primer (5')
	ScPHO5 p-*S. mikatae PHO5 g4* -YFP-pRS313 in DG29	O2049	caaatagagcaagcaaattcgagattaccaATGTTCAATTCGATTCTTTA	
		O2050	accagtgaataattcttcacctttagacatCTATTGTCTCAGTAAACTG	
DG336		O1946	GGTTTGGTTGAGTTTCACCC	Check Primer (5')
	ScPHO5 p-*ScPHO5* -YFP-pRS313 in DG29	O2051	caaatagagcaagcaaattcgagattaccaATGtttaaatctgttgttta	
		O2052	accagtgaataattcttcacctttagacatctattgtctcaatagactgg	
DG337		O1933	CAACTTAACTGCCGAATAC	Check Primer (5')
	ScPHO5 p-*ScPHO3* -YFP-pRS313 in DG29	O2053	caaatagagcaagcaaattcgagattaccaatgtttaagtctgttgttta	
		O2054	accagtgaataattcttcacctttagacatttattgttttaatagggtat	
DG338		O1934	GTACGTTCCTCAAGGTGCTC	Check Primer (5')
	ScPHO5 p-*S. pombe PHO1* -YFP-pRS313 in DG29	O2055	caaatagagcaagcaaattcgagattaccaATGttcttgcaaaatttatt	
		O2056	accagtgaataattcttcacctttagacatttaataaggataaacagcag	
DG339		O1981	tcactgacaatactcctgag	Check Primer (5')
	ScPHO5 p-*S. pombe PHO4* -YFP-pRS313 in DG29	O2057	caaatagagcaagcaaattcgagattaccaATGaagttaagtggtatttc	
		O2058	accagtgaataattcttcacctttagacatctaagtctagtagtagacgg	
DG340		O1984	gatcgtaaggtattcttagc	Check Primer (5')
	ScPHO5 p-*Y. lipolytica PHO5* -YFP-pRS313 in DG29	O2059	caaatagagcaagcaaattcgagattaccaATGagcaagtaccgaaaact	
		O2060	accagtgaataattcttcacctttagacatctacaactctccctcgcaca	
DG341		O1987	TAAGACCTTCCCTCTGGACC	Check Primer (5')
	ScPHO5 p-Ancestral *PMU2/3* -YFP-pRS313 in DG29	O2066	caaatagagcaagcaaattcgagattaccaATGATCTTGCATAGATTGTT	
		O2067	accagtgaataattcttcacctttagacatTTAAGAAACAACCAACATTG	
DG343		O2042	CATTCAGATGTTATTGAATC	Check Primer (5')
	ScPHO5 p-*K. lactis KLLA0_D00258g* -YFP-pRS313 in DG29	O2128	caaatagagcaagcaaattcgagattaccaATGAAGCAGATCAAAAACGCAG	
		O2129	accagtgaataattcttcacctttagacatTTACTTGTTACTAACGGGACCG	
DG367		O2130	GGTTGCACCTCAGGTCCAGG	Check Primer (5')
	Check for integration of phosphatase ORFs (3')	O245	GGGACAACACCAGTGAATAATTCTTCACC	
Primers to put promoters in front of *YFP*				
	3 Kb *CgPMU2* p-*YFP*-pRS313	O318A	ggtggcggccgctctagaactagtggatcc**cacttctattactcctatcacttg**	
DB346		O321	accagtgaataattcttcacctttagacat**tgtaacgagagtggatattt**	
	1 Kb *CgPMU3* p-*YFP*-pRS313	O1479	ggtggcggccgctctagaactagtggatcc**gggcctgacgctgttacaac**	
DB347		O1478	accagtgaataattcttcacctttagacatt**gtaacgagagtggatatat**	
qPCR Primers				
	ScPHO5	O151	TGCTTGTAACTCATGTCCTGC	

	O152	TTGAGGTCAAGTTCAAACCCT
ScPHO3	O2068	GTAATGCGTGCCCAGGATGG
	O2069	ACGTACCAATTCATCTTCGG
ScACT1	O155	TCCTACGAACTTCCAGATGGT
	O156	GGCAGATTCCAAACCCAAAA
CgPMU1	O191	gtgcacacgtgtgatgaacgtg
	O192	cattggttgatcatctgtaggc
CgPMU2	O664	gtgatgttactgttcattttgattatcctg
	O641	gatacatcgatcacagtgtaaactag
CgPMU3	O195	ctctagcagaataccaggatc
	O196	ctacgagaattgattgatcatc
CgACT1	O75	gaccaaactacttacaactcc
	O76	ccactttcgtcgtattcttgcttg
SpPHO1	O69	gctaatagccttgcaaattccctc
	O70	ctagcattgcaaagagtgtcaaag
SpPHO4	O2070	ccagtcgaggctgctcttggg
	O2071	gacattgcgagttaaaattag
SpACT1	O66	ggtattcatgaggctacttacaac
	O67	ccgctctcatcatactcttgcttg
CgTHI4	O1119	ggacatgaacaatgccgaagc
	O1120	ctcagcgaagtgcttcaagat
CgTHI20	O1285	CTACATCAGGTTCTTCCCTA
	O1286	ATTCTGTCCAAAGGAACTTC
CgTHI10	O1287	CGTGGTTGGGTGGTCTATGT
	O1288	ATCCAGAGTTGTTGACCGTA
CgPET18	O1291	ACCCAGCTCTTATTTCTTAC
	O1292	TAGACTCACGTCCTATCTAC
CgTHI6	O1289	ACATCGGCGTTGGTACATTA
	O1290	TGTGGAATTGCAGCTAGATC