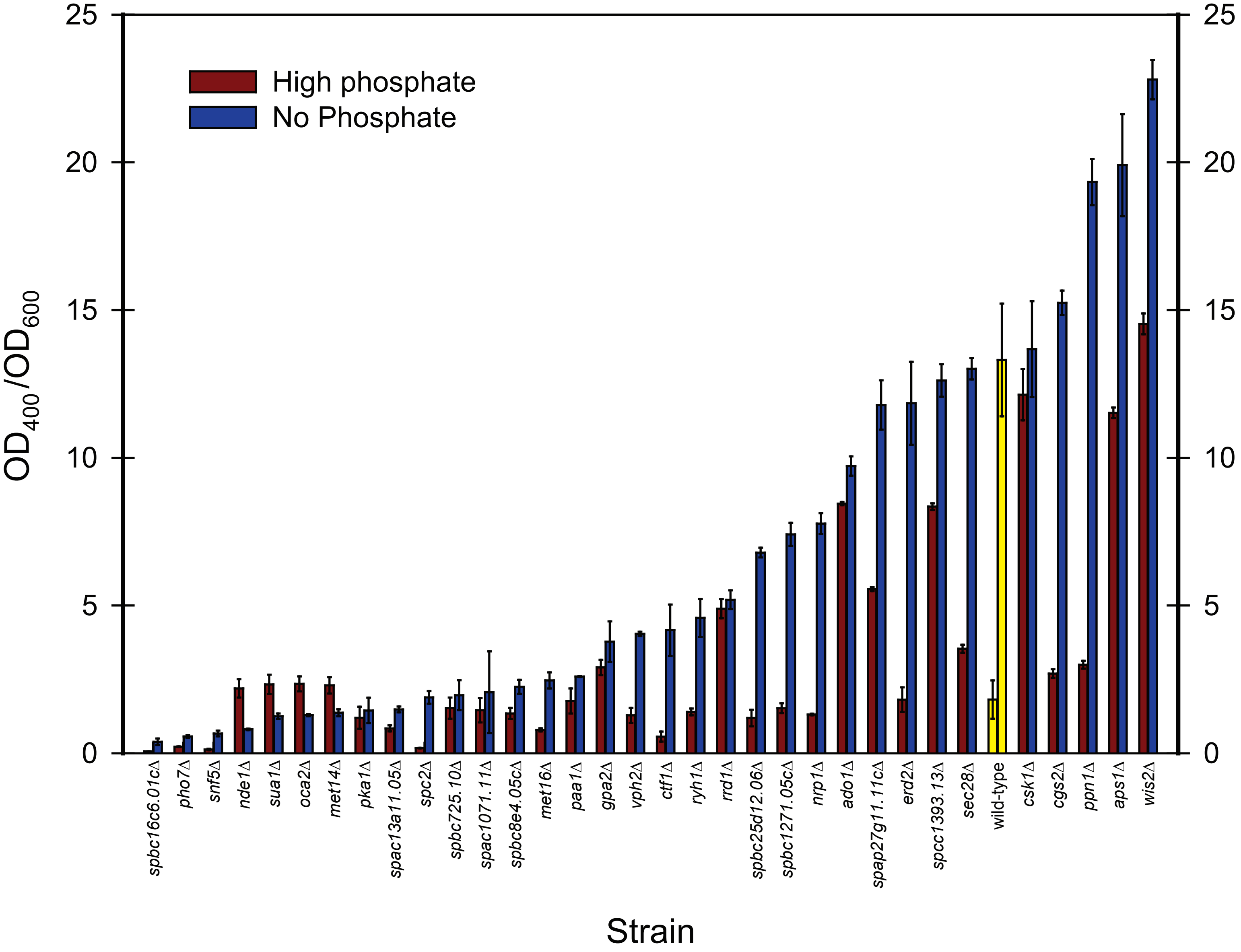
Figure S1



25
20
15
10
5
0
OD$_{400}$/OD$_{600}$
High phosphate
No Phosphate
spbc16c6.01cΔ
pho7Δ
snf5Δ
nde1Δ
sua1Δ
oca2Δ
met14Δ
pka1Δ
spac13a11.05Δ
spc2Δ
spbc725.10Δ
spac1071.11Δ
spbc8e4.05cΔ
met16Δ
paa1Δ
gpa2Δ
vph2Δ
ctf1Δ
ryh1Δ
rrd1Δ
spbc25d12.06Δ
spbc1271.05cΔ
nrp1Δ
ado1Δ
spap27g11.11cΔ
erd2Δ
spcc1393.13Δ
sec28Δ
wild-type
csk1Δ
cgs2Δ
ppn1Δ
aps1Δ
wis2Δ
Strain

Figure S1. Histogram of acid-phosphatase activity. Mutants' phosphatase activity was measured using PNPP as a substrate after 16 hours of growth in high- and no-phosphate conditions. The strains were ordered by their phosphatase activity during phosphate starvation from least to most activity. All tests were performed in triplicate and the error is SE. Wild-type (DP3) is shown in yellow.

TABLE S1. All mutants scored.

S. pombe Systematic Name	Product
	Uninducible screen
SPAC4G8.11c	F1-F0 ATPase assembly protein; similar to S. cerevisiae YLR393W
SPAC13A11.05	peptidase family M17; no apparent S. cerevisiae ortholog
SPBC106.10	cAMP-dependent protein kinase catalytic subunit Pka1 (PMID 8144551); non-essential (PMID 12618370); similar to S. cerevisiae YJL164C and YPL203W and YKL166C
SPBC530.01	GTPase activating protein (predicted); TBC domain protein; target Rab-like GTPase (predicted); similar to S. cerevisiae YOR070C
SPBC1711.14	meiotic recombination protein Rec15; no apparent orthologs
SPBC3B9.11c	mRNA cleavage and polyadenylation specificity factor complex subunit Ctf1; rrm RNA recognition motif; similar to S. cerevisiae YGL044C
SPBC1D7.04	RNA annealing factor Mlo3; similar to S. cerevisiae YDR381W; non-essential (PMID 15990877); rrm RNA recognition motif
SPAC3H8.09c	poly(A) binding protein; rrm RNA recognition motif; similar to S. cerevisiae YPL190C
SPAC17H9.04c	RNA-binding protein; zinc finger protein; zf- ranBP; rrm RNA recognition motif; similar to S. cerevisiae YDL167C
SPAC2F7.08c	chromatin remodeling complex subunit Snf5 (predicted); similar to S. cerevisiae YBR289W
SPAC1782.11	adenylyl-sulfate kinase (predicted); similar to S. cerevisiae YKL001C
SPAC1D4.01	sequence orphan
SPBC1271.14	glutamate N-acetyltransferase (predicted); non- essential (PMID 12618370); similar to S. cerevisiae YMR062C
SPAC1782.08c	exonuclease Rex3 (predicted); similar to S. cerevisiae YLR107W
SPAC16C9.07	serine/threonine protein kinase Ppk5 (predicted); non-essential (PMID 15821139); related to S. pombe pom1; DYRK family; no apparent orthologs
SPAC31G5.17c	40S ribosomal protein S10; similar to S. cerevisiae YOR293W and YMR230W
SPBC13E7.03c	post-transcriptional regulator Vts1 (predicted); RNA hairpin binding protein (predicted); SAM domain (sterile alpha motif); similar to S. cerevisiae YOR359W
SPAC3A11.07	NADH dehydrogenase; similar to S. cerevisiae YMR145C and YDL085W and YML120C
SPBC14C8.05c	glucan-alpha-1,4-glucosidase; glycosyl hydrolase family 15; expressed during sporulation; meiotic expression upregulated; predicted N-terminal signal sequence; similar to S. cerevisiae YIL099W
SPBC1604.20c	kinesin-like protein Tea2; kinesin family; KIP2 subfamily; similar to S. cerevisiae YPL155C
SPAC9.02c	N-acetyltransferase; GNAT family; arylalkylamine N-acetyltransferase (predicted); similar to S. cerevisiae YDR071C
SPAC1093.01	PPR domains; predicted N-terminal signal sequence; no apparent orthologs (cannot be distinguished)
SPBC1198.14c	fructose-1,6-bisphosphatase Fbp1 (PMID 2157626); similar to S. cerevisiae YLR377C
SPBC25H2.03	HEAT repeat; similar to S. cerevisiae YLR386W
SPBC27B12.11c	transcription factor (predicted); zinc finger protein; zf-fungal Zn(2)-Cys(6) binuclear cluster domain; no apparent orthologs (cannot be distinguished)
SPBC27.08c	sulfate adenylyltransferase (ATP) (PMID 14723223); similar to S. cerevisiae YJR010W
SPBC29A3.02c	phosphoribosyl-AMP cyclohydrolase/phosphoribosyl- ATP pyrophosphohydrolase HiS07; similar to S. cerevisiae YCL030C; similarity to YCL030C is at the N-term, S. pombe his2 is similar to YCL030C at the C-term

SPBC8E4.05c	3-carboxy-cis,cis-muconate cycloisomerase (predicted); no apparent S. cerevisiae ortholog
SPBC2D10.05	glucan 1,3-beta-glucosidase; glycosyl hydrolase family 5; similar to S. cerevisiae YBR056W
SPBP4G3.02	acid phosphatase Pho1 (PMID 4092931); predicted N-terminal signal sequence; GPI anchored protein (predicted) (PMID 12845604); glycoprotein (PMID 2381421); similar to S. cerevisiae YAR071W and YHR215W and YDL024C and YBR093C and YBR092C; localization cell
SPBC30D10.16	phrenate dehydratase (predicted); similar to S. cerevisiae YNL316C
SPCC1739.10	conserved fungal protein; similar to S. pombe SPAC13G7.04c (paralog); 3 predicted transmembrane helices; similar to S. cerevisiae YOL019W and YFR012W and YMR063W; predicted N-terminal signal sequence
SPAC17A5.16	conserved eukaryotic protein; no apparent S. cerevisiae ortholog
SPBC428.05c	argininosuccinate synthase (predicted); non- essential (PMID 12618370); similar to S. cerevisiae YOL058W
SPCC1672.04c	mitochondrial copper ion transport protein; CHCH domain; similar to S. cerevisiae YLL018C-A
SPBC24C6.05	coatomer epsilon subunit (predicted); TPR repeat protein (inferred from context); similar to S. cerevisiae YIL076W
SPCC1739.06c	uroporphyrin methyltransferase (predicted); similar to S. cerevisiae YKR069W
SPCC285.09c	cAMP-specific phosphodiesterase Cgs2; similar to S. cerevisiae YGL248W
SPAC1071.04c	signal peptidase subunit (predicted); 2 predicted transmembrane helices; similar to S. cerevisiae YML055W
SPAC4C5.02c	GTPase Ryh1; similar to S. cerevisiae YLR262C
SPCC16A11.15c	sequence orphan
SPAC13D6.02c	zinc finger protein; zf-CCHC type (zinc knuckle) (7); similar to S. cerevisiae YNL255C
SPAC13G6.10c	conserved fungal protein; serine-rich protein; glycoprotein (predicted); predicted N-terminal signal sequence; similar to N. crassa B24p11.210; no apparent S. cerevisiae ortholog
SPAPB1A10.03	Tap cofactor p15; NTF2 domain; non-essential (PMID 14963046); similar to S. cerevisiae YKL186C; ouble mutant rae1delta/nxt1delta lethal (PMID 14963046)
SPBC725.10	similar to peripheral-type benzodiazepine receptor; 3 predicted transmembrane helices; no apparent S. cerevisiae ortholog; non-essential (PMID 12618370)
SPBC36.04	cysteine synthase (PMID 14981292); similar to S. cerevisiae YGR012W
SPCC1020.10	serine/threonine protein kinase Oca2 (predicted); similar to S. cerevisiae YNL183C and YOR267C and YDL025C and YDL214C; non-essential (PMID 15821139)
SPAC227.01c	EXS family protein; similar to S. cerevisiae YDR414C; 4 predicted transmembrane helices
SPBC660.11	single-stranded telomeric binding protein Tgc1 (PMID 12519786); rrm RNA recognition motif; functionally complements S. cerevisiae cdc13-1 (PMID 12519786); similar to N. crassa NCU07734.1; no apparent S. cerevisiae ortholog (cannot be distinguished)
SPCC757.10	endoplasmic reticulum membrane involved in assembly of the V-ATPase; similar to S. cerevisiae YKL119C
SPBC106.17c	homoserine O-acetyltransferase (predicted); abhydrolase family; non-essential (PMID 12618370); deletion could not be obtained (PMID 12618370); similar to S. cerevisiae YNL277W
SPAC23E2.01	iron-sensing transcription factor Fep1; zinc finger protein; zf-GATA type; expression constitutive irrespective of the nitrogen source (PMID 8799335); no apparent S. cerevisiae ortholog (cannot be distinguished)
SPAC19A8.11c	sequence orphan
SPBC30D10.13c	pyruvate dehydrogenase e1 component (beta subunit); similar to S. cerevisiae YBR221C
SPCC736.07c	sequence orphan
SPAC4D7.06c	siroheme synthase (predicted); similar to S. cerevisiae YBR213W
SPBC428.02c	branched chain amino acid aminotransferase Eca49; non-essential (PMID 12618370); similar to S. cerevisiae YHR208W and YJR148W

SPBP8B7.22	HDEL receptor; similar to S. cerevisiae YBL040C; 6 predicted transmembrane helices; predicted N-terminal signal sequence
SPAC25B8.05	pseudouridylate synthase (predicted); similar to S. cerevisiae YFL001W
SPAC22G7.07c	mRNA (N6-adenosine)-methyltransferase (predicted); conserved eukaryotic protein; similar to S. cerevisiae YGL192W
SPCC1281.04	pyridoxal reductase (predicted); aldo/keto reductase family 8; similar to S. pombe SPAC9E9.11; similar to S. cerevisiae YPR127W
SPAC13G7.06	phosphoadenosine phosphosulfate reductase; similar to S. cerevisiae YPR167C
SPBC16C6.01c	lysine methyltransferase (predicted); SET domain; no apparent S. cerevisiae ortholog
SPAC20H4.07	RecA family ATPase Rhp57; RecA family; AAA family ATPase; helix-hairpin-helix (inferred from context); involved in the stimulation of Rad51 (Rhp51) mediated strand exchange; similar to S. cerevisiae YDR004W
SPBC25D12.06	RNA helicase (predicted); similar to A. thaliana RH22; no apparent S. cerevisiae ortholog
SPAC1071.11	NADH-dependent oxidoreductase (predicted); no apparent S. cerevisiae ortholog
SPAC17H9.13c	glutamate 5-kinase (predicted); PUA domain; similar to S. cerevisiae YDR300C and YHR033W
SPAC30.02c	elongator associated protein (predicted); similar to S. cerevisiae YKL110C
SPAC29B12.08	sequence orphan; serine/proline-rich protein
SPAC23H3.13c	heterotrimeric G protein alpha-2 subunit Gpa2 (PMID 1340462); similar to S. cerevisiae YER020W
SPAC959.07	40S ribosomal protein S04; similar to S. cerevisiae YJR145C and YHR203C
SPCC1259.01c	40S ribosomal protein S18; similar to S. cerevisiae YDR450W and YML026C
SPAC1F7.13c	60S ribosomal protein L2A; similar to S. cerevisiae YFR031C-A and YIL018W
SPAC29B12.04	pyridoxine biosynthesis protein; similar to S. cerevisiae YMR096W and YFL059W and YNL333W
SPCC24B10.06	glycoprotein (predicted); possibly S. pombe specific; GPI anchored protein (predicted) (PMID 12845604) (pers. comm. Birgit Eisenhaber); predicted N-terminal signal sequence
SPCC24B10.21	triosephosphate isomerase; similar to S. cerevisiae YDR050C
SPAPB1E7.02c	DNA polymerase alpha accessory factor Mcl1; WD repeat protein; essential (PMID 15643072); non-essential (PMID 15915339); similar to S. cerevisiae YPR135W
SPCC285.10c	hypothetical protein; similar to S. cerevisiae YMR171C and YKL124W; SPRY domain; predicted N-terminal signal sequence
SPAC22F3.10c	glutamate--cysteine ligase Gcs1 (PMID 8619315); similar to S. cerevisiae YJL101C

Constitutive screen	
SPAC1D4.06c	cyclin-dependent kinase activating kinase Csk1 (PMID 9857180); similar to S. cerevisiae YKL139W; non- essential (PMID 8467814)
SPAC513.03	M-factor precursor (PMID 8196631); pheromone; no apparent orthologs
SPBC13G1.08c	Ash2-trithorax family protein; SPRY domain; zinc finger protein; zf-PHD finger; non-essential (PMID 12488447); similar to S. cerevisiae YLR015W
SPBC119.06	copper chaperone Sco1; similar to S. cerevisiae YBR037C and YBR024W
SPAC3G9.15c	conserved eukaryotic protein; similar to S. cerevisiae YLR051C
SPBC354.09c	protease (predicted); peptidase family M28; similar to transferrin receptor protein; PA (protease associated) domain; similar to S. cerevisiae YJR126C and YPL176C and YOR256C; non-essential (PMID 12618370)
SPAC8E11.07c	tubulin specific chaperone (cofactor A) (PMID 10978278); non-essential (PMID 10978278); similar to S. cerevisiae YOR265W
SPAP27G11.11c	dubious; unusual amino acid sequence; below 100 amino acid size threshold

SPCC1393.13	conserved eukaryotic protein; DUF89; similar to S. cerevisiae YMR027W; similar to S. pombe SPAC806.04C (paralog)
SPBC713.07c	vacuolar polyphosphatase (predicted); similar to S. cerevisiae YDR452W; predicted N-terminal signal sequence
SPBC36.07	RNA polymerase II (elongator subunit) (predicted); disease assocaited, familial dysautonomia; similar to S. cerevisiae YLR384C
SPBC17A3.10	zinc finger protein; pex2/pex 12 family; zf- C3HC4 type (RING finger); ubiquitin-protein ligase (E3) (predicted); similar to S. cerevisiae YDR265W
SPAC13G6.14	diadenosine 5',5'''-p1,p6-hexaphosphate hydrolase Aps1 (PMID 10090752); dual function MutT hydrolase; non-essential (PMID 12387729); deletion mutant results in decreased in vitro Ap6A hydrolase activity (PMID 12387729); degrades PP-InsP5 (PMID 12387729);
SPCC1450.07c	D-amino acid oxidase (predicted); no apparent S. cerevisiae ortholog
SPAC4F10.04	protein phosphatase type 2A, intrinsic regulator (predicted); similar to S. cerevisiae YIL153W
SPAC637.07	translation initiation factor eIF3d Moe1; no apparent S. cerevisiae ortholog
SPAC16E8.05c	sequence orphan; transcriptionally regulated by Mei4
SPAC19G12.15c	trehalose-6-phosphate phosphatase Tpp1; glycosyl transferase family 20; similar to S. pombe SPAC3G6.09C; similar to S. cerevisiae YDR074W
SPAC1B3.03c	cyclophilin; TPR repeat protein (inferred from context); induced by heat shock; peptidyl-prolyl cis-trans isomerase; similar to S. cerevisiae YLR216C and YJR032W
SPCC338.14	adenosine kinase (predicted); similar to S. cerevisiae YJR105W
SPAC24H6.06	pre-initiation complex subunit Sld3 (PMID 12006645); interacts physically with MCM proteins (PMID 12006645); similar to S. cerevisiae YGL113W
SPAC22F8.12c	sequence orphan; serine-rich protein; predicted N-terminal signal sequence
SPAC21E11.06	translation initiation factor eIF2B delta subunit; similar to S. cerevisiae YGR083C

TABLE S2. Mutants identified in both screens

S. pombe Systematic Name	*S. pombe* Standard Name	*S. cerevisiae* ortholog(s)	*S. cerevisiae* Standard Name	Product	Is the gene inactivated with KAN?	Is the phenotype linked to KAN knockout?
			Uninducible			
spbc16c6.01c		none apparent		lysine methyltransferase *	no	yes
spbc27b12.11c	Pho7	none apparent		zinc finger domain - transcription factor *	yes	yes
spac2f7.08c	Snf5	YBR289W	Snf5	SWI/SNF complex subunit Snf5	yes	yes
spac3a11.07		YMR145C, YDL085W, YML120C	Nde1	NADH dehydrogenase	yes	not determined
spbc27.08c	Sua1	YJR010W	Met3	sulfate adenylyltransferase	no	yes
spcc1020.10	Oca2	YNL183C, YOR267C, YDL025C, YDL214C	Npr1	serine/threonine protein kinase Oca2 *	yes	no
spac1782.11	Met14	YKL001C	Met14	adenylyl-sulfate kinase *	no	yes
spbc106.10	Pka1	YJL164C, YPL203W, YKL166C	Tpk1	cAMP-dependent protein kinase catalytic subunit Pka1	yes	yes
spac13a11.05		none apparent		peptidase family M17	no	yes
spac1071.04c	Spc2	YML055W	Spc2	signal peptidase subunit Spc2 *	yes	yes
spbc725.10		none apparent		tspO homolog/ peripheral benzodiazepine receptor homolog, involved in the transport cytoplas/mitochondrial of haem *	yes	not determined
spac1071.11		none apparent		NADH-dependent flavin oxidoreductase *	yes	no
spbc8e4.05c		none apparent		fumarate lyase superfamily	yes	no
spac13g7.06	Met16	YPR167C	Met16	phosphoadenosine phosphosulfate reductase	yes	yes
spac9.02c		YDR071C	Paa1	polyamine N-acetyltransferase *	yes	no
spac23h3.13c	Gpa2	YER020W	Gpa2	heterotrimeric G protein alpha-2 subunit Gpa2	yes	yes
spcc757.10	Vph2	YKL119C	Vph2	endoplasmic reticulum membrane protein involved in assembly of the V-ATPase *	yes	yes
spbc3B9.11c	Ctf1	YGL044C	Rna15	mRNA cleavage and polyadenylation	yes	yes

				specificity factor complex subunit Ctf1		
spac4c5.02c	Ryh1	YLR262C	Ypt6	GTPase Ryh1	yes	yes
spac4f10.04		YIL153W	Rrd1	protein phosphatase type 2A, intrinsic regulator *	yes	yes
spbc25d12.06		none apparent		RNA helicase *		no
spbc1271.05c		YOR052C		zf-AN1 type zinc finger protein	yes	not determined
spac17h9.04c		YDL167C	Nrp1	RNA-binding protein	yes	yes
				Constitutive		
spcc338.14		YJR105W	Ado1	adenosine kinase *	yes	yes
spap27g11.11c		none apparent		dubious; unusual amino acid sequence- below 100 amino acid size threshold	yes	no
spbp8b7.22	Erd2	YBL040C	Erd2	HDEL receptor	no	yes
spcc1393.13		YMR027W		DUF89 family protein	yes	yes
spbc24c6.05	Sec28	YIL076W	Sec28	coatomer epsilon subunit *	yes	yes
spac1d4.06c	Csk1	YKL139W	Ctk1	cyclin-dependent kinase activating kinase Csk1	yes	yes
spcc285.09c	Cgs2	YGL248W	Pde1	cAMP-specific phosphodiesterase Cgs2	yes	not determined
spbc713.07c		YDR452W	Ppn1	vacuolar polyphosphatase *	yes	yes
spac13g6.14	Aps1	YOR163W	Ddp1	diadenosine 5',5'''-p1,p6-hexaphosphate hydrolase Aps1	yes	yes
spac1b3.03c	Wis2	YLR216C, YJR032W	Cpr6	cyclophilin family peptidyl-prolyl cis-trans isomerase Wis2	yes	no

* = predicted

TABLE S3. Primers used in this study.

Primer	Sequence	Purpose
		Delete *pho1*$^+$ (DP55)
DWO21	ctgcttctttggttacaaccCACAGGAAACAGCTATGACC GGTCATAGCTGTTTCCTGTGggttgtaaccaaagaagcag	
DWO22	gcatttacaagtcgtacgcgtatg	
DWO23	ggataaacagcagccacagcGTTGTAAAACGACGGCCAGT ACTGGCCGTCGTTTTACAACgctgtggctgctgtttatcc	
DWO24	gtgcacgtataggtttgtac	
		Delete *snf5*$^+$ (DP82)
O400	ctttactttttttttaaatct**CGGATCCCCGGGTTAATTAA**	core 5'
O401	gataaagattcttccaaaattgta**GAATTCGAGCTCGTTTAAAC**	core 3'
O402	cttcacgtcctatgaacctac	5'end homology 5'
O403	TTAATTAACCCGGGGATCCGagatttaaaaaaaaagtaaag	5'end homology 3'
O404	GTTTAAACGAGCTCGAATTCtacaattttggaagaatctttatc	3'end homology 5'
O405	gcaaagatgaatttaacgag	3'end homology 3'
O406	gttatttacaaaacttcccgctc	Chk primer 500 bp
		Delete *pho7*$^+$ (DP81)
O393	CATATTTCTTTTGTCTTTTTCGTTTGT**CGGATCCCCGGGTTAATTAA**	core 5'
O394	gaaaaacaaaggtaatatgcgcaaaa**GAATTCGAGCTCGTTTAAAC**	core 3'
O395	gtaccaagttgttgatcataaagg	5'end homology 5'
O396	ttaattaacccggggatccgacaaacgaaaaagacaaaagaaatatg	5'end homology 3'
O397	GTTTAAACGAGCTCGAATTCttttgcgcatattacctttgtttttc	3'end homology 5'
O398	catctgtacgatcacatttatcc	3'end homology 3'
O399	cgacttcgccctaacacgat	Chk primer 500 bp
		Delete *asp1*$^+$ (DP102)
O831	AAGCGTTATTAAATATTTTAACGTAGTTGAATAATAAAGG**CGGATCCCCGGGTTAATTAA**	core 5'
O832	GTTATCAAAACATTCGTAAAAAGGGTAAAAGCGGTTAATT**GAATTCGAGCTCGTTTAAAC**	core 3'
O833	GCTTTTACCCTTTTTACGAATG	3' homology 5'
O834	GAATCATTTTGGCGCCAAGCACC	3' homology 3'
O835	CATAGAAGCATTACTGCGAAAC	check primer
O780	TTAATTAACCCGGGGATCCG	Pringle Chk

		Confirming deletion of genes / qPCR primers
O444	G AAT ATG GAA ACA ATG CAC C	*pho7*$^+$ (ZnFinger)
O445	GAATCGGCTTGGTTTTGATGGAAG	
O448	GAGTTTTGACTCACTAAACG	*snf5*$^+$
O449	CTCATTAATGCAATCATGACAAC	
O450	GCTGCTAAGCCAGGAGATG	SPAC13A11.05
O451	CCGCTGTACAACAACCAC	
O452	GTCTTCCAGCTATATGCTG	SPBC25D12.06
O453	CTTAACCAGTACTCCATCAG	
O505	GGT GAT AAG TCC GAG ACT GCC	SPAC1B3_03c
O506	GTTACCAGCCTTAGCAAGTGC	
O507	GGT TTA GTA GTC GAT GAA TAC	SPAC3A11_07
O508	GTTACGCAAGGAGTATAATTC	
O509a	GGCTGATGAATCTGTTCAGCA	SPAC13G6_14
510a	GCTTCCTCATCTCTGGGTAAT	
O511	GCT CAG AAG TTT GGT GAG AAG	SPAC13G7_06
O512	CCAACGTCCGGCACGTTCATC	
O513	GGT TGT GGA TAT CAC AAT TTC	SPAC17H9_04c
O514	CATATTAGAGTAATGCGGAGC	
O515	GGC CTC GCA TTT GGC ATT GAG	SPAC1071_04c
O516	GTACTTTGAAATTTCCGCCTC	
O517	CGA GTA ATC GTT CAT CTT CTG	SPAC1071_11
O518	GGATGTGCTGCAGTAGTTCCG	
O519	CCT ATT TCA TGC GTT TAC ATC	SPBC8E4_05c
O520	GTAATTTGTAACTTGGCGCTC	
O521	CCA ACT ACA TAC GCA AAT GAC	SPBC16C6_01c
O522	GACTAAACGAGACCTATTCTC	
O523	GCT CAG GAA ATC GGT ATC ACC	SPBC27_08c
O524	GTTTACGGTAGTCCACTCAGC	
O525	GAT TAT TTA GCC CCG GAA ATC	SPBC106_10
O526	CGTAGCTACATCAGCATAAGC	
O527	CAG TCT CAA TCA GAT TAT GAG	SPBC713_07c
O528	GCCACTCTGTAATTTGAATTG	
O529	GCT TCT CTC GTT CCA GTC GCC	SPBC725_10
O530	GGAAGCCGTTGGTGCAAGAGG	
O531	GCT GAT TAT GGC ATT ATC CAC	SPBC1271_05c
O532	GCAATCATGATCTTCCATAAG	
O533	CCC TAT ATC ATG AAT CTT AGC	SPCC338_14
O534	GCCGCTAACCTTGATGCATTC	
O535	GAT CCT CGT GCA GTG GAT ATC	SPCC1020_10
O536	CATATGGCACATCGAAATATC	
O537	ACT TTC GAC TTT CCC AGA TTG	SPAC1D4_06c-intronsx2

O538	GCAGATACTTTAGGGAATGAC	
O539a	G CAA GTG ACT CAA GAA GAA GG	SPAC4C5_02c-intronsx3
O540a	GCTTTCATTCTCGTTAGGCTG	
O541	GAC TTT GGT ACG GGT CAT GAG	SPAC4F10_04-intron
O542	GACCTTTGACCATATAGGAAC	
O543	CTT GAC TTC TAG AAC AGG TAG	SPAC9_02c-intron
O544	CAAGTTTCATCCCCAAACTTG	
O545	GAT CAT TTG CAA ATT CGA ATG	SPAC23H3_13c-intron
O546	CCGATTTATAGAAGGGTTCAC	
O547	GCG TCT GGA AAG TCT ACA ATC	SPAC1782_11-intron
O548	CTTGTACAAACCCTTTGGATC	
O549a	GTT TAA AAT TGA TTC ATA TTC	SPAP27G11_11c-intron
O550a	GGTTGATTTAATCCAATATTG	
O551	CCG ACT TCT ATC CCA TTG GCC	SPBC3B9_11c-intronsx2
O552	CCGCTTCCCTTCATTGCCCTG	
O553	CTG CTG AAC AGA CAT TGA AAC	SPBC24C6_05-intron
O554	GATCGTTCAACTTCAGTGTAG	
O555	GTC TTG ATA CTT TTC GAA CTG	SPBP8B7_22-intronsx2
O556	CTGTTCGGCGATATACGACTG	
O557	CGT CGA ACC CGA TAT GGT AGC	SPCC285_09c-intronsx2
O558	GAACTTTTGGAAGACAACGAC	
O559a	CTA TGT GCG TTT TCA GCA ATC	SPCC757_10-intron
O560a	CTTCAAAGATGGAATGGCTCC	
O561	CGA AGG ATG TAC CCT GGT TTG	SPCC1393_13-intron
O562	CAACGACGGCGTATTTACCAG	
		qPCR
O66	ggtattcatgaggctacttacaac	qPCR on *act1*$^+$ 5'
O67	ccgctctcatcatactcttgcttg	qPCR on *act1*$^+$ 3'
O69	gctaatagccttgcaaattccctc	qPCR on *pho1*$^+$ 5'
O70	ctagcattgcaaagagtgtcaaag	qPCR on *pho1*$^+$ 3'
O72	gatttgcttgttttgttattgcc	qPCR on *pho84*$^+$ 5'
O73	ccacttgctatcacattgaactttg	qPCR on *pho84*$^+$ 3'
O848	CCTTGGACACTGATATTGGCG	qPCR on *fbp1*$^+$ 5'
O849	TGAAATTAATATATTCCTCG	qPCR on *fbp1*$^+$ 3'
O850	GAGTATGATGACGCTTGCTATTC	qPCR on *isp6*$^+$ 5'
O851	CAGGAATAGACAAGAGTACATC	qPCR on *isp6*$^+$ 3'
O503	GACATGGAGGCCCAGAATAC	For amplifying the NAT cassette to switch KAN to NAT in delete strains
O504	TGGATGGCGGCGTTAGTATC	

		Mating type check
MT1	AGAAGAGAGAGTAGTTGAAG	Mtype for *Sz. pombe*
MP	ACGGTAGTCATCGGTCTTCC	
MM	TACGTTCAGTAGACGTAGTG	
		pUR18-YFP complementation plasmids
O495	catgcctgcaggtcgactctagaggatCCCCGGGTTAATTAAC**atgtctaaaggtgaagaatta**	PCR YFP (5') to put into pUR18
O496	**cacaggaaacagctatgaccatgattacgaattcgagctcggta**tatattaccctgttatccc	PCR YFP (3') to put into pUR18
O500	gccaagcttgcatgcctgcaggtcgactctagaggatCCCCGGGCCGTATACGATACTTTTAAC	PCR *pho7*$^+$ (5') with no stop for YFP tag in pUR18
O502	taattcttcacctttagacatTTGTCTAAAGGGATGATTC	PCR *pho7*$^+$ (3') with no stop for YFP tag in pUR18
O736	gccaagcttgcatgcctgcaggtcgactctagaggatATGGATAAGGATATAGGCTCTGC	PCR *snf5*$^+$ into pUR19YFP plasmid
O737	taattcttcacctttagacatAGTATTTCTATCCAAAACC	