

Supplementary Table S1: Genes induced at least 1.5-fold in 3 of 4 samples tested when lowering *rpb4* expression levels.

Primer name	Common name	Systematic name	Annotation
C167.06c		SPAC167.06c;SPAC57A7.02c	Protein of unknown function
C11C11.06c		SPBC11C11.06c	Protein of unknown function
C23C4.16c	atg15	SPAC23C4.16c	Protein of unknown function, similar to a region of <i>S. cerevisiae</i> Atg15p
phz1	phz1;pzh1	SPAC57A7.08	Serine-threonine protein phosphatase
C56F2.06		SPBC56F2.06	Protein of unknown function
P8B7.24c	atg8	SPBP8B7.24c	Similar to <i>S. cerevisiae</i> Atg8p
C16E8.16		SPAC16E8.16	Protein required for RNA polymerase II-mediated transcription
ssm4	ssm4	SPAC27D7.13c;SPAC637.01c	Microtubule-associated coiled-coil protein with a role in meiosis
C365.12c	ish1	SPBC365.12c	Member of the late embryogenesis abundant (LEA) group 4 family
C21C3.19		SPBC21C3.19	Protein of unknown function
C16E9.16c		SPBC16E9.16c	
isp6	isp6;prb1	SPAC4A8.04	Putative subtilase-type proteinase involved in sexual differentiation
C1B3.06c		SPAC1B3.06c	Protein of unknown function, has moderate similarity to uncharacterized <i>C. albicans</i> Spx2p
CUNK4.15		SPACUNK4.15	Protein of unknown function
ada1	ada1	SPBC106.04	AMP deaminase, hydrolyzes AMP to IMP and ammonia
b8647-5		SPCC10D6.07c;SPCC737.04	Protein of unknown function
C27D7.11c		SPAC27D7.11c	Protein of unknown function, has high similarity to uncharacterized <i>S. pombe</i> Spac27d7.10cp
C19C7.04c		SPBC19C7.04c	Protein of unknown function
C11C11.05		SPBC11C11.05	Member of the yeast cell wall synthesis protein KRE9 or KNH1 family
C191.01		SPCC191.01;SPCC417.13	Protein of unknown function
rad25	rad25	SPAC17A2.13c	14-3-3- protein involved in G2/M phase transition and DNA damage checkpoint control
C23D3.07		SPAC23D3.07	Similar to proteasome subunit beta2_sc (<i>S. cerevisiae</i> Pup1p)
hsp9	hsp9;scf1	SPAP8A3.04c	Heat shock-induced protein
tps1	ggs1;tps1	SPAC328.03	Trehalose-6-phosphate synthase
C577.10		SPBC577.10	Similar to proteasome subunit beta7_sc (<i>S. cerevisiae</i> Pre4p)
pcr1: mts2	pcr1;mts2	SPAC21E11.03c	Transcription factor that plays roles in mating, meiosis and stress response
hsp16	hsp16	SPBC3E7.02c	Heat shock protein that may be regulated by Ras1p
gpx1	gpx1	SPBC32F12.03c	Glutathione peroxidase, may play a role in adaptation to oxidative stress
C17H9.11		SPAC17H9.11	Protein with moderate similarity to glia maturation factor-beta (human GMFB)
C338.12		SPCC338.12	Member of the subtilisin N-terminal region containing family
PB8E5.04c		SPAPB8E5.04c	Protein containing an ML domain

C25H1.01c		SPAC23H3.15c;SPAC25H1.01c	Protein of unknown function
P35G2.02		SPBP35G2.02	Member of the DUF1000 domain of unknown function family
C19G12.09		SPAC19G12.09	Protein containing an aldo-keto reductase family domain
P31B10.06		SPCP31B10.06	Protein containing two C2 domains, which may be involved in calcium-dependent phospholipid binding
cta1	cta1;ctl1	SPCC757.07c	Catalase, involved in oxidative stress resistance
misc_RNA_1.1.38.RC		SPNCRNA.103	
C4H3.03c		SPAC4H3.03c	Member of the glycosyl hydrolase 15 family
C3A11.10c		SPAC3A11.10c	Member of the membrane dipeptidase (peptidase family M19) family
C24H6.08		SPAC24H6.08	Protein of unknown function
rRNA_2.2.16			
ntp1	ntp1	SPBC660.07	Neutral trehalase, requires calcium for activity and oligomerization
atf31	atf31	SPAC22F3.02	Transcription factor
C576.04		SPCC576.04	Member of the UPF0005 uncharacterized protein family
C4D7.02c		SPAC4D7.02c	Member of the glycerophosphoryl diester phosphodiesterase family
cmb1	cmb1	SPAC4G9.11c	HMG box mismatch-binding protein, likely to be involved in DNA repair
rst2	rst2	SPAC6F12.02	Transcriptional activator that positively regulates the transcription of ste11 and fbp1
C725.10		SPBC725.10	Member of the tryptophan-rich sensory protein and mitochondrial peripheral benzodiazepine receptor family
C725.03		SPBC725.03	Protein of unknown function
C119.03		SPBC119.03	Protein with moderate similarity to catechol-O-methyltransferase (rat Comt)
alp11	alp11;alp11B8.14c	SPAC13D6.05;SPAC4G9.01	Cytoskeleton-associated protein required for the maintenance of microtubule structure
ypt7	ypt7	SPBC405.04c	Protein involved in endocytosis and vacuole function
C6F6.05		SPAC6F6.05	Protein with high similarity to defender against apoptotic cell death 1 (mouse Dad1)
C26H8.12		SPBC26H8.12	Member of the cytochrome C and C1 heme lyase family
PB16A4.06c		SPCPB16A4.06c	Protein of unknown function
cta3	cta3	SPBC24E9.06;SPBC839.06	Probable Ca ²⁺ -ATPase
C660.06		SPBC660.06	Protein of unknown function
C26F1.07		SPAC26F1.07	Protein with high similarity to aldehyde reductase (human AKR1A1)
C1952.16	rga9	SPAC1952.16	Probable GTP-ase activating protein (GAP) for Rho4p and Cdc42p
C1198.07c		SPBC1198.07c	Glycosylphosphatidylinositol (GPI)-anchored protein
C21B10.08c		SPAC21B10.08c;SPBC21B10.08c	Protein of unknown function
C22E12.03c		SPAC22E12.03c	Member of the DJ-1 or PfpI family
PB1C11.02		SPCPB1C11.02	Member of the amino acid permease family of membrane transporters
C338.18		SPCC338.18	Protein of unknown function
C9E9.04		SPAC9E9.04	Protein of unknown function
C12C2.04		SPBC12C2.04	Protein of unknown function

C21D10.11c		SPBC21D10.11c	Protein with high similarity to cysteine desulfurase (<i>S. cerevisiae</i> Nfs1p)
C1006.01	psp3	SPAC1006.01	Subtilase-type serine peptidase
C22F8.05		SPAC22F8.05	Member of the glycosyltransferase 20 and trehalose-phosphatase families
C126.06	twf1	SPCC126.06	Protein containing a cofilin or tropomyosin-type actin-binding protein domain
pB18E9.04c		SPAPB18E9.04c	Protein with low similarity to <i>S. cerevisiae</i> Prp3p
cgs1	cgs1	SPAC8C9.03	Regulatory subunit for cAMP-dependent protein kinase A
C409.02c		SPBC1709.19c;SPBC409.02c	Protein with high similarity to <i>C. elegans</i> LPD-8
met6	met6	SPBC56F2.11	Putative homoserine o-acetyltransferase acting at the first step in methionine-specific biosynthesis
C31G5.18c		SPAC31G5.18c	Protein of unknown function
C16A3.02c		SPBC16A3.02c	Member of the zinc-binding dehydrogenase family
rhp57	rhp57;slr2	SPAC145.01;SPAC20H4.07	RecA-like protein involved in DNA recombinational repair and sporulation
C17D11.08		SPBC17D11.08	Protein containing four WD domains (WD-40 repeats)
itr2	itr2	SPAC20G8.03	Essential myo-inositol transporter
C31H12.01		SPCC1183.11;SPCC31H12.01	Member of the mechanosensitive ion channel family
ubpd	ubp21;ubpD;ubp15	SPBC713.02c	Ubiquitin-specific protease that may regulate Prp4p function through deubiquitination
C63.12c		SPCC63.12c	Similar to proteasome subunit beta3_sc (<i>S. cerevisiae</i> Pup3p)
C4A8.02c		SPAC4A8.02c	Member of the uncharacterized protein family UPF0047
C16A11.15c		SPCC16A11.15c	Protein of unknown function
C119.15		SPBC119.15	Similar to xeroderma pigmentosum group A protein binding protein 1 (human XAB1)
C1952.13	ned1	SPAC1952.13	Protein required for normal nuclear morphology and chromosome stability
C14G10.03c	ump1	SPCC14G10.03c	Member of the proteasome maturation factor UMP1 family
C36.02c		SPBC36.02c	Member of the major facilitator superfamily
tal1	tal1	SPCC1020.06c	Transaldolase
C4C3.10c		SPBC4C3.10c	Similar to proteasome subunit beta1_sc (<i>S. cerevisiae</i> Pre3p)
C13C5.01c		SPAC13C5.01c;SPAC31A2.17c	Similar to proteasome subunit alpha3_sc (protease yscE subunit Y13, <i>S. cerevisiae</i> Pre9p)
prl44		SPNCRNA.44	
C30C2.08		SPAC30C2.08	Protein of unknown function
C14C4.01c		SPAC14C4.01c;SPAC19D5.08c	Protein of unknown function
C216.03		SPBC216.03	Protein of unknown function
slt1	slt1	SPAC17G6.13	Protein of unknown function

Supplementary Table S2: Genes repressed at least 3-fold in 3 of 4 samples tested when lowering *rpb4* expression levels.

Primer name	Common name	Systematic name	Annotation
C1259.08		SPCC1259.08	Protein of unknown function
frp1	frp1	SPBC1683.09c	Ferric reductase, involved in ferric iron uptake
C11D3.02c		SPAC11D3.02c	Protein containing an acetyltransferase (GNAT) domain
PB10D8.01		SPBPB10D8.01	membrane transporter
C965.13		SPCC965.13	Member of the major facilitator superfamily
C1683.05		SPBC1683.05	Member of the cytosine, purines, uracil, thiamine, or allantoin permease family
mfm2	mfm2	SPAC513.03	Precursor polypeptide for the mating pheromone M factor that is produced by h- cells
C1B3.16c	vht1	SPAC1B3.16c	High affinity H ⁺ /biotin symporter, required for growth under low external biotin conditions
C1198.02	dea2	SPBC1198.02	Adenine deaminase that functions in the purine salvage pathway
C11D3.14c		SPAC11D3.14c	Protein with high similarity to 5-oxo-L-prolinase (rat Oplah)
C212.10		NULL_SPAC212.10	
C887.17		SPBC887.17	Member of the xanthine or uracil permeases family of membrane transporters
C11D3.08c		SPAC11D3.08c	Member of the amino acid permease family of membrane transporters
C19C2.04c	ubp32;ubp11	SPBC19C2.04c	Member of the ubiquitin carboxyl-terminal hydrolase family
C29B12.10c		SPAC29B12.10c	Protein with high similarity to <i>S. cerevisiae</i> Opt1p
P8B7.18c		SPBP8B7.18c	Member of the TENA or THI-4 protein family, has low similarity to <i>S. cerevisiae</i> Thi20p
misc_RNA_1.1.8.RC		SPNCRNA.128	RNase P K-RNA
ilv1	ilv1	SPBP35G2.07	Acetolactate synthase (acetohydroxyacid synthase)
C23C4.06c		SPAC23C4.06c	Protein of unknown function
C3H7.16		SPBC28E12.06c;SPBC3H7.16	Member of the Beige or BEACH domain-containing family
C947.06c		SPBC947.06c	Member of the sugar (and other) transporter family and the major facilitator superfamily
C2E1P3.05c		SPAC2E1P3.05c	Protein containing two fungal-type cellulose binding domains
C4A8.10		SPAC4A8.10	Member of the DUF676 domain of unknown function family
pho1	pho1	SPBP4G3.02	Non-specific acid phosphatase precursor
pho4	pho4	SPBC428.03c	Thiamine-repressible acid phosphatase
C1093.03		SPAC1093.03	Member of the SacI homology domain containing family
mae1	mae1	SPAPB8E5.03	Malate transporter
mae2	mae2	SPCC794.12c	Malate:NAD ⁺ oxidoreductase (oxaloacetate-decarboxylating), malic enzyme
C4F6.09	str1	SPBC4F6.09	Probable ferrichrome-iron transporter
C359.03c		SPAC359.03c;SPBC359.03c	Protein with high similarity to general amino acid permease (<i>S. cerevisiae</i> Gap1p)
C1039.02		SPAC1039.02	Protein of unknown function, appears to localize to membranes

C1039.06		SPAC1039.06	Protein containing an alanine racemase N-terminal domain
C1709.06		SPBC1709.06	Member of the dihydrouridine synthase (Dus) family
C359.05		SPBC359.05	Putative ATP-dependent permease
C947.04		SPBC947.04	Protein of unknown function, has low similarity to a region of flocculin (<i>S. cerevisiae</i> Flo1p)
sou1	sou1	SPAC8E11.10	Protein with high similarity to <i>C. albicans</i> Sou1p
P16F5.08c		SPBP16F5.08c	Protein with low similarity to <i>C. elegans</i> C46H11.2, which is involved in lipid storage
PB1C11.01		SPCPB1C11.01	Protein with high similarity to <i>S. cerevisiae</i> Mep2p
PB1C11.03		SPCPB1C11.03	Member of the major facilitator superfamily, has low similarity to <i>S. cerevisiae</i> Dal5p
C13G6.03	gpi7	SPAC13G6.03	Protein with low similarity to <i>S. cerevisiae</i> Las21p
C23D3.12		SPAC23D3.12	Member of the sugar (and other) transporter family and the major facilitator superfamily
C132.04c		SPCC132.04c	Protein containing a glutamate, leucine, phenylalanine or valine dehydrogenase domain
PJ760.03c	adg1	SPAPJ760.03c	Ace2-dependent gene 1, required for normal cell separation during cytokinesis
C11D3.18c		SPAC11D3.18c	Member of the major facilitator superfamily
C823.14		SPAC823.14	Protein of unknown function
C36.03c		SPBC36.03c	Member of the major facilitator superfamily
C5H10.01		SPAC5H10.01	Member of the DUF1445 domain of unknown function family
C5H10.03		SPAC5H10.03	Protein containing a phosphoglycerate mutase family domain
C5H10.10		SPAC5H10.10	Protein containing an NADH:flavin oxidoreductase or NADH oxidase family domain
C922.04		SPAC922.04	Protein of unknown function
C922.06		SPAC922.06	Protein containing a short chain dehydrogenase domain
prl3		SPNCRNA.03	non-coding RNA (predicted), prl03
misc_RNA_2.2.48.RC			
pex7	pex7	SPAC1834.12;SPAP17D4.01	Peroxisomal targeting signal 2 receptor, peroxin-7
C965.14c		SPCC965.14c	Member of the cytidine and deoxycytidylate deaminase zinc-binding region family
gln1	gln1	SPAC23H4.06	Glutamine synthetase
C13G6.06c		SPAC13G6.06c	Protein with high similarity to <i>S. cerevisiae</i> Gcv2p
P8B7.05c		SPBP8B7.05c	Protein containing a carbonic anhydrase domain
C337.07c		SPBC337.07c	Protein containing a zinc carboxypeptidase domain
rng3	rng3	SPCC613.04c	Protein involved in formation of the contractile ring during cytokinesis
PB10D8.02c		SPBPB10D8.02c	Member of the sulfatase family, which hydrolyze sulfate esters
PB10D8.04c		SPBPB10D8.04c	Member of the C4-dicarboxylate transporter or malic acid transport protein family
C1271.07c		SPBC1271.07c	Protein containing an acetyltransferase (GNAT) domain
C750.08c		SPAC750.08c	Protein containing a malic enzyme NAD binding domain
C186.03		SPAC186.03	Protein with high similarity to L-asparaginase II (<i>S. cerevisiae</i> Asp3-2p)
C1F8.03c	str3	SPAC1F8.03c	Protein that may be involved in iron-siderochrome transport

C14C4.09.B C70.08c C1B2.03c	agn1	SPAC14C4.09 SPCC70.08c SPAC1B2.03c	Endo-(1,3)-alpha-glucanase involved in degradation of septum edging during cell separation Protein of unknown function Protein with high similarity to <i>S. cerevisiae</i> Sur4p
aes1 C285.05 C1683.06c C212.09c C1F8.07c	aes1	SPAPB21E7.07;SPBPB21E7.07 SPCC285.05 SPBC1683.06c SPAC212.09c SPAC1F8.07c	Member of the phenazine biosynthesis-like protein family Member of the purine nucleoside permease (NUP) family Protein containing an inosine-uridine preferring nucleoside hydrolase domain pseudo-malic enzyme with 2 frameshifts Protein containing a thiamine pyrophosphate enzyme N-terminal TPP binding domain
C2F3.09 C30.03c C16D10.06 C30D10.07c	hem1 tsn1;tsn	SPAC2F3.09 SPAC30.03c SPBC16D10.06 SPBC30D10.07c	Protein with high similarity to 5-aminolevulinate synthase (<i>S. cerevisiae</i> Hem1p) Translin, a protein that binds single-stranded RNA (GU) and DNA (GT) repeats Member of the ZIP zinc transporter family, which may be metal transporters Protein containing a biotin or lipoate A or B protein ligase family domain
C646.06c C191.13 C922.01 C757.14 C8E4.03	agn2 hpm1;mmf2;hpf1	SPBC646.06c SPCC1450.02;SPCC191.13 SPAC1039.10;SPAC922.01 SPBC757.14;SPCC613.01;SPCC757.14 SPBC8E4.03	Protein required for endolysis of the ascus cell wall Putative transcription factor, has similarity to <i>S. cerevisiae</i> Bdf1p Protein containing an endoribonuclease L-PSP domain Member of the major facilitator superfamily Protein containing an arginase family domain
alp6 C25B2.08 C215.01 C530.09c C30D11.11	alp6	SPBC428.20c;SPBC902.01c SPBC25B2.08 SPBC215.01;SPBC3B9.20 SPBC530.09c SPAC30D11.11	Member of the gamma-tubulin complex Protein of unknown function Member of the TBC domain containing family Protein of unknown function, has a region of low similarity to a region of <i>S. cerevisiae</i> Mrl1p Member of the hemolysin-III related family
map3 C1F12.08 C1271.14 C56F8.02 C56F8.10	map3	SPAC3F10.10c SPAC1F12.08 SPBC1271.14 SPAC56F8.02 SPAC56F8.10	Pheromone M factor receptor that is required for mating Protein of unknown function Protein with high similarity to <i>S. cerevisiae</i> Arg7p Protein with low similarity to AMP binding luciferase-like protein (human KIAA1463) Methylenetetrahydrofolate reductase (MTHFR)
C21E11.04 C530.07c C1142.05 C977.17	ppr1	SPAC21E11.04 SPBC530.07c SPAC1142.05 SPAC977.17	Protein required for resistance to the L-proline analog L-azetidine-2-carboxylic acid (AZC) Protein of unknown function Integral membrane component of the high-affinity copper transport complex Protein with high similarity to <i>S. cerevisiae</i> Yfl054p
tf2-5 PB8E5.07c C23H4.01c C3C7.07c	Tf2-5	SPAPB15E9.03c SPAPB8E5.07c SPAC23H4.01c;SPAP27G11.01 SPAC3C7.07c	Protein containing two HEAT repeats Member of the emp24 family Member of the arginine-tRNA-protein transferase C terminus and N terminus containing families

C4H3.01		SPAC4H3.01	Protein containing a DnaJ domain
bfr1: hba2	hba2;bfr1	SPCC18B5.01c;SPCPJ732.04c	ABC transporter involved in multidrug resistance
C1039.08		SPAC1039.08	Protein containing a serine acetyltransferase N-terminal domain
PB2B2.01		SPBPB2B2.01	Member of the amino acid permease family of membrane transporters
C922.07c		SPAC922.07c	Protein with high similarity to aldehyde dehydrogenase (<i>S. cerevisiae</i> Ald2p)
C6G9.03c		SPAC6G9.03c	Protein with weak similarity to regulator of Ty transposition (<i>S. cerevisiae</i> Rtt106p)
C145.02		SPAC145.02;SPAC20H4.08	Protein of unknown function
pB18E9.05c		SPAPB18E9.05c	Protein of unknown function
C70.03c		SPCC70.03c	Member of the proline dehydrogenase family
isp7	isp7	SPAC25B8.13c	Protein involved in sexual differentiation
C4C5.01		SPAC4C5.01	Protein containing a haloacid dehalogenase-like hydrolase domain
P7G5.06		SPAP7G5.06	Protein with high similarity to general amino acid permease (<i>S. cerevisiae</i> Gap1p)
C14F5.01		SPBC14F5.01;SPBC1861.10	Protein of unknown function
C3H1.11		SPAC3H1.11	Protein containing two zinc finger C2H2 type repeats
eng1	eng1	SPAC821.09	Endo-beta-1,3-glucanase required for primary septum degradation and cell separation
C18G6.11c	rrn3	SPAC18G6.11c	Protein involved in initiation of transcription of rDNA promoter
tnr3	tnr3;TPK	SPAC6F12.05c	Thiamine pyrophosphokinase
C569.07		SPCC569.07	Similar to aromatic amino acid aminotransferase I (<i>S. cerevisiae</i> Aro8p)
C1683.13c		SPBC1683.13c	Putative transcriptional activator, contains zinc finger domain
fip1	fip1	SPAC1F7.07c	Protein with high similarity to <i>C. albicans</i> Ftr2p, which is an iron permease
C584.13		SPAC8A4.11;SPCC584.13	Similar to GABA permease (<i>C. albicans</i> Gpt1p), which is a polyamine transporter
misc_RNA_1.1.46.RC		SPNCRNA.75	non-coding RNA (predicted)
C3H7.12		SPBC3H7.12	Protein of unknown function
mei2	mei2	SPAC27D7.03c	RNA-binding protein involved in meiosis
C18G6.05c		SPAC18G6.05c	Protein containing 20 HEAT repeats
gpa2: git8	gpa2;git8	SPAC23H3.13c	G-protein, alpha subunit, of the Gpa2p/Git5p/Git11p heterotrimeric G protein
yip1	yip12;yip1-b;yip1	SPAPB17E12.02	Protein that may be involved in mRNA metabolism or pre-RNA splicing
C57A7.13		SPAC57A7.13	Member of the G-patch domain family, contains two RNA recognition motifs
C8E4.01c		SPBC8E4.01c;SPBP4G3.01	Member of the major facilitator superfamily and the sugar (and other) transporter family
sum3: ded1: slh3: moc2	moc2;sum3;dep1	SPCC1795.11	Putative helicase, essential for G2/M phase checkpoint control
C11D3.07c		SPAC11D3.07c	Protein containing a fungal specific transcription factor domain
C18H10.15	ppk23	SPBC18H10.15	Protein with high similarity to cyclin dependent kinase 10 (human CDK10)
C13B11.03c		SPCC13B11.03c	Protein containing a metallo-beta-lactamase superfamily domain
C11D3.11c		SPAC11D3.11c	

C6G10.08	idp1	SPAC6G10.08	Protein with high similarity to mitochondrial isocitrate dehydrogenase (<i>S. cerevisiae</i> Idp1p)
C8D2.10c	pi055;rmt3	SPBC8D2.10c	Arginine methyltransferase, associates with the translational machinery
C1539.05		SPBC1539.05	Member of the Sec34-like family, has weak similarity to <i>S. cerevisiae</i> Cog3p
PB7E8.01		SPBP7E8.01;SPBPB7E8.01	Protein of unknown function
C1683.07	mal1	SPBC1683.07	Protein with high similarity to alpha-glucosidase (<i>C. albicans</i> Mal2p)
C18.01c	adg3	SPCC18.01c;SPCC74.07c	Ace2-dependent gene 3, required for normal cell separation during cytokinesis
PB15E9.01c		SPAPB15E9.01c;SPAPB18E9.06c	Protein with weak similarity to <i>S. pombe</i> Nup124p
C17D1.06		SPBC17D1.06;SPCC17D1.06	Protein with high similarity to DEAD-box protein 3 (<i>S. cerevisiae</i> Dbp3p)
C12D12.06	srb11	SPBC12D12.06	Putative G1-to-S phase-specific cyclin, component of a mediator subcomplex
C12C2.07c	SPC12C2.07c	SPBC12C2.07c	Protein with high similarity to putrescine aminopropyltransferase (<i>S. cerevisiae</i> Spe3p)
C4G3.18		SPCC4G3.18	Protein of unknown function
PB24D3.06c		SPAPB24D3.06c	Protein of unknown function
C1683.04		SPBC1683.04	Protein with high similarity to <i>C. pseudotropicalis</i> Bglp
C1773.17c		SPBC1773.17c;SPBP26C9.01c	Protein containing D-isomer specific 2-hydroxyacid dehydrogenase NAD domains
C1271.08c		SPBC1271.08c	Protein of unknown function

Supplementary Table S3: Functional classification of genes affected by *rpb4*

Functional category	Induced genes	Repressed genes
Metabolism	26	58
Signal Transduction, Cell Communication and Transcription	11	10
Cellular Biogenesis and Organization	6	9
Cellular Transport and Transport Facilitation	11	36
Protein synthesis, folding, modification, targeting and degradation	15	10
Cell cycle, cell growth and cell division	10	11
Others	10	9

Functional distribution of genes whose expression was modulated in response to *rpb4* expression levels. The total numbers of induced and repressed genes do not add up to the total number of genes identified, because the functions of many genes are still unknown, while others encode proteins that function in more than one category and have been assigned to multiple groups.