Appendix I: Strains used in this study

Strain	Source
972 h-	Laboratory collection
cdc25-22 h-	Laboratory collection
cdc10-129 h-	Laboratory collection
cdc25-22 sep1∆::ura4 h-	Matthias Sipiczki
ace2∆::kanMX6 ade6-M21?h-	This study
ace2Δ::kanMX6 sep1::ura4 ade6-M21? leu1-32 h?	This study
atfl∆∷ura4 ura4-D18 h-	Nic Jones
$cdc10$ - $C4h^+$	Paul Nurse
cig1∆::ura4 cig2∆::ura4 puc1∆::ura4	Sergio Moreno
leu1-32 h- pREP3X-fkh2	This study
leu1-32 h- pREP3X-ace2	This study
leu1-32 h- pREP3X-fhl1	This study
leu1-32 h- pREP3X-sep1	This study
mbx1∆::kanMX6 leu1-32 ura4-D18 ade6-M210 his7-366 h-	Jonathan Miller
meu3∆::kanMX6 ade6-M21?h-	This study
meu19::kanMX6 ade6-M21?h-	This study
nda3-KM311 h-	Laboratory collection
pcr1∆::ura4 h-	Nic Jones
prr1∆::his7 his7? h-	Nic Jones
sep1∆::ura4 h-	Matthias Sipiczki
SPAC8C9.01Δ::kanMX6 h90 (fhl1)	Laboratory collection
SPAC8C9.01\(\Delta::kanMK6 \) sep1::ura4 h?	This study
SPBC16G5.15c∆::ura4 leu1-32 ura4-D18 ade6-M210/216	Brian Morgan
his7-366 h+/h-	
SPBC16G5.15c∆::ura4 leu1-32 ura4-D18 ade6-M21? his7-	This study
366 h-	

Appendix II: List of buffers, solutions, media and antibiotics

Buffers and stock solutions	Composition				
	For 1 liter: 3.0 g potassium hydrogen phthalate, 2.2 g				
Edinburgh Minimal madium (EMM)	Na ₂ HPO ₄ , 5.0 g NH ₄ Cl, 20g D-glucose, 20 ml salts				
Edinburgh Minimal medium (EMM)	stock (X50), 1 ml vitamin stock (X1000), 0.1 ml				
	mineral stock (X10000)				
0.5 M EDTA	For 1 liter: 186.1 g disodium				
U.S WI EDIA	ethylenediaminetetracetate \cdot 2H ₂ O				
Formal saline	0.9% saline, 3.7% formaldehyde				
Freezing mix	YE containing 250 mg of Glutamic Acid, 50%				
rreezing iinx	glycerol				
Hybridization buffer	5 x SSC, 6 x Denhardt's 60 mM TrisHCl pH 7.6,				
Trybridization burier	0.12% sarkosyl, 48% formamide; filter sterilized				
10X LiAc	1M Lithium Acetate, pH 7.5				
Luria Bertani medium (LB)	For 1 liter: 10g NaCl, 10 g tryptone, 5 g yeast extract,				
Luria Dertam medium (LD)	pH 7.0				
	For 1 liter: 5.0 g H ₃ BO ₃ , 4.0 g MnSO ₄ , 4.0 g ZnSO ₄ ·				
Mineral stock (X10000)	$7H_2O$, 2.0 g FeCl ₃ · $6H_2O$, 0.4 g $H_2MOO_4 \cdot H_2O$, 1.0				
	g KI, 0.4 g CuSO ₄ · 5H ₂ O, 10 g citric acid				
2X Printing buffer	300 mM sodium phosphate, pH 8.5				
PEG/LiAc/TE	For 20 ml: 2 ml 10X LiAc, 2 ml 10X TE, filter-				
TEG/EIAC/TE	sterilized				
Phosphate Buffer Saline (PBS)	For 1 liter: 8.0 g NaCl, 0.2 g KH ₂ PO ₄ , 1.44 g				
Thosphate Duffer Samie (TDS)	Na ₂ HPO ₄ , 0.2 g KCl, pH 7.4				
Salt stock (X50)	For 1 liter: 53.5 g MgCl ₂ · 6H ₂ O, 0.74 g CaCl ₂ ·				
Sait stock (ASO)	2H ₂ 0, 50 g KCl, 20 g Na ₂ SO ₄				
	For 100 ml: 2.0g Bacto-tryptone, 0.5g Bacto-yeast				
SOC medium	extract, 1ml 1M NaCl, 0.25ml 1M KCl, 1ml Mg2+				
500 inculum	stock (1M MgCl2 . 6H2O, 1M MgSO4 . 7H2O),				
	filter-sterilized, 1ml 2M glucose, filter-sterilized				
20X SSC	3 M NaCl, 300 mM Na-citrate, pH 7.0				

1X TAE	40 mM Tris-acetate, 1 mM EDTA, pH 7.2				
1X TE	10 mM Tris/HCl, pH 8.0, 1 mM EDTA				
1X TES	10 mM Tris pH 7.5, 10 mM EDTA pH 8.0, 0.5%				
IX IES	SDS				
Vitamin stock (1000X)	For 1 liter: 1.0 g Na pantothenate, 10 g nicotinic acid,				
Vitaliili Stock (1000A)	10 g inositol, 10 mg biotin				
Washing solution 1	2X SSC				
Washing solution 2	0.1X SSC, 0.1% SDS				
Washing solution 3	0.1X SSC				
	For 1 liter: 5 g Difco Yeast Extract, 30 g glucose, pH				
Yeast Extract (YE)	5.6. Supplements: 250 mg histidine, leucine,				
	adenine, uracil and lysine				
Yeast Extract (YE) agar	YE plus 20 l/liter Difco agar				

Appendix III: Primers used in this study

PRIMERS for GENE DELETION

Primer name	Sequence					
Meu19_F	5'-agttttaacgaccgctacgtagtgtaatgctacaaaataagtctac					
IVICUTY_I	$t caga tattat g cag c c g tact cat c t g at ttt g c \underline{g} \underline{g} \underline{a} \underline{t} \underline{c} \underline{c} \underline{c} \underline{c} \underline{g} \underline{g} \underline{g} \underline{t} \underline{t} \underline{a} \underline{t} \underline{t} \underline{a} \underline{a} \underline{t} \underline{a} \underline{e} \underline{c}$					
Meu19_R	5'-gcttactcataatttcttctttaaaaaatcgatgtgacattgtgaatacata					
WCu17_K	aaccgtcaataatctactgctaaaatgcgaattcgagctcgtttaaac-3'					
Meu3_F	5'-taacgctaatgtcatacaacaccgtattcgtctgatttgtctacaaaaatgta					
Wicus_i	aacaaacaattattttatcgcattgatcggatccccgggttaattaa					
Meu3_R	5'-ctactcattatttcctcattaaaagatcgacttggcactgaaaacaaatgaac					
Wicus_K	cgccgatatcctatattgttacaaagcgaattcgagctcgtttaaac-3'					
Ace2_F	5'-attteteteategttetetettgatttetetaegeattgeaetagataetegeta					
Acc2_I	tcctaagtaaacaagacaatgtcgcggatccccgggttaattaa					
Ace2_R	5'-aattgtcacagcattagttcatgtacgatgcttgaatttgaatttatataaaac					
Acez_K	aaattaaaaacaataatattagtaagaattcgagctcgtttaaac-3'					
	5'-					
Fhl1_F	gctttctagtctcattgtgctttcaattggctagaagtttagcttactataaaaaa					
	aggaagtctttgggtcattaaggccggatccccgggttaattaa					
Fhl1_R	5'-ccaagttgtgcaatcactgtcaaaaaaagaaaaatgaaacagcttatgcat					
1 1111_1X	gctggtaagtgtaattttcggcactaattggaattcgagctcgtttaaac-3'					

The underlined sequence represents the sequence homologous to the plasmid multiple cloning site.

PRIMERS for CHECKING GENE DELETIONS

Primer name	Sequence
Ace2_check_R	5'-gttatacacaatactagggtgatg-3'
Meu3_check_R	5'-cgtttcaatattgaaattcttacag-3'
Meu19_check_R	5'-tcgcatctttagattaacatatagg-3'
Kan_check_R	5'-gtcacatcatgccctgagc-3'

PRIMERS for CLONING - OVEREXPRESSION

Primer name	Sequence
C16g5.15 forward	5'-ctcgagatgactgttcgcagactcgaaagc-3'
C16g5.15 reverse	5'-gggataagatattaaacaaggtg-3'
C6g10.12c forward	5'-ctcgagatgtcgctttcatat-3'
C6g10.12c reverse	5'-tcattagtgctgtctgcgatc-3'
C1142.08 forward	5'-ctcgagatgcctgttgcagag-3'
C1142.08 reverse	5'-tcaggtataagaggatgatgtctc-3'
Sep1 forward	5'-ctcgagatcttcctcatgaat-3'
Sep1 reverse	5'-ttagaatagtgttgaagtttgac-3'

The sequence in bold corresponds to the *Xho*I restriction site.

Appendix IVa: Time courses experimental conditions

Experiment	Strain	Timepoints	Sample label	Reference	Ref label	Media	Temp (°C)	Sample OD	Array batch number
Elutriation I	972 h-	20	СуЗ	Asynchronous 972 h-	Cy5	EMM	30	0.65	137 & 140
Elutriation II	972 h-	20	Cy5	Asynchronous 972 h	Cy3	EMM	30	0.24	228 & 232
Elutriation III	972 h-	20	Cy5	Asynchronous 972 h	Cy3	EMM	30	0.15	489
cdc25 b&r I	cdc25-22 h-	18	Cy3	Asynchronous cdc25-22 h-	Cy5	YE	25	0.34	40 & 70
cdc25 b&r I dye swap	cdc25-22 h-	18	Cy5	Asynchronous cdc25-22 h-	Cy3	YE	25	0.34	40 & 70
cdc25 b&r II	cdc25-22 h-	19	Cy5	Asynchronous cdc25-22 h-	Cy3	EMM	25	0.19	292
cdc25 elu + b&r	cdc25-22 h-	22	Cy5	Asynchronous cdc25-22 h-	Cy3	EMM	25	0.22	226, 228 & 232
cdc10 elu + b&r	cdc10-129 h-	22	Cy5	Asynchronous <i>cdc10-129</i> h-	Cy3	EMM	25	0.30	331 & 334
cdc10::ura4	cdc10::ura4 leu1-32 ura4-D18 ade6-M210 + pREP1-HA-res1(1-192)	3	Cy5	Untreated cdc10::ura4	СуЗ	EMM ade	30	0.2	477
cig1Δ cig2Δ puc1Δ elu	cig1::ura4 cig2::ura4 puc1::ura4	6	Cy5	Asynchronous cig1::ura4 cig2::ura4 puc1::ura4 h-	Cy3	EMM	30	0.15	477
HU b&r	972 h-	4	Cy3	Untreated 972 h-	Cy5	EMM	32	0.08	489
nda3	nda3-KM311 h-	3	Cy5	Untreated nda3	Cy3	EMM		0.23	477
sep1 b&r	cdc25-22 sep1::ura4 h-	20	Cy5	cdc25-22 sep1::ura4 h-	Cy3	EMM	25	0.12	331 & 334
wt b&r	972 h-	18	Cy3	972 h-	Cy3	EMM	25	0.15	782 & 784

 $0.5 \text{ OD} = 1 \text{ X } 10^7$

Appendix IVb: Mutant strains experimental conditions

Experiment	Strain	Sample label	Reference	Ref label	Media	Temp (°C)	Sample OD	Array batch number
ace2 #1		Cy5		Cy3		32	0.22	489-48
ace2 #2		Cy3		Cy5			0.23	489-7
ace2 #3	ace2∆::kanMX6 ade6-M21?h-	Cy5	972 h-	СуЗ	EMM ade		0.23	489-14
ace2 #4		Cy5		Cy3			0.24	489-12
ace2 #5		Cy5		Су3			0.33	668-2
ace2 sep1 #1	ace2∆::kanMX6 sep1::ura4 ade6-	Cy5	972 h-	СуЗ	EMM ura ade leu	30	0.26	668-9
ace2 sep1 #2	M21? leu1-32	Cy5	9/2 n-	СуЗ	Elviivi ura ade ieu	30	0.32	668-10
atf1 #1	atf1∆∷ura4 ura4-D18 h-	Cy5	972 h-	Cy3	YE	25	0.18	596-21
atf1 #2	uy1\(\text{\D}\)uru4 uru4-\(\text{\D}\)10 n-	Cy5	9/2 n-	СуЗ	YE	23	0.21	599-2
cdc10-C4 #1		Cy5		СуЗ	— EMM	25	0.23	489-10
cdc10-C4 #2	cdc10-C4 leu1-32 h+	Cy5	$972 h^+$	Cy3			0.24	489-11
cdc10-C4 #3	cac10-C4 leu1-32 n+	Cy3	9/2 11	Cy5			0.23	334-19
cdc10-C4 #4		Cy5		СуЗ			0.24	334-17
fh11 #1		Cy3		Cy5			0.23	334-22
fh11 #2	SPAC8C9.01∆::kanMX6 h90	Cy5	972 h-	СуЗ	EMM	25	0.23	334-11
fhl1 #3		Cy5		СуЗ			0.22	668-41
fkh2 #1	SPBC16G5.15c::ura4 leu1-32 ura4-	Cy5	972 h-	СуЗ	YE	30	0.20	560-42
fkh2 #2	D18 ade6-M21? his7-366 h-	Cy5] 9/2 n-	Cy3	IE		0.20	560-45
mbx1 #1	mbx1::kanMX6 leu1-32 ura4-D18	Cy5	972 h-	СуЗ	EMM lay uro ada his	25	0.23	334-18
mbx1 #2	ade6-M210 his7-366 h-	Cy3] 9/2 N-	Cy5	EMM leu ura ade his	23	0.22	334-20

Experiment	Strain	Sample label	Reference	Ref label	Media	Temp (°C)	Sample OD	Array batch number
meu3 #1	- meu3∷kanMX6 ade6-M21?h-	Cy5	972 h-	Cy3	EMM ade	32	0.23	489-49
meu3 #2	meus::kanMA0 aaeo-M21?n-	Су3	9/2 n-	Cy5	Elviivi ade	32	0.23	489-8
meu19 #1	meu19::kanMX6 ade6-M21?h- Cy5 972 h- Cy3 EMM ade	EMM ade	32	0.22	489-50			
meu19 #2	meu19kanw1x0	Су3	9/2 n-	Cy5	EMINI ade	32	0.25	489-9
pcr1 #1	noul ways 4 h	Cy5	972 h-	Cy3	YE	25	0.24	489-17
pcr1 #2	pcr1::ura4 h-	Cy5	9/2 n-	Cy3	I E	23	0.21	560-46
prr1 #1	nuulAhig7 hig72 h	Cy3	972 h-	Cy5	EMM	25	0.23	334-21
prr1 #2	- prr1∆::his7 his7? h-	Cy5	9/2 n-	Cy3	Elviivi	23	0.22	334-12
sep1 #1		Cy5		Cy3			0.24	489-13
sep1 #2	sep1∆ h-	Cy3	972 h-	Cy5	- EMM	25	0.25	334-23
sep1 #3		Cy5	9/2 11-	Cy3	Elviivi		0.24	334-14
sep1 #4		Cy5		Cy3			0.23	668-5
fhl1 sep1 #1	SPAC8C9.01A::kanMK6 sep1::ura4	Cy5 972 h- Cy3 EMM ura ade leu	30	0.23	668-39			
fhl1 sep1 #1	ade6-M21? leu1-32 h-	Cy5	9/2 n-	Cy3	Elviivi ura ade leu	30	0.23	668-27
ace2 OE #1	leu1-32 h- pREP3X-ace2	Cy5		Cy3		32	0.06	596-3
ace2 OE #2	teur-52 n- pres 5A-ace2	Cy5		Cy3		32	0.12	560-31
fhl1 OE #1	leu1-32 h- pREP3X-fhl1	Cy5		Cy3		32	0.03	596-4
fhl1 OE #2	teur-52 n- picer 52-ymr	Cy5	leu1-32 h- pREP3X	Cy3 EMM,	EMM, 15 μM	_	0.08	560-47
fkh2 OE #1	leu1-32 h- pREP3X-fkh2	Cy5	ιεμ1-32 π- μκΕ1 3Α	Cy3	thiamine	32	0.07	596-20
fkh2 OE #2	teal 52 n- pied 5A-jim2	Cy5		Cy3		32	0.04	596-10
sep1 OE #1	leu1-32 h- pREP3X-sep1	Cy5		Cy3		32	0.23	596-22
sep1 OE #2	1	Cy5		Cy3		32	0.17	596-19

 $0.5 \text{ OD} = 1 \text{ X } 10^7$

Appendix V: Additional measurements defining cell cycle synchrony in timecourse experiments and additional clustering

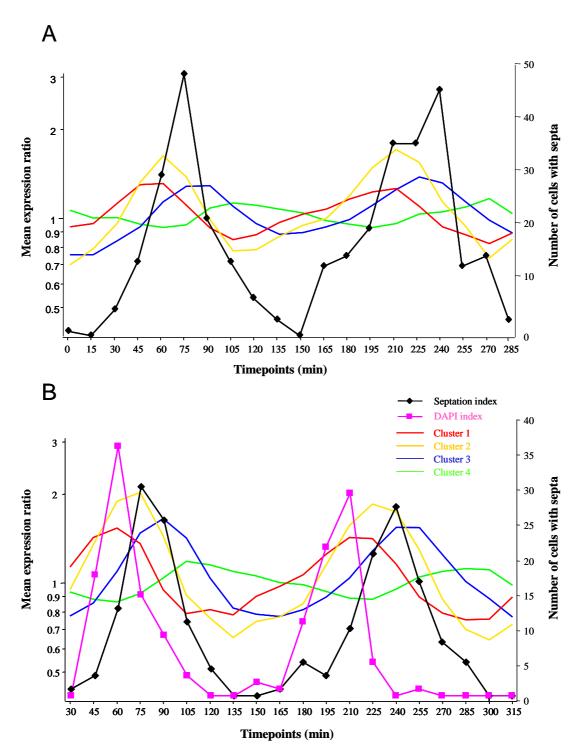


Fig. V.1 Additional measurements for elutriation experiments.

Panel A and B refer to two independent biological experiments, elutriations 1809 and 1012 respectively. For each graph, septation index and average expression profiles for the four clusters are shown. In panel b the DAPI index is also shown

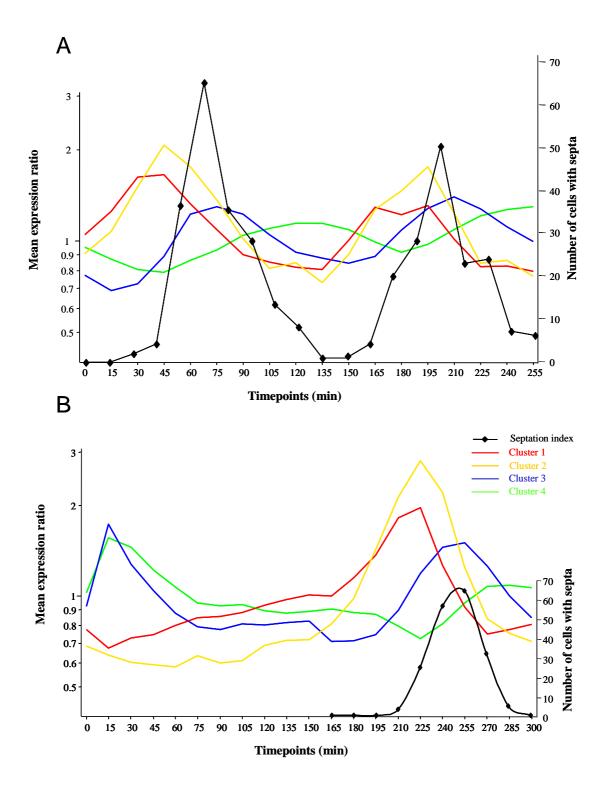


Fig. V.2 Additional measurements for *cdc25* experiments.

Panel A refers to a *cdc25* 'block and release' experiment (1601), panel B refers to a *cdc25* elutriation + 'block and release' (1402). For each graph, septation index and average expression profiles for the four clusters are shown.

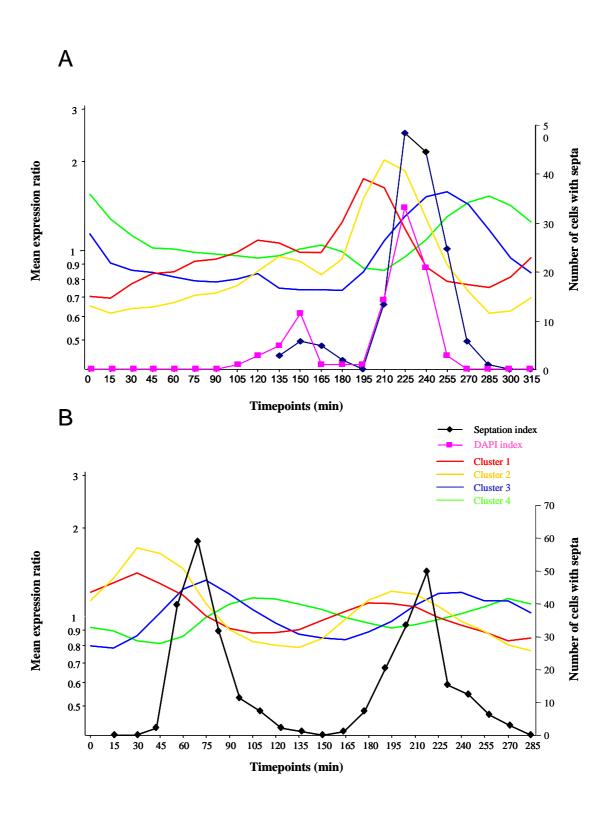


Fig. V.3 Additional measurements for *cdc25* and *cdc10* experiments.

Panel A refers to a $sep1\Delta$ cdc25 'block and release' experiment (2009), panel B refers to a cdc10 elutriation + 'block and release' (509). For each graph, septation index and average expression profiles for the four clusters are shown.

Wild type elutriation

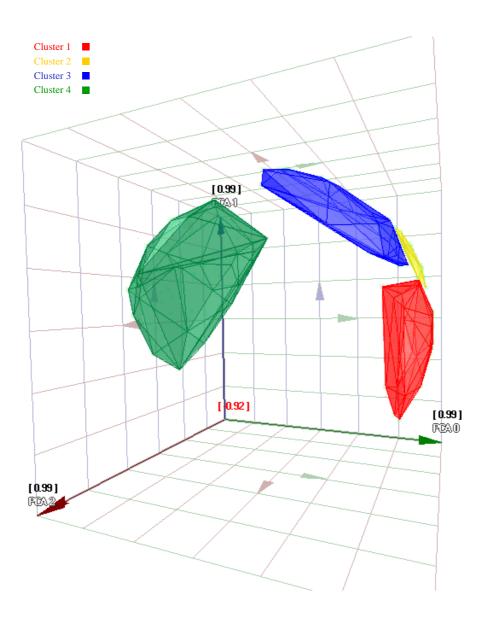


Fig. V.4 3-dimensional representation of the four clusters of cell cycle regulated genes for an elutriation experiment.

Each coloured area represents a cluster of genes. Classification is shown for one elutriation experiment (2201). This graph was obtained using Principal Component Analysis (PCA) in Arrayminer.

cdc25 'block and release'

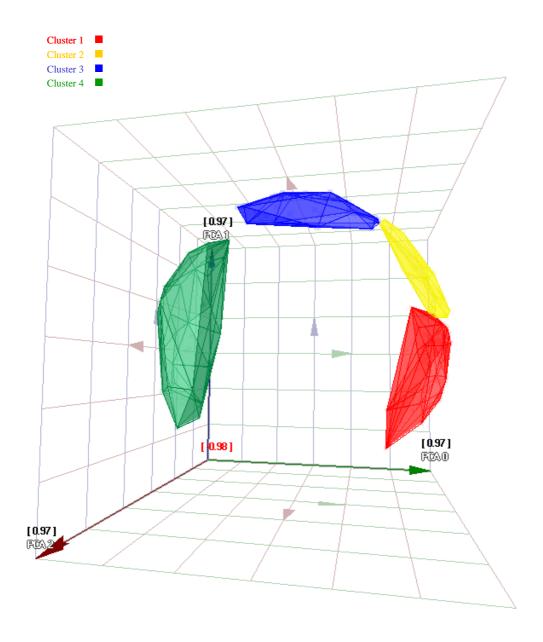


Fig. V.5 3-dimensional representation of the four clusters of cell cycle regulated genes for a *cdc25* 'block and release' experiment.

Each coloured area represents a cluster of genes. Classification is shown for one *cdc25* 'block and release' experiment (2001). This graph was obtained using Principal Component Analysis (PCA) in Arrayminer.

Appendix VI: List of 407 genes periodically expressed during the cell cycle

ste7 SPAC23E2.03c sso1; psy1 SPCC825.03c slp1 SPAC821.08c	Protein required for mating and meiosis Syntaxin-like component of the plasma membrane docking/fusion complex WD-domain protein of the spindle defect checkpoint and APC	1	FLEX FLEX
	docking/fusion complex WD-domain protein of the spindle defect checkpoint and APC	1	FLEX
slp1 SPAC821.08c	• • • •		
	activator	1	FLEX
sid2; pld5 SPAC24B11.11c	Protein kinase involved in regulation of cytokinesis	1	FLEX
ark1; sex1 SPCC330.16; SPCC320.13c	Aurora kinase involved in regulation of mitosis	1	
rum1 SPBC32F12.09	Inhibitor of the Cdc2p cyclin-dependent kinase complex	1	FLEX, Novel 2
rhp51; rad51 SPAC644.14C	Required for DNA repair and meiotic recombination	1	MCB 1
plo1 SPAC23C11.16	Polo kinase involved in regulation of mitosis and cytokinesis	1	FLEX, Novel 3
myo3; myp2 SPAC4A8.05c	Myosin-3 isoform, heavy chain (Type II myosin)	1	
mus81 SPCC4G3.05c	Holliday junction resolvase subunit	1	
msh6 SPCC285.16c	Protein involved in mismatch repair (mutS family)	1	FLEX
mob1 SPBC428.13c	Protein involved in regulation of cytokinesis	1	FLEX, MCB 1, Novel 2
meu29 SPAC25H1.05	Unknown function	1	Ace2, FLEX
meu16	Non-coding RNA	1	
SPBC1685.15c; SPBC649.01c	Kinesin motor protein; KIP3 subfamily	1	FLEX
klp5 SPBC2F12.13	Kinesin motor protein; KIP3 subfamily	1	FLEX, MCB 1
imp2 SPAC13F4.08c; SPBC11C11.02	Protein required for medial ring disassembly after cytokinesis	1	FLEX, MCB 1, Novel 1
etd1 SPAC1006.08	Protein required for cytokinesis	1	FLEX, MCB 1
chs2 SPBC1734.17; SPBC1709.01	Member of chitin synthase family, involved in cell wall maintenance	1	MCB 1
cdc20; pol2 SPBC25H2.13c	DNA polymerase epsilon catalytic subunit	1	FLEX, MCB 2
cdc15; rng1 SPAC20G8.05c	Protein involved in cytokinesis	1	FLEX
bet1 SPAC23C4.13	Member of SNARE domain containing family	1	FLEX
apc15; apc16 SPBC83.04	Component of APC/cyclosome complex	1	FLEX

	SPCC757.12	Protein containing an alpha amylase N-terminal catalytic domain	1	Novel 2
ace2	SPAC6G10.12c	Zinc finger transcription factor	1	FLEX
	SPAC5D6.02c	Unknown function	1	
	SPCC576.02	Member of aspartate and glutamate racemases family	1	FLEX
	SPAC30D11.01c; SPAC56F8.01	Member of glycosyl hydrolases family 31, involved in carbohydrate metabolism	1	
	SPBC4F6.12	LIM domain protein, low similarity to paxillin focal adhesion protein that regulates integrin or growth factor-mediated responses	1	
wis3; spo12	SPAC3F10.15c	Protein likely to play role in regulating cell cycle progression, possibly at G2 to M phase transition	1	FLEX, Novel 1
	SPBC27.05	Unknown function	1	
	SPAC23H4.19; SPAC1705.03c	Putative cell wall biogenesis protein	1	FLEX, Novel 1, Novel 2
	SPBC19G7.04	Unknown function, possible transcriptional regulator, may contain HMG box	1	FLEX
	SPAC19B12.02c	Protein with high similarity to 1,3-beta-glucanosyltransferase, member of glycolipid anchored surface protein (GAS1) family	1	FLEX
	SPBC16G5.15c	Fork head protein type transcription factor	1	FLEX
ho4	SPAC16A10.04	Rho protein involved in regulation of cytoskeleton, cytokinesis, and cell wall integrity	1	FLEX, Novel 1
nde6	SPAC15A10.10	Protein likely to play a role in meiosis or sporulation, requires Mei4p for transcriptional activation	1	FLEX
	SPAC15A10.09c	Unknown function	1	FLEX, MCB 1, Novel 1
nac1	SPAC13G7.04c	Transmembrane protein involved in cell separation	1	FLEX, Novel 2
	SPAC11E3.13c	Member of glycolipid anchored surface protein (GAS1) family, possible involvement in cell wall maintenance	1	MCB 1
	SPBC1198.07c	Putative glycosylphosphatidylinositol (GPI)-anchored protein involved in cell wall biosynthesis	1	FLEX
top1	SPBC1703.14c	DNA topoisomerase I, involved in chromatin organisation	1	FLEX, Novel 1
spn2	SPAC821.06	Septin homolog, involved in cell separation	1	
sad1; sta1	SPBC16H5.01c; SPBC12D12.01	Spindle pole body associated protein	1	

psc3	SPAC17H9.20; SPAC607.01	Cohesin complex component, required for sister chromatid cohesion and normal mitosis	1	MCB 1
	SPBC32H8.09	Protein containing WD domain G-beta repeat	1	
ndk1	SPAC806.07	Nucleoside diphosphate kinase	1	
dis1	SPCC736.14	Microtubule-associated protein required for chromosome segregation (functions with Klp5p and Klp6p in kinetochore-spindle attachment)	1	
csk1	SPAC1D4.06c	Cyclin-dependent kinase activating kinase (CAK) involved in activating Cdc2p (activity partially redundant with Mcs6p-Mcs2p complex)	1	
crk1; mcs6; mop1	SPBC19F8.07	Cyclin-dependent kinase activating kinase (CAK) involved in activating Cdc2p kinase, putative transcription initiation factor TFIIH subunit	1	
cid13	SPAC821.04c	Cytoplasmic poly(A) polymerase involved in regulation of ribonucleotide reductase (suc22) mRNA, TRF family of nucleotidyltransferases	1	Novel 1
cdr1; nim1	SPAC644.06c	Protein kinase involved in regulation of mitosis	1	
cdc25; sal2	SPAC24H6.05	Tyrosine phosphatase that activates Cdc2p kinase, involved in G2/M transition and DNA damage checkpoints	1	
cdc13	SPAC19G10.09C; SPBC582.03	Cyclin that promotes entry into mitosis from G2 phase, forms complex with Cdc2	1	
aph1	SPCC4G3.02	Diadenosine tetraphosphatase, catalyzes hydrolysis of dinucleoside polyphosphate compounds	1	
	SPBPB2B2.09c	Member of the ketopantoate reductase PanE or ApbA family, involved in thiamine biosynthesis	1	
rps602; rps6	SPAPB1E7.12	Protein with high similarity to ribosomal S6 proteins	1	
	SPAC824.04	Protein containing three WD domains (WD-40 repeat)	1	
	SPAP8A3.11c	Member of GTP1 or OBG family of GTP-binding proteins, similarity to developmentally regulated protein with possible role in neurogenesis	1	
	SPAP27G11.08c	Unknown function	1	FLEX
	SPAC9.11	Unknown function	1	
	SPBC646.06c	Member of glycosyl hydrolase family 71, putative glucanase	1	FLEX, Novel 2
	SPAC589.09	Protein containing a CRAL-TRIO domain, putative	1	

		phosphatidylinositol metabolism		
	SPAC589.02c	Component of mediator subcomplex that may function in negative regulation of transcription	1	
	SPCC4G3.06c	Unknown function, possible mitochondrial ribosomal protein of large subunit	1	FLEX
	SPBC4F6.11c	Unknown function	1	MCB 1
	SPBC4F6.05c	Member of legume-like lectin family	1	
	SPBC428.12c	Putative RNA binding protein	1	
	SPBC1306.02; SPBC4.08	Protein containing eight WD domains (WD-40 repeat), possible role in activated transcription by RNA polymerase II	1	FLEX
	SPBC3H7.13	Member of forkhead associated (FHA) domain family, similarity to S. pombe spindle checkpoint protein Dma1p	1	
ртс2	SPAC2F7.04	Mediator complex component, involved in regulating RNA polymerase II activity	1	
	SPBC27B12.06	Protein with possible role in glycosylphosphatidylinositol biosynthesis	1	FLEX
	SPBC26H8.13c	Unknown function	1	
	SPAC24H6.01c;	Unknown function, similarity to putative glycerol transporter	1	FLEX, MCB 1
	SPAPB21F2.01	involved in phospholipid biosynthesis	1	FLEA, MCB 1
	SPAC24C9.05c	Unknown function	1	
	SPAC23G3.04	Unknown function	1	Novel 3
spn7; mde8	SPBC21.08c; SPBC19F8.01c	Septin homolog, involved in cell separation	1	FLEX
	SPBC19C2.10	Protein containing an Src homology 3 (SH3) domain, putative actin binding	1	
spp2; pri2	SPBC17D11.06	DNA primase, large (non-catalytic) subunit	1	
	SPBC1709.13c	Member of SET domain containing family	1	
	SPAC1687.19c	Probable tRNA-guanine transglycosylase	1	FLEX
	SPAC1687.17c	Member of the Der1-like family, putative transmembrane protein with signal peptide	1	FLEX
	SPAC1687.10	Unknown function	1	
	SPBC1685.03	Member of signal peptidases type I family, which cleave signal peptides from secreted proteins	1	

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	SPAC13G7.10	Protein with two Myb-like DNA-binding domains	1	FLEX
	SPAC13G6.03	Member of type I phosphodiesterase or nucleotide pyrophosphatase family	1	
	SPAC13C5.05c	Member of phosphoglucomutase or phosphomannomutase C- terminal domain containing family	1	
ds5	SPAC110.02	Protein required for maintenance of sister chromatid cohesion	1	MCB 1
nik1	SPBC660.14	Protein kinase that inhibits Cdc2p kinase	2	FLEX, MCB 1, MCB 2
ol1; swi7	SPAC3H5.06c	DNA polymerase alpha catalytic subunit	2	FLEX, Histone
,	SPAC644.05c	Protein similar to dUTP pyrophosphatase, which maintains dUTP at low levels to prevent misincorporation into DNA	2	MCB 1, MCB 2
	SPAC1071.09c	Protein containing a DnaJ domain, which mediates interaction with heat shock proteins	2	
	SPBC1289.01c; SPBC1539.11c	Unknown function, putative involvement in chitin biosynthesis	2	MCB 1
	SPCC1322.04	Putative UTP-glucose-1-phosphate uridylyltransferase	2	FLEX
	SPCC1322.10	Unknown function, similar to cell-surface proteins and proteoglycans	2	FLEX
	SPAC14C4.09	Unknown function, putative glucanase	2	
	SPBC16A3.07c	Unknown function	2	MCB 1, MCB 2
	SPBC1709.12	Unknown function	2	Ace2
	SPAC17H9.18c	Unknown function	2	FLEX
	SPCC74.07c; SPCC18.01c	Member of SUN family, contains predicted N-terminal signal sequence	2	Ace2, FLEX
	SPCC18.02	Protein with similarity to synaptic vesicle-associated acetylcholine transporter	2	
	SPAC23A1.01c; SPAC19G12.16c	Unknown function, similarity to podocalyxin like, a transmembrane sialomucin important for lymphocyte adhesion and homing	2	Ace2, FLEX, MCB 1
	SPBC21B10.13c; SPAC21B10.13c	Homeobox domain (homeodomain) protein, putative transcription factor	2	
	SPAC23H4.01c; SPAP27G11.01	Unknown function, contains a pleckstrin homology (PH) domain	2	Ace2, FLEX
	SPBC27.04	Unknown function	2	Novel 1
ms2	SPCC4F11.01;	Protein that binds binds chromatin at centromere and is	2	MCB 1
	,			

	SPCC290.04	involved in chromosome segregation		
	SPBC2A9.07c	Unknown function	2	
	SPAC2E1P5.03	Protein containing a DnaJ domain, which mediates interaction with heat shock proteins	2	Ace2, MCB 1
	SPBC31F10.17c	Unknown function	2	FLEX, Novel 1
	SPBC32F12.10	Protein with phosphoglucomutase or phosphomannomutase C-terminal domain	2	FLEX
	SPBC3E7.12c	Unknown function, possible role in regulation of chitin synthase	2	Ace2, MCB 1
rgf3	SPCC645.06c	Protein containing a pleckstrin homology (PH) and a RhoGEF (GTPase exchange factor) domain	2	
	SPBC651.04	Unknown function	2	FLEX
mrc1; huc1	SPAC694.06c	Protein required for DNA replication checkpoint	2	MCB 1, MCB 2
	SPBC83.18c	Protein containing a C2 domain, which may be involved in calcium-dependent phospholipid binding	2	Ace2
	SPCC965.14c	Member of cytidine and deoxycytidylate deaminase zinc-binding region family	2	FLEX
cdc18	SPBC14C8.07c	Protein that couples cell cycle signals to DNA replication machinery and induces replication	2	MCB 1, MCB 2
cdc22	SPAC1F7.05	Ribonucleoside-diphosphate reductase large chain, likely required for initiation of DNA replication	2	MCB 1, MCB 2
cdm1	SPBC12D12.02c	DNA polymerase delta subunit	2	FLEX, Novel 2
cdt1	SPBC428.18	Protein that coordinates completion of S phase with onset of mitosis	2	MCB 1, MCB 2
cdt2	SPAC17H9.19c	Protein required for DNA replication	2	MCB 1, MCB 2
cig2; cyc17	SPAPB2B4.03	Major G1/S-phase cyclin, promotes onset of S phase	2	FLEX
cut2	SPBC1815.02c; SPBC14C8.01c	Securin; required for sister chromatid separation	2	Ace2, FLEX
dfp1; him1; rad35	SPCC550.13	Regulatory subunit of the Hsk1p-Dfp1p kinase copmlex involved in S phase initiation	2	FLEX, MCB 1
eng1	SPAC821.09	Endo-beta-1,3-glucanase required for cell separation	2	FLEX
exg1	SPBC1105.05	Putative exo-beta-1,3-glucanase	2	Novel 2
fin1	SPAC19E9.02	NimA family kinase; regulates spindle formation and recruitment of Plo1p to SPB, promotes chromatin condensation	2	FLEX
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klp8	SPAC144.14	Protein containing a kinesin motor domain	2	
meu19		Non-coding RNA	2	
	SPAP14E8.02	Unknown function	2	MCB 1, MCB 2
par2; pbp2	SPAC6F12.12	Protein phosphatase PP2A, B' regulatory subunit, required for cytokinesis, morphogenesis, and stress tolerance	2	Ace2
rep2	SPBC2F12.11c	Zinc finger transcriptional activator, MBF transcriptional complex	2	
rpc17	SPAPB1E7.10	Unknown function	2	
	SPBPB2B2.13	Protein similar to galactokinase, which catalyzes first step in galactose metabolism	2	
	SPAPJ760.03c	Unknown function	2	Ace2, FLEX
mid2	SPAPYUG7.03c	Protein required for septin function and stability during cytokinesis	2	Ace2, MCB 1
rad21	SPCC338.17c	Cohesin complex subunit, double-strand-break repair protein	2	
rph1; pfh1; pif1	SPBC887.14c	ATP-dependent DNA helicase involved in telomere maintenance, DNA replication, and DNA repair	2	
psm3; smc3	SPAC10F6.09c	Cohesin complex subunit, involved in sister chromatid cohesion and progression through mitosis	2	MCB 2
ste9; srw1	SPAC144.13c	Protein required for mating and sporulation, may regulate anaphase promoting complex	2	
ssb1; rad11	SPBC660.13c	Single-stranded DNA-binding protein subunit, required for DNA replication	2	MCB 1, MCB 2, Novel 1
ulp1	SPBC19G7.09	Ubl2p-specific protease	2	FLEX, MCB 1
	SPAC343.20	Unknown function	2	
	SPCC63.13	Protein containing a DnaJ domain, which mediates interaction with heat shock proteins	2	
	SPBC839.02; SPBC24E9.02	Unknown function, contains an N-terminal arrestin (or S- antigen) domain, possibly fungal specific	2	
cdc4	SPAP8A3.08	EF-hand component of actomyosin contractile ring, required for cytokinesis	2	Ace2, Novel 3
cdc10	SPBC336.12c	Component of MBF transcriptional activation complex involved in control of START	2	
bgs4; cwg1	SPCC1840.02c	Putative 1,3-beta-glucan synthase component, cell wall synthesis	2	
	SPAC11E3.10	Unknown function, member of VanZ-like family	2	
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	SPAC22F8.04	Unknown function	2	MCB 1
	SPAC22G7.02	Unknown function	2	Ace2, Novel 3
	SPAC27D7.12c	Unknown function	2	MCB 1
	SPBC2A9.13	Unknown function	2	Ace2
	SPAC2F7.14c	Protein similar to 3'-5' exoribonuclease required for 3' processing of ribosomal 5.8S rRNA and component of 3'-5' exosome complex	2	MCB 1
	SPBC32C12.03c	Protein with protein kinase domain, similar to S. pombe Kin1p, a putative serine-threonine protein kinase involved in regulating cell polarity	2	FLEX, MCB 2
	SPCC4F11.03c	Unknown function	2	MCB 1
	SPAC4H3.11c	Unknown function	2	Histone
	SPCC553.12c; SPCC794.13	Unknown functionl	2	MCB 1
	SPCC794.15	Unknown function	2	
	SPBC9B6.07; SPAC9B6.07	Unknown function, possible role in maturation of 25S rRNA	2	
chs5	SPAC6G9.12	Protein with fibronectin domain involved in cell surface binding, and BRCT domain found in checkpoint proteins, similar to chitin synthase	2	FLEX
cnp1; sim2	SPBC1105.17	CENP-A-like protein, histone H3 variant specific to inner centromeres and required for chromosome segregation	2	FLEX, MCB 2
eso1; eco1	SPBC16A3.11	DNA polymerase eta, involved in sister chromatid cohesion	2	FLEX, MCB 1
	SPBPB21E7.10; SPAPB21E7.10	Unknown function	2	
pob1	SPBC1289.04c	Protein required for cell polarity and cell separation	2	Ace2
	SPCC1795.10c	Unknown function	3	Ace2
	SPBC17G9.06c	Unknown function	3	Ace2
	SPBC19C7.04c	Unknown function	3	
	SPCC338.12	Unknown function	3	Ace2, MCB 1, Novel 3
hht1	SPAC1834.04	Histone H3.1	3	Histone, MCB 1
hht2	SPBC8D2.04	Histone H3.2	3	Histone
hht3; clo5	SPBC1105.11c	Histone H3.3	3	Histone
hhf1; ams1	SPAC1834.03c	Histone H4.1	3	Histone, MCB 1
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hhf2; ams3	SPBC8D2.03c	Protein similar to histone H4.1, contains a core histone domain	3	Histone
hhf3; ams4	SPBC1105.12	Histone 4.3	3	Histone
nta1	SPCC622.08c	Histone H2A-alpha	3	Histone, MCB 1
hta2	SPAC19G12.06c	Histone H2A-beta	3	Histone
htb1	SPCC622.09	Histone H2B-alpha	3	Histone, MCB 1
oht1	SPBC11B10.10c	Histone H2A variant	3	
	SPBPJ4664.02	Unknown function, possible cell surface glycoprotein	3	
orl36		Non coding RNA	3	
sap1	SPCC1672.02c	DNA-binding protein required for growth and mating type switching	3	
sod2	SPAC977.10	Sodium/proton antiporter	3	
	SPAC1F7.03	Unknown function	3	
	SPCC306.08c	Malate dehydrogenase, mitochondrial precursor	3	
	SPAC1142.02c; SPAC17G6.19c	Unknown function, contains three TPR domains	3	FLEX
	SPBC1105.14	Protein containing two zinc finger DNA binding domains, possible role in proteasome regulation	3	
	SPAC12G12.07c	Unknown function, domain similar to integrin-a cytoplasmic region	3	
	SPBC1348.10c; SPAC1348.10c	Member of lysophospholipase catalytic domain family, putative lysophospholipase precursor	3	MCB 1
	SPAC806.09c; SPAC1639.01c	SUR4 family protein, putative fatty acid elongation protein	3	Ace2
	SPBC16G5.05c	Protein containing MSP domain, possible type II integral ER membrane protein involved in inositol regulation	3	
	SPCC1906.01	Mannose-1-phosphate guanyltransferase	3	
	SPBC19G7.16	Member of IWS1 C terminus containing family, possible roles in in transcription regulation and transcription elongation	3	Novel 3
	SPBC21B10.09; SPAC21B10.09	Protein similar to acetyl-CoA transporter	3	
	SPAC22G7.01c; SPAPJ696.03c	Protein containing metallopeptidase family M24 domain, similar to x-prolyl aminopeptidase	3	
	SPBPJ758.01; SPBC23E6.01c	Protein with RNA recognition motifs, similar to U1 snRNA- associated protein that suppresses splicing defects and mediates	3	

		recombination		
	SPBC28F2.11	Protein with a high mobility HMG-box domain	3	
	SPBC31F10.16	Unknown function	3	Ace2
	SPBC337.20; SPBC1734.04	Protein similar to cis Golgi protein, putative involvement in protein glycosylation in the golgi	3	MCB 1
	SPAC343.13	Member of PET112 family, may be involved in mitochondrial gene translation	3	
	SPAC631.01c	Member of F-actin capping protein beta subunit family	3	
	SPAC6F6.13c	Unknown function, DUF726 domain	3	Ace2
	SPBC83.11	Unknown function, possible role in binding phosphatidylinositol	3	
	SPAC977.09c	Member of lysophospholipase catalytic domain containing family, similar to phospholipase B, which deacylates phosphatidylinositol	3	MCB 1
cam1	SPAC3A12.14	Calmodulin, essential calcium-binding regulatory protein	3	Histone
csx2	SPBC17G9.08c	Protein with putative arf GTPase activation domain and pleckstrin homology domain, similar to GTPase activating protein for ARF	3	Ace2
сур4	SPBP8B7.25	Protein similar to cyclophilin B, a peptidyl prolyl cis-trans isomerase	3	
pas1	SPAC57A10.01; SPAC19E9.03	Cyclin involved in regulation of mating, interacts with Pef1p and Cdc2p kinases	3	
php5	SPBC3B8.02	CCAAT-binding factor subunit, required for growth on non- fermentable carbon sources	3	
rad25	SPAC17A2.13c	14-3-3- protein involved in DNA damage checkpoint control	3	MCB 1
rer1	SPAC22E12.05c	Protein similar to component of COPII-coated vesicles, member of retention of ER proteins family	3	
spd1	SPAC29B12.03	Negative regulator of S phase	4	
rds1	SPAC343.12	Stress response protein	4	
psu1	SPAC1002.13c	Protein required for cell wall integrity, member of SUN protein family	4	
	SPAC13G6.10c	Unknown function	4	MCB 1
	SPAP7G5.06	Protein similar to amino acid permease, a proton symport transporter for all naturally-occurring L-amino acids	4	
	SPAC5H10.06c	Protein similar to alcohol dehydrogenase IV, which is involved in carbohydrate metabolism	4	

	SPAC1039.02	Unknown function, possible membrane protein	4	
	SPAC1039.01	Member of amino acid permease family of membrane transporters	4	
	SPBC119.10	Asparagine synthetase	4	Novel 3
	SPCC1235.11	Unknown function, member of UPF0041 uncharacterized protein family	4	
	SPCC126.09	Member of ZIP zinc transporter family, possible metal transporter and vacuolar membrane protein	4	
	SPBC1271.07c	Protein containing acetyltransferase (GNAT) domain	4	FLEX
	SPBC1271.08c	Unknown function	4	
	SPAC139.02c	Probable mitochondrial oxaloacetate transporter	4	
	SPBC13G1.09	Member of bystin family, possible role in 35S pre-rRNA processing into 18S rRNA	4	
	SPCC1494.06c	Member of the DEAD or DEAH box ATP-dependent RNA helicase, possible role in rRNA processing	4	
	SPCC1682.08c	Protein containing six Pumilio-family RNA binding domains, possible role in mRNA metabolism	4	
	SPBC16D10.06	Member of ZIP zinc transporter family	4	
	SPCC1739.01; SPCC1906.05	Member of zinc finger family, which bind DNA or RNA	4	
	SPCC1795.12c	Unknown function	4	FLEX
	SPBC17D1.06; SPCC17D1.06	Member of the DEAD or DEAH box ATP-dependent RNA helicase	4	FLEX
pof6	SPCC18.04	Protein involved in cell division, contains F-box domain	4	Novel 3
	SPCC18.05c	Protein containing nine WD domains (WD-40 repeat), possible membrane receptor	4	Novel 3
	SPCC1827.06c	Aspartate semialdehyde dehydrogenase	4	FLEX
rrn3	SPAC18G6.11c	Protein involved in initiation of transcription of rDNA promoter	4	
	SPAC1F12.05	Unknown function	4	
	SPAC212.08c	Telomeric protein of unknown function, possibly S. pombe specific	4	
	SPAC212.10	Pseudogene; malic acid transport protein; truncated C at terminal	4	
	SPAC24B11.10c	Unknown function, possible protoplast regeneration protein that stimulates chitin synthase III activity	4	
	SPBC25B2.08	Unknown function	4	FLEX

	SPAC2C4.18;	Protein with RNA recognition motif, possible splicing factor that	4	
	SPAC25G10.01	activates pre-mRNA splicing		
	SPBC29A3.01	Member of P-type ATPase, similar to copper-transporting ATPase	4	
	SPAC2C4.11c	Unknown function	4	
	SPAC323.07c	Member of the MatE family of integral membrane proteins	4	Novel 3
	SPBC365.16	Unknown function	4	
	SPBC3B8.06	Unknown function	4	
	SPCC548.06c	Protein similar to putative H+-glucose symporter involved in glucose transport	4	Novel 3
arg5	SPBC56F2.09c	Protein similar to amidotransferase small subunit of carbamoylphosphate synthetase	4	
	SPCC594.04c	Unknown function	4	
gmh2	SPAC5H10.13c	Protein similar to alpha-1,2-galactosyltransferase	4	MCB 1
	SPAC6B12.07c	Protein with zinc finger and N-terminal domain that may be involved in G protein associated signal transduction	4	
	SPAC6G9.02c	Protein with five Pumilio-family (Puf) RNA binding domains	4	
	SPCC757.11c	Unknown function	4	
ibp1	SPBC24E9.07; SPBC839.07	Protein phosphatase, rhodanese-like domain	4	Novel 3
	SPAC869.02c	Member of globin family of oxygen transporters, similar to flavohemoglobin that protects from stress	4	
	SPBC8E4.03	Protein with arginase family domain, similar to agmatine ureohydrolase	4	
	SPAC9.10	Member of amino acid permease family of membrane transporters	4	
cig1	SPCC645.01; SPCC4E9.02	B-type cyclin involved in G1 to S phase transition	4	FLEX, MCB 1
csx1	SPAC17A2.09c	Protein containing three RNA recognition motifs, similar to U1 snRNA-associated protein	4	
dak1; dak2	SPAC977.16c	Dihydroxyacetone kinase, isoenzyme II	4	Novel 3
gpd2	SPAC23D3.04c	Glycerol-3-phosphate dehydrogenase	4	Novel 3
mae1	SPAPB8E5.03	Malate transporter	4	
	SPCP1E11.08	Protein similar to nuclear protein involved in ribosome biogenesis	4	
	SPBP8B7.15c	Protein similar to Polyadenylation Factor I complex component	4	
		T and confidences		

		required for mRNA cleavage and polyadenylation		
pac2	SPAC31G5.11	Regulatory protein involved in sexual development via cAMP-independent pathway	4	
	SPAPB24D3.09c	Protein with ABC transporter domains, similar to brefeldin A resistance protein involved in multidrug resistance	4	
	SPBPB2B2.06c	Protein with calcineurin-like phosphoesterase domain	4	
	SPBP7E8.01; SPBPB7E8.01	Unknown function	4	
TF2-1		Retrotransposable element; tf2-type transposon	4	
TF2-10		Retrotransposable element; tf2-type transposon	4	
TF2-2		Retrotransposable element; tf2-type transposon	4	
TF2-3; TF2-4		Retrotransposable element; tf2-type transposon	4	
TF2-5		Retrotransposable element; tf2-type transposon	4	
TF2-6		Retrotransposable element; tf2-type transposon	4	
TF2-7		Retrotransposable element; tf2-type transposon	4	
TF2-8		Retrotransposable element; tf2-type transposon	4	
TF2-9		Retrotransposable element; tf2-type transposon	4	
bgl2	SPAC26H5.08c	Protein similar to beta-glucosidase, a cell wall endo-beta-1,3-glucanase	4	
	SPBC11C11.05	Member of yeast cell wall synthesis protein KRE9 or KNH1 family	4	FLEX
	SPAC11D3.04c	Unknown functionhypothetical protein; sequence orphan; shows expression on microarray	4	
	SPBC1271.10c	Protein similar to membrane transporter	4	
	SPBC12C2.12c; SPBC21D10.03c	Protein similar to glyoxalase I, contains glyoxalase, bleomycin resistance protein or dioxygenase family domains	4	
	SPBC1347.09	Unknown function	4	
	SPAC1486.09	Protein similar to protein that functions in 20S proteasome maturation and 26S proteasome assembly	4	FLEX
	SPCC1494.07	Unknown function	4	Novel 3
	SPCC1494.08c	Unknown function	4	Novel 2
	SPAC14C4.12c	Unknown function, contains SWIRM domain	4	
	SPAC1527.03	Unknown function, contains La domain	4	
	SPAC16C9.03	Possible role in nuclear export of 60S ribosomal subunits	4	

SPBC16D10.02	Putative DNA-(amino)methyltransferase	4	Novel 3
SPBC1711.07	Protein containing three WD domains (WD-40 repeat), possible role in ribosome assembly	4	MCB 1
SPAC17A2.06c	Unknown function, similar to protein involved in vacuolar sorting	4	
SPBC17D11.08	Unknown function, four WD domains (WD-40 repeats)	4	
SPCC1827.05c	Protein with RNA recognition motif, similar to nucleolar protein	4	
SPCC18B5.07c; SPBC18B5.07c	Member of RanBP1 domain containing family, similar to nuclear pore protein (nucleoporin)	4	
SPCC1919.05	Protein containing nine TPR domains, similar to superkiller 3, which protects cells from RNA viruses	4	
SPAC19B12.11c	Unknown function, similar to putative nuclear pore protein involved in bud site selection	4	FLEX, Novel 1
SPAC19G12.09	Protein with aldo-keto reductase family domain, similar to aldehyde reductase	4	
SPAC1B3.08	Member of PCI (proteasome, COP9-complex and eIF3) or PINT (Proteasome, Int-6, Nip-1 and TRIP-15) domain family	4	MCB 1
SPAC823.03; SPAC1E11.03	Protein with kinase domain, similar to CDC-like kinase 2, which may regulate mRNA splicing	4	
SPBC215.13	Unknown function, similar to protein involved in vesicle formation in endoplasmic reticulum	4	MCB 1
SPAC222.09	Unknown function	4	
SPAC23H4.15	Member of DUF663 protein of unknown function family, possible role in rRNA processing and 40S ribosomal subunit biogenesis	4	FLEX
SPBC24C6.10c	Unknown function	4	
SPBC19F5.05c; SPBC25D12.01c	Unknown function	4	
SPAC27D7.09c	Unknown function	4	
SPAC26F1.07	Protein similar to aldehyde reductase that reduces carbonyl- containing substrates and metabolizes xenobiotics	4	
SPAC27D7.11c	Unknown function	4	Novel 3
SPAC27F1.06c	Protein with FKBP-type peptidyl-prolyl cis-trans isomerase domain	4	Ace2
SPBC29A10.08	Glycolipid-anchored surface protein precursor	4	
SPAC29B12.08	Unknown function	4	MCB 1

	SPAC31A2.07c	Putative RNA helicase, possible role in ribosome biogenesis	4	
	SPAC31G5.02	Possible role in role cell wall organization and biogenesis	4	
	SPCC31H12.01; SPCC1183.11	Member of mechanosensitive ion channel family	4	
	SPAC328.05	Protein containing three RNA recognition motifs, possible role in protein-nucleus export	4	FLEX
gps2	SPBC365.14c	Putative UDP-glucose 4-epimerase involved in UDP-galactose synthesis and protein glycosylation	4	
	SPAC3G9.05	Unknown function, similar to cell polarity and cell fusion protein	4	
	SPBC405.02c; SPBC4C3.01	Unknown function	4	FLEX
	SPCC417.05c	Unknown function, similar to protein that stimulates chitin synthase III activity	4	
	SPBC428.10	Unknown function, similar to cell surface flocculin required for invasive and pseudohyphal growth	4	Novel 3
	SPAC521.02	Unknown function	4	
sst1	SPAC521.04c	Member of sodium or calcium exchanger protein family of membrane transporters	4	
	SPCC553.10	Unknown function	4	FLEX, MCB 1
	SPAC57A10.09c	Protein similar to DNA-binding and DNA-bending protein involved in transcriptional activation, contains HMG family domain	4	
	SPAC637.13c	Unknown function, pleckstrin homology (PH) domain	4	
	SPBC651.01c; SPBC725.18c	Unknown function, similar to a putative nucleolar GTP-binding protein required for ribosomal subunit biogenesis	4	FLEX
	SPBC660.06	Unknown function	4	
	SPAC688.11	Protein with actin binding domains, similar to talin-like protein required for hyphal growth	4	
	SPCC794.03	Member of amino acid permease family of membrane transporters	4	
	SPCC794.11c	Protein with actin binding domain, possible role in formation of clathrin coats at the Golgi and endosomes	4	MCB 1
	SPAC821.03c	Unknown function	4	
	SPAC9.07c	Putative GTP-binding protein	4	
	SPAC9E9.04	Unknown function, contains predicted N-term signal sequence and transmembrane helices	4	FLEX

cbh2	SPBC14F5.12c	DNA binding protein, possible role in chromosome segregation, role in histone tail modifications at centromere	4	
cdc2; swo2	SPBC11B10.09	Cyclin-dependent kinase, regulates cell cycle transitions G1/S and G2/M	4	
cds1	SPCC18B5.11c	Protein kinase involved in unreplicated DNA checkpoint response	4	FLEX
	SPACUNK4.15	Unknown function	4	Ace2
dim1	SPBC336.02	Protein similar to ribosomal RNA adenine dimethylases	4	
git3	SPCC1753.02c	Protein involved in cAMP pathway and required for growth under high osmotic stress	4	
myo52; myp5; myo4	SPCC1919.10c	Class V myosin, involved in polarized cell growth and vacuole fusion	4	FLEX, MCB 1
•	SPAC31G5.12c	Unknown function, similar to negative effector of RNA polymerase III	4	
nrd1	SPAC2F7.11	Protein containing four RNA recognition motifs	4	
	SPAPB15E9.01c; SPAPB18E9.06c	Unknown function	4	
	SPAPB18E9.03c	Unknown function	4	
	SPAPB18E9.05c	Unknown function	4	
pcr1; mts2	SPAC21E11.03c	Transcription factor that plays roles in mating, meiosis and stress response	4	
pim1; ptr2; dcd1	SPBC557.03c	GTP-exchange factor (GEF) for Spi1p, required for nucleo- cytoplasmic transport, microtubule function and cytokinesis	4	
pka1; git6	SPBC106.10	Catalytic subunit of the cAMP-dependent protein kinase	4	
rdp1	SPAC1B1.01	Protein containing a C2H2 type zinc finger domain, binds to DNA damage response elements	4	Ace2
ssp1	SPCC297.03	Protein kinase that mediates rapid osmotic stress response at cell surface	4	
thi1; ntf1	SPAC6G10.01; SPAC1486.10	Regulatory protein for thiamine repressible genes, required forsynthesis of thiazole moiety of thiamine	4	MCB 1
	SPAC6F12.03c	Member of SNARE domain containing family	4	
top2	SPBC1A4.03c	DNA topoisomerase II	4	MCB 1
trx1; trx2	SPAC7D4.07c	Putative thioredoxin involved inresponse to heavy metals	4	FLEX
uvi15	SPBC649.04	Protein essential for stationary phase survival, induced by stress	4	Novel 2

vip1	SPAC10F6.06	Protein containing an RNA recognition motif	4	
	SPCC320.02c; SPCC1235.01	Unknown function	N(1)	FLEX, Histone
prl3		Non-coding RNA	N(1)	
hsk1	SPBC776.12c	Protein kinase of the Hsk1p-Dfp1p complex involved in S phase initiation	N(1,2)	
	SPCC338.08	Unknown function	N(1,2)	
mfm2	SPAC513.03	Precursor polypeptide for mating pheromone M factor produced by h- cells	N(1,2)	
spk1	SPAC31G5.09c	MAP kinase (MAPK) acting in the mating and sporulation pathways	N(1,2)	
byr2; ste8	SPBC2F12.01; SPBC1D7.05	MAP kinase kinase kinase acting upstream of MAPKK Byr1p and MAP kinase Spk1p in pheromone signaling pathway	N(1,2)	
	SPAC1006.06	Protein with RhoGEF domain, similar to Rho GDP-GTP exchange factor activated by cell wall defects	N(1,2)	
	SPAC12G12.06c	Probable RNA 3'-terminal phosphate cyclase	N(1,2)	
	SPCC1322.09	Unknown function	N(1,2)	MCB 2
	SPAC14C4.05c	Unknown function	N(1,2)	FLEX, MCB 2
	SPBC1683.07	Protein similar to alpha-glucosidase	N(1,2)	Ace2
hril	SPAC20G4.03c	Translation initiation factor 2 alpha kinase, may play role in negative regulation of eIF2alpha in response to stress	N(1,2)	
	SPBC365.01	Unknown function, CRAL-TRIO domain and a CRAL or TRIO N terminus domain	N(1,2)	
din1	SPAC19D5.06c	Unknown function	N(1,2)	Novel 2
mei2	SPAC27D7.03c	RNA-binding protein involved in meiosis	N(1,2)	
spm1; pmk1	SPBC119.08	MAP kinase involved in maintenance of cell wall integrity	N(1,2)	FLEX
	SPCC965.06	Protein similar to potassium voltage-gated channel	N(1,2,3)	Novel 1
cnd2	SPCC306.03c	Subunit of condensin complex involved in chromosome condensation	N(1,3)	
isp6; prb1	SPAC4A8.04	Putative subtilase-type proteinase, role in sexual differentiation+E49	N(1,3,4)	
	SPAC869.05c	Member of sulfate transporter family, similar to sulfate permease	N(1,4)	
	SPAC1002.17c	Protein with phosphoribosyl transferase domain, possible role in pyrimidine salvage pathway	N(1,4)	

	SPAC1610.04	Unknown function	N(1,4)	
	SPCC16C4.06c	Protein with tRNA pseudouridine synthase domains	N(1,4)	Novel 1
sim4	SPBC18E5.03c	Centromere-associated protein required for chromosome segregation and silencing	N(1,4)	
	SPBC19G7.07c	Member of PPR repeat containing family	N(1,4)	
	SPCC330.15c;	Member of pyridoxal phosphate dependent enzyme family, similar	N(1,4)	
	SPCC320.14	to racemase that catalyzes the racemisation of L-serine to D-serine		
	SPBC428.17c	Unknown function	N(1,4)	
	SPCC553.07c	Member of impB, mucB or samB family, possible role as translesion DNA repair polymerase	N(2,3)	
	SPBC800.11	Protein with inosine-uridine preferring nucleoside hydrolase domain	N(2,3)	
	SPAC750.05c	Telomeric protein of unknown function, highly similar to S. pombe SPAC977.01, SPAC1348.02 and SPBPB2B2.19c	N(2,3)	
	SPBC1348.02; SPAC1348.02	Telomeric protein of unknown function, highly similar to S. pombe SPAC977.01, SPAC750.05C and SPBPB2B2.19c	N(2,3)	
	SPBPB2B2.19c	Telomeric protein of unknown function, highly similar to S. pombe SPAC977.01, SPAC1348.02 and SPAC750.05C	N(2,3)	Histone
	SPAC977.01	Telomeric protein of unknown function, highly similar to S. pombe SPAC1348.02, SPAC750.05C and SPBPB2B2.19c	N(2,3)	FLEX
	SPBC409.22c; SPBC1306.01c	Protein with elongation factor Tu GTP binding domain, similar to mitochondrial translation elongation factor G	N(2,3)	
	SPAC17G6.03	Protein with calcineurin-like phosphoesterase domain	N(2,3)	
	SPBC18E5.07	Unknown function	N(2,3)	Novel 2
	SPBC21B10.07; SPAC21B10.07	Protein with glycosyl hydrolase family 16 domain	N(2,3)	
	SPAC2E1P3.04	Protein with possible role in detoxifying extracellular amines and nitrogen metabolism	N(2,3)	Ace2, Novel 3
	SPAC29A4.05	Protein similar to calmodulin 1, which regulates the calcium- dependent activity of enzymes including phosphatases	N(2,4)	
	SPAC631.02	Protein with two bromodomains, which interact with acetylated lysine	N(3,4)	
	SPBC1271.09	Member of sugar (and other) transporter family, possible role in inositol metabolism	N(3,4)	Novel 3

	SPCC364.07; SPCC4G3.01	Protein similar to 3-phosphoglycerate dehydrogenase, which catalyzes first step in synthesis of serine	N(3,4)	
	SPAC3A11.10c	Member of Rnal dipeptidase family, zinc-dependent metalloproteinases that hydrolyze various dipeptides	N(3,4)	
	SPAC664.03	Member of Paf1 family, components of RNA polymerase II associated complexes	N(3,4)	Ace2, FLEX
pro1	SPAC821.11	Protein similar to gamma-glutamyl phosphate reductase involved in proline biosynthesis	N(3,4)	
fim1	SPBC1778.06c	Fimbrin, role in actin organization during medial ring formation and polarized growth	N(3,4)	
	SPBPB21E7.09; SPAPB21E7.09	Protein similar to L-asparaginase II	N(4)	FLEX, MCB 1, Novel 3

^a Gene descriptions are based on the information in PombePD (www.incyte.com/control/tools/proteome) and *S. pombe* GeneDB (www.genedb.org/genedb/pombe/index.jsp) databases.

Genes are sorted according to the cluster they belong to; genes in bold are of 'high amplitude' and the unclassified genes (N) are listed at the bottom of the list.