

**Supplementary Table 14:****(A) Different dispensability for one to one orthologous genes in the two yeasts**

	<b>Process</b>	<b>Number of orthologous pairs</b>	<b>S. p essential S. c non-essential</b>	<b>S. c essential S. p non-essential</b>
1	Mitochondrial translation	69	69	0
2	Other mitochondrial function	21	17	4
3	Iron-sulphur cluster assembly	5	3	2
4	V-type ATPase	12	12	0
5	Golgi /ER transport function	27	14	13
6	RNA processing & nuclear export	57	25	32
7	Proteasome/APC/ubiquitin associated	11	8	3
8	Neddylation associated	4	4	0
9	SUMOylation associated	4	0	4
10	Spindle/kinetochore/centromere associated	17	6	11
11	tRNA modification	5	2	3
12	Mitotic exit & SIN signalling, cytokinetic process	11	3	8
13	DNA replication checkpoint	5	0	5
14	Signal transduction, various	24	14	10
15	DNA replication/recombination/repair	11	7	5
16	Transcription and other chromatin associated	30	14	16
17	Cytoplasmic translation	9	3	6
18	Glycosylation and other ER associated	14	11	3
19	N-acetyltransferase related	4	2	2
20	Cortical actin cytoskeleton related	2	2	0
21	Tubulin specific chaperone	4	4	0
22	Proteolysis (peptidases)	2	2	0
23	Tryptophan metabolism	7	7	0
24	Methionine threonine glutamate metabolism	9	9	0
25	Other amino acid metabolism	4	3	1
26	Purine/pyrimidine metabolism & salvage	3	2	1
27	Ergosterol metabolism	4	3	1
28	Heme metabolism	3	0	3
29	Miscellaneous metabolism	7	4	3
30	Other processes	16	12	4
31	Unknown processes	10	6	4
<b>Total</b>		<b>411</b>	<b>268</b>	<b>143</b>

Classification of the 411 orthologous pairs with different dispensability in the two yeasts (blue in **Fig. 4a**) into a biological process. 'GO slim' was used to identify processes that may have a similar number of essential genes in each organism but where the specific essential genes differ. Out of 31 biological terms, 22 are shown in **Fig. 4b** in the main text.

**(B)** List of orthologous pairs with different dispensability in the two yeasts

Systematic ID	Gene name	Gene product
<b>Essential in fission yeast, but non-essential in budding yeast</b>		
<b>1. Mitochondrial translation</b>		
SPAC27E2.06c		mitochondrial methionine-tRNA ligase
SPAC3A12.19		mitochondrial ribosomal protein subunit L27
SPBC14C8.16c	bot1	mitochondrial ribosomal protein subunit S35
SPBC30D10.12c	rsm27	mitochondrial ribosomal protein subunit S27
SPCC18B5.08c		mitochondrial isoleucine-tRNA ligase
SPCC736.03c		mitochondrial phenylalanyl-tRNA synthetase
SPCC576.06c		mitochondrial tyrosine-tRNA ligase
SPCC18.08		mitochondrial lysine-tRNA ligase
SPBC24C6.03		mitochondrial proline-tRNA ligase (predicted)
SPBC1198.10c		mitochondrial asparagine-tRNA ligase Slm5
SPAC24C9.09		mitochondrial threonine-tRNA ligase
SPAC4G8.09		mitochondrial leucine-tRNA ligase
SPAC343.13		mitochondrial glutamyl-tRNA amidotransferase
SPAC3G9.13c	msw1	mitochondrial tryptophan-tRNA ligase Msw1 (predicted)
SPAPB1A10.11c		glutamyl-tRNA synthetase, mitochondrial
SPBC646.03		glutamyl-tRNA amidotransferase
SPBC9B6.04c	tuf1	mitochondrial translation elongation factor EF-Tu Tuf1
SPBC1306.01c		mitochondrial translation elongation factor G
SPAP8A3.11c		mitochondrial GTPase Mtg2
SPBC83.06c		mitochondrial ribosomal protein subunit L36
SPAC12G12.08	mrpl6	mitochondrial ribosomal protein subunit L16
SPAC1486.07c	mrpl19	mitochondrial ribosomal protein subunit L19
SPAC16E8.10c		mitochondrial ribosomal protein subunit S7
SPAC1751.02c	rsm19	mitochondrial ribosomal protein subunit S19
SPAC1952.14c	mrpl25	mitochondrial ribosomal protein subunit L25
SPAC24C9.13c	mrp1	mitochondrial ribosomal protein subunit Mrp10
SPAC23H3.07c	mrp2	mitochondrial ribosomal protein subunit S14
SPAC2F7.15	rsm24	mitochondrial ribosomal protein subunit S24
SPAC31A2.03	mrpl11	mitochondrial ribosomal protein subunit L11
SPAC31A2.08	mrp2	mitochondrial ribosomal protein subunit L23
SPAC29A4.03c		mitochondrial ribosomal protein subunit S9
SPCC16A11.11	mrpl31	mitochondrial ribosomal protein subunit L31
SPCC16C4.15	rml2	mitochondrial ribosomal protein subunit L2
SPCC1739.02c	mrpl22	mitochondrial ribosomal protein subunit L22
SPAC4F8.02c	mrpl4	mitochondrial ribosomal protein subunit L40
SPAC4F8.05c	mrpl28	mitochondrial ribosomal protein subunit L28
SPAC4F8.06		mitochondrial ribosomal protein subunit S12
SPAC4G9.17c	mrps5	mitochondrial ribosomal protein subunit S5
SPAC343.02	img1	mitochondrial ribosomal protein subunit L19
SPAC343.08c	mrp17	mitochondrial ribosomal protein subunit Mrp17
SPCC1393.11		mitochondrial ribosomal protein subunit L20
SPAC644.17c	mrpl9	mitochondrial ribosomal protein subunit L9
SPBC14C8.10	mrpl24	mitochondrial ribosomal protein subunit L28
SPBC1539.01c		mitochondrial ribosomal protein subunit L15
SPBC1604.13c	mrpl32	mitochondrial ribosomal protein subunit L32

SPBC16A3.04	rsm25	mitochondrial ribosomal protein subunit Rsm25
SPBC19C2.12	mrpl51	mitochondrial ribosomal protein subunit L51
SPBC1271.13	mrpl8	mitochondrial ribosomal protein subunit L8
SPBC11B10.04c	mrps28	mitochondrial ribosomal protein subunit S28
SPBC1105.03c	mrpl16	mitochondrial ribosomal protein subunit L16
SPAP19A11.05c	mrp7	mitochondrial ribosomal protein subunit L27
SPBC16G5.04	mrpl23	mitochondrial ribosomal protein subunit L13
SPBC21C3.04c		mitochondrial ribosomal protein subunit L34
SPBC2F12.02c	mrpl7	mitochondrial ribosomal protein subunit L7
SPBC2F12.10		mitochondrial ribosomal protein subunit L35
SPBC839.09c	mrp21	mitochondrial ribosomal protein subunit Mrp21
SPBC887.07	mrpl38	mitochondrial ribosomal protein subunit L38
SPCC18B5.04	rsm18	mitochondrial ribosomal protein subunit S18
SPCC1919.08c	mrpl33	mitochondrial ribosomal protein subunit YmL33
SPCC736.10c	mrps8	mitochondrial ribosomal protein subunit S8
SPCC645.09	mrpl37	mitochondrial ribosomal protein subunit L37
SPCC4G3.06c	mrpl4	mitochondrial ribosomal protein subunit L4
SPCC1795.07		mitochondrial ribosomal protein subunit S37
SPCC126.05c	mrpl17	mitochondrial ribosomal protein subunit L17
SPBC409.14c	mrps17	mitochondrial ribosomal protein subunit S17
SPBC3B9.14c	mrpl3	mitochondrial ribosomal protein subunit L3
SPBC354.06	mrps16	mitochondrial ribosomal protein subunit S16
SPBC29A3.15c	rsm23	mitochondrial ribosomal protein subunit S23
SPBP4H10.15		aconitate hydratase/mitochondrial ribosomal protein subunit L49
<b>2. Other mitochondrial processes</b>		
SPBC119.18		mitochondrial distribution and morphology protein Mdm35
SPBC1718.06	msp1	mitochondrial GTPase Msp1
SPBC8D2.15		mitochondrial lipoic acid synthetase (predicted)
SPAC22E12.10c	etp1	mitochondrial type I [2Fe-2S] ferredoxin Etp1/cytochrome oxidase cofactor Cox15, fusion
SPBC4F6.17c		mitochondrial heatshock protein Hsp78 (predicted)
SPBC776.07		mitochondrial Mam33 family protein
SPAP8A3.10		mitochondrial intermembrane space protein sorting protein
SPBC28F2.06c	mdm12	Mdm10/Mdm12/Mmm1 complex subunit Mdm12
SPBC27B12.01c	mmm1	Mdm10/Mdm12/Mmm1 complex subunit Mmm1 (predicted)
SPAC17H9.17c	mdm1	Mdm10/Mdm12/Mmm1 complex subunit Mdm10 (predicted)
SPBC19C2.11c		mitochondrial outer membrane protein (predicted)
SPBC18H10.17c		mitochondrial protein Mhr1 (predicted)
SPCC1682.09c		mitochondrial guanine nucleotide transporter
SPAC26H5.12	rpo41	mitochondrial DNA-directed RNA polymerase
SPAC2F3.04c	rim1	mitochondrial single-stranded DNA binding protein Rim1
SPAC1002.08c	mtf1	mitochondrial RNA polymerase specificity factor
SPBC30D10.08	mgm11	mitochondrial DNA repair protein
<b>3. Iron sulfur cluster assembly</b>		
SPCC645.03c	isa1	iron-sulfur protein Isa1
SPBC3B9.17	isa2	iron-sulfur protein Isa2
SPAC21E11.07		iron-sulphur cluster biogenesis protein (predicted)
<b>4. V-type ATPase</b>		
SPAC11E3.07	vma4	V-type ATPase subunit E

SPAC17A2.03c	vma6	V-type ATPase subunit d
SPAC1B3.14	vma3	V-type ATPase subunit c
SPAC2C4.13	vma16	V-type ATPase subunit c''
SPAC343.05	vma1	V-type ATPase subunit A
SPAC637.05c	vma2	V-type ATPase V1 subunit B
SPAC732.01	vma11	V-type ATPase proteolipid subunit
SPAPB2B4.05	vma5	V-type ATPase subunit C
SPAC7D4.10	vma13	V-type ATPase subunit H
SPCC965.03	vma8	V-type ATPase subunit D (predicted)
SPBC3B9.18c	vma7	V-type ATPase subunit F (predicted)
SPCC757.10	vph2	endoplasmic reticulum membrane involved in assembly of the V-ATPase
<b>5. Golgi transport function</b>		
SPAC144.15c	cog1	Golgi transport complex subunit Cog1 (predicted)
SPBC776.10c	cog6	Golgi transport complex peripheral subunit Cog6 (predicted)
SPBC19G7.14c	cog5	Golgi transport complex subunit Cog5 (predicted)
SPBC11B10.03	cog8	Golgi transport complex subunit Cog8 (predicted)
SPAC2F3.10		GARP complex subunit Vps54 (predicted)
SPAC3A12.15	vps53	GARP complex subunit Vps53 (predicted)
SPBC336.11		GARP complex subunit Vps52 (predicted)
SPAC3G6.10c		GARP complex subunit Vps51 (predicted)
SPBC2A9.08c	sec22	SNARE Sec22
SPBC31E1.04	pep12	SNARE Pep12
SPAC13G6.05c		TRAPP complex subunit Bet3 (predicted)
SPAC23H4.03c	erv25	COPII-coated vesicle component Erv25 (predicted)
SPBC9B6.08	clc1	clathrin light chain
SPAC26A3.05	chc1	clathrin heavy chain Chc1 (predicted)
<b>6. RNA processing and nuclear export</b>		
SPAC1D4.14	tho2	THO complex subunit Tho2 (predicted)
SPAC1F3.01	rrp6	exosome subunit Rrp6 (predicted)
SPCC1739.07		substrate-specific nuclear cofactor for exosome activity (predicted)
SPAC167.03c	snu66	U4/U6 x U5 tri-snRNP complex subunit Snu66 (predicted)
SPAC2F3.17c	lsm6	U6 snRNP-associated protein Lsm
SPAC16.02c	srp2	mRNA export factor Srp2
SPBC146.07	prp2	U2AF large subunit (U2AF-59)
SPBC1289.02c	uap2	U2 snRNP-associated protein Uap2
SPBC8D2.09c		U2 snRNP-associated protein Msl1 (predicted)
SPBC1861.08c		U2 snRNP-associated protein Lea1 (predicted)
SPCC126.14	prp18	U5 snRNP-associated protein Prp18
SPBC3E7.13c		splicing factor, SYF2 family
SPBC337.06c	cwf15	complexed with Cdc5 protein Cwf15
SPCC550.02c	cwf5	RNA-binding protein Cwf5
SPCC1620.10	cwf26	complexed with Cdc5 protein Cwf26
SPBC28F2.04c	cwf7	splicing factor Cwf7
SPBC31E1.03	hub1	ubiquitin-like protein modifier Hub1
SPAC19D5.04	ptr1	HECT domain
SPBC409.15		rRNA processing protein Tsr2 (predicted)
SPBC16A3.05c	rae1	RNA export factor Rae1
SPBC428.01c	nup17	nucleoporin Nup107

SPBC3B9.16c	nup12	nucleoporin Nup120
SPAC6G10.07		nuclear cap-binding complex large subunit (predicted)
SPBC13A2.01c		nuclear cap-binding complex small subunit
<b>7. Proteasome /anaphase promoting complex /ubiquitin associated</b>		
SPAC23C11.12	hcn1	anaphase-promoting complex subunit Hcn1
SPBC28E12.01c	apc13	anaphase-promoting complex subunit Apc13
SPBC1A4.01	apc1	anaphase-promoting complex subunit Apc10
SPCC1259.15c	ubc11	ubiquitin conjugating enzyme E2-C
SPBC3D6.11c	slx8	SUMO-targeted ubiquitin-protein ligase E3 Slx8 (predicted)
SPCC790.02	pep3	ubiquitin-protein ligase
SPAC17A5.12	ucp7	UBA/TPR/DNAJ domain protein Ucp7
SPCC18.04	pof6	F-box protein Pof6
<b>8. Neddylaton</b>		
SPAC323.06c	uba5	NEDD8 activating enzyme (predicted)
SPBC12D12.08c	ned8	ubiquitin-like protein modifier Ned8
SPCC777.10c	ubc12	NEDD8-conjugating enzyme Ubc12
SPAC24H6.12c	uba3	NEDD8 activating enzyme
<b>10. Spindle/kinetochore/centromere associated</b>		
SPAC1687.20c	mis6	inner centromere protein Mis6
SPAC23H4.11c	cnl2	centromere localized protein Cnl2
SPAC25B8.14	mal2	kinetochore protein Mal2
SPBC336.15	pic1	INCENP-like
SPBP22H7.09c	mis15	kinetochore protein Mis15
SPBC16A3.11	eso1	sister chromatid cohesion protein Eso1
<b>11. tRNA modification</b>		
SPAC23H4.04		tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase
SPAC4F10.03c		2'-O-ribose methyltransferase
<b>12. Mitotic exit signaling and cytokinetic processes</b>		
SPAC6F6.08c	cdc16	two-component GAP Cdc16
SPAC3G9.14	sak1	transcriptional repressor Sak1
SPCC613.04c	rng3	UCS-domain protein
<b>14. Other signal transduction- various</b>		
SPBC800.09	sum2	G2/M transition checkpoint protein Sum2
SPAC11E3.02c		C2 domain protein
SPAP27G11.07c		serine/threonine protein kinase (predicted)
SPAC22E12.17c	glo3	ARF GTPase activating protein
SPAC22F3.05c	alp41	ADP-ribosylation factor Alp41
SPCC777.05	gtr2	Gtr1/RagA G protein Gtr2
SPBC428.16c	rhb1	Rheb GTPase Rhb1
SPCC1840.01c	mog1	Ran GTPase binding protein Mog1
SPBC21D10.05c	ucp3	GTPase activating protein Ucp3 (predicted)
SPCC645.06c	rgf3	RhoGEF Rgf3
SPAC24H6.05	cdc25	serine/threonine protein phosphatase Cdc25
SPCC1739.12	ppe1	serine/threonine protein phosphatase Ppe1
SPCC970.08		inositol polyphosphate kinase (predicted)

SPAC607.04		inositol polyphosphate kinase (predicted)
<b>15. DNA replication/recombination/repair</b>		
SPAC17G8.03c	dpb3	DNA polymerase epsilon subunit Dpb3
SPBC1734.02c	cdc27	DNA polymerase delta subunit Cdc27
SPBC16G5.12c	top3	DNA topoisomerase III
SPBC577.09		ERCC-8 homolog (predicted) (repair)
SPAC23A1.19c		RecQ type DNA helicase Hrql (predicted)
SPAC26A3.03c	rmi1	RecQ mediated genome instability protein Rmi1
SPAC6F12.05c	tnr3	thiamine diphosphokinase Tnr3
<b>16. Transcription and other chromatin associated processes</b>		
SPAC2F3.03c	rpa49	DNA-directed RNA polymerase I complex subunit
SPBC337.14	rpb4	DNA-directed RNA polymerase II complex subunit Rpb4
SPAC22E12.08	rrn1	RNA polymerase I upstream activation factor complex subunit Rrn10
SPBC336.12c	cdc1	MBF transcription factor complex subunit Cdc10
SPBC725.16	res1	MBF transcription factor complex subunit Res1
SPCC1281.05	rsc7	RSC complex subunit Rsc7
SPAC23H3.10	ssr2	SWI/SNF and RSC complex subunit Ssr2 (predicted)
SPBC146.01	med15	mediator complex subunit Med15 (predicted)
SPCC1259.07		transcriptional regulatory protein Rxt3 (predicted)
SPAC25B8.02	sds3	Clr6 histone deacetylase complex subunit Sds3 (predicted)
SPCC1795.08c		histone acetyltransferase complex subunit (predicted)
SPBC36.05c	clr6	histone deacetylase (class I) Clr6
SPBC83.07	jmj3	Lid2 complex subunit Jmj3
SPCC663.05c	cia1	histone chaperone Cia1
<b>17. Cytoplasmic translation</b>		
SPBC36B7.09	gcn2	eIF2 alpha kinase Gcn2 (predicted)
SPAC56F8.03		translation initiation factor IF2 (predicted)
SPBC3B9.01		Hsp70 nucleotide exchange factor (predicted)
<b>18. Glycosylation and other ER associated processes</b>		
SPAC823.07		GPI-phospholipase A2 activity regulator (predicted)
SPAC4F10.10c		mannosyltransferase complex subunit, Anp family (predicted)
SPAC6G10.09		glucosidase I Gls1 (predicted)
SPAC7D4.15c	ost4	oligosaccharyltransferase subunit Ost4 (predicted)
SPBC409.21	sec66	ER protein translocation subcomplex subunit Sec66 (predicted)
SPAC3C7.11c	cnx1	calnexin
SPBC530.12c	pdf1	palmitoyl protein thioesterase-dolichol pyrophosphate phosphatase fusion 1
SPBC1711.10c	npl4	Cdc48-Ufd1-Npl4 complex component Npl4 (predicted)
SPBC1347.05c		DNAJ domain protein Scj1
SPAC1687.02		CAAX prenyl protease (predicted)
SPAC1F5.06		heat shock protein Lhs1 (predicted)
<b>19. N-acetyltransferase related</b>		
SPAC15E1.08		NatA N-acetyltransferase complex subunit Ard1 (predicted)
SPBC1215.02c	arml	NatB N-acetyltransferase complex non catalytic subunit Arml

<b>20. Cortical actin cytoskeleton related</b>		
SPBC1778.08c	arc3	ARP2/3 actin-organizing complex subunit Arc21
SPAC688.11	end4	Huntingtin-interacting protein homolog
<b>21. Tubulin specific chaperone</b>		
SPAC13D6.05	alp11	tubulin specific chaperone cofactor B
SPAC328.08c		tubulin specific chaperone cofactor C (predicted)
SPBC11C11.04c	alp1	tubulin specific chaperone cofactor D
SPAC22H10.10	alp21	tubulin specific chaperone cofactor E
<b>22. Proteolysis</b>		
SPAC22E12.09c	krp1	kexin
SPBC119.17		metallopeptidase
<b>Metabolism various</b>		
<b>23. tryptophan metabolic process</b>		
SPBC1539.09c	trp1	anthranilate synthase component II trp1 4.1.3.27/5.3.1.24/4.1.1.48
SPBC16G5.08	trp4	phosphoribosylanthranilate transferase Trp4 2.4.2.18
SPAC1834.02	aro1	pentafunctional aromatic polypeptide Aro1 (predicted)
SPAC16E8.04c		chorismate mutase (predicted) 5.4.99.5
SPCC1223.14		chorismate synthase (predicted) 4.2.3.5
SPAC19A8.15	trp2	tryptophan synthase trp2 4.2.1.20
SPCC1442.09	trp3	anthranilate synthase component I
<b>24. Methionine/threonine/glutamate folate metabolism</b>		
SPAC56F8.10	met9	methylenetetrahydrofolate reductase Met9
SPCC1827.06c		aspartate semialdehyde dehydrogenase
SPBC4C3.03		homoserine kinase (predicted)
SPBC19F5.04		aspartate kinase (predicted)
SPBC1709.17		folylpolyglutamate synthase
SPCC1753.04	toll	3'(2'),5'-bisphosphate nucleotidase/inositol-1,4-bisphosphate 1-phosphatase
SPBP8B7.29		para-aminobenzoate synthase (predicted)
SPBC1677.03c		threonine ammonia-lyase
SPAC9E9.06c		threonine synthase (predicted)
<b>25. Other amino acid metabolism</b>		
SPBP19A11.01		glycine decarboxylase complex subunit H
SPAC1002.09c	dld1	dihydrolipoamide dehydrogenase Dld1
SPCC1672.01		histidinol-phosphatase (predicted)
<b>26. Purine/pyrimidine metabolism &amp; salvage</b>		
SPAC1486.06		nicotinate phosphoribosyltransferase (predicted)
SPBC1198.02	dea2	adenine deaminase Dea2
<b>27. Ergosterol metabolism</b>		
SPBC16E9.05	erg6	delta-sterol C-methyltransferase Erg6 (predicted)
SPBC16G5.18	erg24	C-14 sterol reductase Erg24

SPAC7D4.09c		steroid dehydrogenase (predicted)
<b>29. Miscellaneous metabolism</b>		
SPAP7G5.02c	gua2	GMP synthase [glutamine-hydrolyzing] (predicted)
SPAC31G5.05c		ribulose phosphate 3-epimerase (predicted)
SPAP27G11.09c		GTP cyclohydrolase (predicted)
SPAC24C9.06c		aconitate hydratase
<b>30. Other processes- various</b>		
SPAP8A3.09c	paa1	protein phosphatase regulatory subunit Paa1
SPBC1105.07c		nuclear pore associated protein Thp1-Sac3 complex subunit (predicted)
SPAC26F1.03	pda1	pyruvate dehydrogenase e1 component alpha subunit Pda1
SPBC17A3.07	pgr1	glutathione reductase
SPBC32F12.06	pch1	cyclin Pch1
SPCC736.12c	mmi1	YTH family protein Mmi1
SPBC887.12		P-type ATPase
SPAC1952.13	ned1	lipin
SPAC19B12.02c		1,3-beta-glucanosyltransferase (predicted)
SPBC13G1.07		palmitoyltransferase (predicted)
SPBC409.13		6,7-dimethyl-8-ribityllumazine synthase (predicted)
SPBC30D10.17c		glucan synthase regulator (predicted)
SPAC22A12.08c		cardiolipin synthase/ hydrolase fusion protein (predicted)
<b>31. Unknown process</b>		
SPAC16E8.02		DUF962 family protein
SPAC2C4.04c		conserved eukaryotic protein
SPAC4H3.08		short chain dehydrogenase (predicted)
SPAC56E4.05	mug69	DUF788 family protein
SPBC13G1.05		DUF747 family protein
SPBC543.04		UPF0171 family protein
<b>Essential in budding yeast, but non- essential in fission yeast (fission yeast names are used.)</b>		
<b>2. Other mitochondrial process</b>		
SPBC713.08	tom13	mitochondrial TOM complex subunit Tom13
SPAC24H6.02c		TIM23 translocase complex subunit Tim15 (predicted)
SPBC13E7.04	atp16	F1-ATPase delta subunit (predicted)
SPAC30C2.06c	dml1	mitochondrial inheritance GTPase (predicted)
<b>3. Iron sulfur cluster assembly</b>		
SPBC21D10.11c	nfs1	iron-sulfur cluster assembly protein Nfs1
SPAC144.08		DNAJ domain protein Jac1 (predicted)
<b>5. Golgi ER/transport functions</b>		
SPBP8B7.22	erd2	HDEL receptor
SPCC126.15c	sec65	signal recognition particle subunit Sec65 (predicted)
SPBC36B7.03	sec63	ER protein translocation subcomplex subunit Sec63 (predicted)
SPAC23A1.15c	sec2	SNARE Sec20
SPAC31A2.13c	sft1	SNARE Sft1
SPBC36B7.07	tlg1	SNARE Tlg1



SPAC6G10.05c		TRAPP complex subunit Trs120 (predicted)
SPCC285.14		TRAPP complex subunit Trs130 (predicted)
SPBC106.20	exo7	exocyst complex subunit Exo70 (predicted)
SPBC409.20c	psh3	ER chaperone SHR3 homologue Psh3
SPAPB21F2.02		Dopey family protein
SPAC6C3.06c		P-type ATPase, calcium transporting
SPBC2A9.06c		di-trans,poly-cis-decaprenylcistransferase
<b>6. RNA processing and export</b>		
SPAC1F5.10		ATP-dependent RNA helicase, eIF4A related (predicted)
SPAC890.05		ribosome biogenesis protein (predicted)
SPBC16H5.08c		ribosome biogenesis ATPase, Arb family ABCF2-like
SPAC4F8.03		SBDS family ribosome maturation protein (predicted)
SPAC57A7.04c	pabp	mRNA export shuttling protein
SPBC1D7.04	mlo3	RNA annealing factor Mlo3
SPCC1840.11	cs14	exosome subunit Csl4
SPAC3G9.04	ssu72	phosphoric ester hydrolase Ssu72 (predicted)
SPCC16C4.03	pin1	peptidyl-prolyl cis-trans isomerase Pin1
SPBC56F2.04	utp2	U3 snoRNP protein Utp20
SPAC22F3.11c	snu23	U4/U6 x U5 tri-snRNP complex subunit Snu23
SPAC3H5.04	aar2	U5 snRNP-associated protein Aar2
SPCC1840.10	lsm8	U6 snRNP-associated protein Lsm8 (predicted)
SPAC14C4.06c		poly(A) binding protein Nab2 (predicted)
SPAC3H8.09c	nab3	poly(A) binding protein Nab3 (predicted)
SPCC613.07		zf-HIT (snoRNA met)
SPAC22F8.09	rrp16	rRNA processing protein Rrp16 (predicted)
SPAC29A4.09		rRNA processing protein Rrp17
SPBC776.17		rRNA processing protein Rrp7 (predicted)
SPAC22G7.05		krr family protein
SPCC613.08		CDK regulator involved in ribosome export (predicted)
SPBC9B6.07		nucleolar protein Nop52 family (predicted)
SPAC6F6.03c		ribosome export GTPase
SPAC22F3.08c	rok1	ATP-dependent RNA helicase Rok1 (predicted)
SPBC2D10.10c	fib1	fibrillarin
SPAC3F10.16c		GTP binding protein, HSR1-related
SPBC365.13c	hba1	Ran GTPase binding protein Hba1
SPAPB1A10.03	nxt1	mRNA export receptor Nxt1
SPBC1921.03c	mex67	mRNA export receptor Mex67
SPAC30D11.04c	nup124	nucleoporin Nup124
SPBC13A2.02		nucleoporin Nup82
SPCC1840.03	sal3	karyopherin Sal3
<b>7. Proteasome/APC/ubiquitin associated</b>		
SPBC106.16		20S proteasome component alpha 4
SPBC577.10		20S proteasome component beta 7
SPBC2D10.20	ubc1	ubiquitin conjugating enzyme Ubc1
<b>9. SUMOylation</b>		
SPBC365.06	pmt3	SUMO
SPAC17A5.07c	ulp2	SUMO deconjugating cysteine peptidase Ulp2 (predicted)
SPAC4C5.04	rad31	SUMO E1-like activator enzyme Rad31
SPBC16H5.03c	fub2	SUMO E1-like activator enzyme Fub2

<b>10. Spindle/kinetochore/centromere associated</b>		
SPAC589.08c	dam1	DASH complex subunit Dam1
SPAC16A10.05c	dad1	DASH complex subunit Dad1
SPAC8C9.17c	spc34	DASH complex subunit Spc34
SPBC27.02c	ask1	DASH complex subunit Ask1
SPAC1805.07c	dad2	DASH complex subunit Dad2
SPBC32F12.08c	duo1	DASH complex subunit Duo1
SPCC1223.15c	spc19	DASH complex subunit Spc19
SPBC1861.01c	cnp3	CENP-C
SPCC736.14	dis1	microtubule-associated protein Dis1
SPAC110.02	pds5	cohesin-associated protein Pds5
SPBC106.01	mph1	dual specificity protein kinase Mph1
<b>11. tRNA modification</b>		
SPAC31A2.02	trm112	tRNA (guanine-N2-)-methyltransferase regulatory subunit Trm112 (predicted)
SPAC9G1.12	cpd1	tRNA (m1A) methyltransferase complex subunit Cpd1
SPAPB18E9.01	trm5	tRNA (guanine) methyltransferase Trm5 (predicted)
<b>12. Mitotic exit &amp; SIN signaling, cytokinetic process</b>		
SPAC1782.09c	clp1	Cdc14-related protein phosphatase Clp1/Flp1
SPAC23C4.08	rho3	Rho family GTPase Rho3
SPAC16E8.09	scd1	RhoGEF Scd1
SPCC1919.10c	myo52	myosin type V
SPAC4F10.11	spn1	septin Spn1
SPAC9G1.11c	spn4	septin Spn4
SPBC16A3.01	spn3	septin Spn3
SPAC4F10.15c	wsp1	WASp homolog
<b>13. DNA replication checkpoint</b>		
SPAC9E9.08	rad26	ATRIP
SPBC216.05	rad3	ATR checkpoint kinase
SPCC18B5.11c	cds1	replication checkpoint kinase Cds1
SPBC651.10	nse5	Smc5-6 complex non-SMC subunit Nse5
SPAC11E3.08c	nse6	Smc5-6 complex non-SMC subunit Nse6
<b>14. Signal transduction- various</b>		
SPBC577.06c		phosphatidylinositol kinase (predicted)
SPBC83.18c		C2 domain protein
SPBC725.02	mpr1	response regulator phosphotransferase
SPBC26H8.08c	grn1	GTPase Grn1
SPCC553.08c		GTPase Ria1 (predicted)
SPBC12C2.02c	ste2	sterility protein Ste20
SPAPYUG7.02c	sin1	stress activated MAP kinase interacting protein Sin1
SPBC21B10.05c	pop3	WD repeat protein Pop3
SPAC18B11.04	ncs1	related to neuronal calcium sensor Ncs1
SPBC19C7.03	cyr1	adenylate cyclase
<b>15. DNA replication/recombination/repair</b>		
SPBC16D10.03	pgp2	metallopeptidase Pgp2
SPBC1778.02	rap1	telomere binding protein Rap1

SPBC609.05	pob3	FACT complex component Pob3
SPCC23B6.05c	ssb3	DNA replication factor A subunit Ssb3
SPBC13G1.13	tfb2	transcription factor TFIIH complex subunit Tfb2
<b>16. Transcription and chromatin associate</b>		
SPAC25G10.03	zip1	transcription factor Zip1
SPAC1142.08	fh11	fork head transcription factor Fhl1
SPCC1682.07	ssl1	transcription factor TFIIH complex subunit Ssl1
SPAC1002.15c	pmc5	mediator complex subunit Pmc5
SPBC31F10.09c	nut2	mediator complex subunit Med10
SPAC1071.06	arp9	SWI/SNF and RSC complex subunit Arp9
SPBC30B4.04c	sol1	SWI/SNF complex subunit Sol1
SPBC1734.15	rsc4	RSC complex subunit Rsc4
SPAC1F3.07c	rsc58	RSC complex subunit Rsc58
SPCC4G3.15c		CCR4-Not complex subunit Not2 (predicted)
SPAC1F3.07c	rsc58	RSC complex subunit Rsc58
SPCC4G3.15c		CCR4-Not complex subunit Not2 (predicted)
SPCC16C4.14c	sfc4	transcription factor TFIIIC complex subunit Sfc4
SPBC19G7.16	iws1	transcription elongation factor complex subunit Iws1 (predicted)
SPBC947.13	rba5	RNA polymerase II associated protein (predicted)
SPAC1F7.01c	spt6	transcription elongation factor Spt6
<b>17. Cytoplasmic translation</b>		
SPAC21E11.06	tif224	translation initiation factor eIF2B delta subunit
SPBC17G9.09	tif213	translation initiation factor eIF2 gamma subunit
SPCC1919.09	tif6	translation initiation factor eIF6
SPBC800.08	gcd1	translation initiation factor eIF-3 gamma subunit Gcd10
SPCC830.07c	psi1	DNAJ domain protein Psi1
SPCC1223.07c		aspartate-tRNA ligase (predicted)
<b>18. Glycosylation and other ER associated</b>		
SPBC1289.08		UDP-N-acetylglucosamine diphosphorylase (predicted)
SPBPJ4664.06	gpt1	UDP-glucose-glycoprotein glucosyltransferase Gpt1
SPAC5D6.06c		UDP-GlcNAc transferase associated protein Alg14
<b>19. N-acetyltransferase assooated</b>		
SPBC106.07c		N alpha-acetyltransferase Nat2 (predicted)
SPAC20G8.09c		N-acetyltransferase Nat10 (predicted)
<b>25. Other amino acid metabolism</b>		
SPBC56F2.12	ilv5	acetohydroxyacid reductoisomerase
<b>26. Purine/pyrimidine metabolism &amp; salvage</b>		
SPAC15E1.04		thymidylate synthase (required for DNA replication in S.c)
<b>27. Ergosterol metabolic process</b>		
SPBC29A10.01	ccr1	NADPH-cytochrome p450 reductase
<b>28. Heme metabolism</b>		
SPAC1805.06c	hem2	porphobilinogen synthase Hem2 (predicted)
SPCC4B3.05c	hem12	uroporphyrinogen decarboxylase Hem12 (predicted)

SPAC24B11.13	hem3	hydroxymethylbilane synthase
<b>29. Miscellaneous metabolism</b>		
SPAC926.09c	fas1	fatty acid synthase beta subunit Fas1
SPAC17G8.06c		dihydroxy-acid dehydratase
SPCC1235.04c		FAD synthetase
<b>30. Other processes</b>		
SPAC25G10.09c		actin cortical patch component, with EF hand and WH2motif (predicted)
SPBC14F5.09c	ade8	adenylosuccinate lyase Ade8
SPBC8D2.18c		adenosylhomocysteinase (predicted)
SPCC24B10.21	tpi1	triosephosphate isomerase
<b>31. Unknown processes</b>		
SPBC25H2.15		programmed cell death protein homolog (cytoplasmic/nuclear/nucleolar)
SPBC337.10c		anamorsin family protein (cytoplasmic/nuclear)
SPAC23C11.10		conserved eukaryotic protein
SPAC1296.06		NADPH cytochrome reductase with potential role in replication (predicted)

Two genes SPAC6F12.05C and SPBC16A3.11 are single copy essential genes in fission yeast, but their budding yeast orthologues are tandem fusions and it is possible that essentiality is conserved in both organisms.