Table S1. Genes associated with H4K20me1, me2 and me3

Systematic name	Description	H4K20 me1
SPBC1348.10c	phospholipase (predicted)	3.81
SPCC4B3.12	histone lysine methyltransferase Set9	2.69
SPBC9B6.02c	retrotransposable element/transposon Tf2-type	2.55
SPAC13G6.04	TIM22 inner membrane protein import complex subunit Tim8 (predicted)	2.51
SPBC29A10.13	F0-ATPase subunit D (predicted)	2.16
SPBC3B9.10	SNARE Vti1 (predicted)	1.99
SPAC9G1.15c	mitotic spindle organizing protein Mzt1 (predicted)	1.98
SPAC11E3.04c	ubiquitin conjugating enzyme Ubc13	1.96
SPAC26A3.11	amidohydrolase	1.94
SPBC3B9.22c	DASH complex subunit Dad4	1.89
SPCC18.19c	oligosaccharyltransferase complex zeta subunit Ost5 (predicted)	1.89
SPAC22F3.15	GatB/YqeY domain protein	1.78
SPBC725.17c	RNA polymerase I transcription factor subunit Rrn11 (predicted)	1.77
SPAC17H9.17c	Mdm10/Mdm12/Mmm1 complex subunit Mdm10 (predicted)	1.73
SPAPB1A10.03	mRNA export receptor Nxt1	1.71
SPBC15D4.11c	mitochondrial Mam33 family protein (predicted)	1.70
SPBC1604.11	F0-ATPase subunit F (predicted)	1.68
SPAC589.11	mitochondrial translation release factor (predicted)	1.66
SPCC1620.13	phosphoglycerate mutase family (predicted)	1.62
SPCC18.16c	riboflavin kinase Fmn1	1.56
SPAC17H9.16	mitochondrial TOM complex subunit Tom22 (predicted)	1.54
SPAC17A2.07c	sequence orphan	1.54
SPAC3A12.04c	RNase P and RNase MRP subunit p30 (predicted)	1.53
SPAC17G8.05	mediator complex subunit Med20	1.49
SPBC9B6.04c	mitochondrial translation elongation factor EF-Tu Tuf1	1.47
SPBC16A3.14	superoxide dismutase%2C mitochondrial ribosomal protein subunit (predicted)	1.45
SPBC4C3.04c	guanyl-nucleotide exchange factor (predicted)	1.43
SPAC3C7.14c	ubiquitinated histone-like protein Uhp1	1.43
SPAC20G8.07c	C-8 sterol isomerase Erg2	1.41
SPBC106.15	isopentenyl-diphosphate delta-isomerase Idi1	1.40
SPBC17D11.07c	19S proteasome regulatory subunit Rpn2 (predicted)	1.39
SPBC646.06c	glucan endo-1%2C3-alpha-glucosidase Agn2	1.37
SPAC637.10c	19S proteasome regulatory subunit Rpn10	1.37
SPAC6B12.06c	mitochondrial genome maintenance protein Rrg9 (predicted)	1.37
SPAC1527.02	Golgi transport protein Sft2 (predicted)	1.37
SPAPB17E12.02	SMN family protein Yip12	1.34
SPBC2G5.04c	COPII-coated vesicle component Erv41 (predicted)	1.34
SPAC1805.08	dynein light chain Dlc1	1.34
SPAC8C9.19	conserved fungal protein	1.34
SPAC25H1.05	sequence orphan	1.31

SPAC4G9.15	ketoreductase (predicted)	1.31
SPCC1906.04	wtf element Wtf20	1.30
SPBC776.03	homoserine dehydrogenase (predicted)	1.30
SPBP19A11.03c	19S proteasome regulatory subunit Mts4	1.30
SPAC4D7.06c	siroheme synthase (predicted)	1.29
SPBC1198.02	adenine deaminase Dea2	1.29
SPAC15A10.12c	TRAPP complex subunit 2-like (predicted)	1.29
SPBC4F6.17c	mitochondrial heatshock protein Hsp78 (predicted)	1.28
SPAC1B1.03c	karyopherin Kap95	1.27
SPAP27G11.13c	snoRNP pseudouridylase box H/ACA snoRNP complex protein (predicted)	1.27
SPAC664.13	sequence orphan	1.26
SPAC17G8.02	uridine ribohydrolase (predicted)	1.26
SPAC16A10.05c	DASH complex subunit Dad1	1.24
SPCC1739.02c	mitochondrial ribosomal protein subunit L22 (predicted)	1.23
SPAC1851.02	1-acylglycerol-3-phosphate O-acyltransferase Slc1 (predicted)	1.23
SPBC1198.11c	RNA polymerase I transcription termination factor Reb1	1.23
SPBC19C7.06	cytoplasmic proline-tRNA ligase Prs1 (predicted)	1.22
SPBC16H5.08c	ribosome biogenesis ATPase%2C Arb family ABCF2-like (predicted)	1.22
SPAC2E1P3.03c	retrotransposable element/transposon Tf2-type	1.22
SPAC3G9.02	3-oxoacyl-	1.22
SPAC17G6.14c	ATP-dependent RNA helicase Uap56	1.22
SPAP8A3.08	myosin II light chain	1.21
SPAPB1A10.16	conserved fungal protein	1.21
SPAC977.04	truncated C terminal region of membrane transporter	1.21
SPBC30D10.09c	HVA22/TB2/DP1 family protein	1.20
SPAC1751.03	translation initiation factor eIF3m	1.19
SPCC364.06	nucleosome assembly protein Nap1	1.19
SPAC27E2.10c	DNA replication factor C complex subunit Rfc3	1.19
SPAC1782.05	protein phosphatase type 2A regulator%2C PTPA family Ypa2	1.18
SPBP23A10.02	V-ATPase assembly factor Pkr1 (predicted)	1.17
SPCC1450.06c	monothiol glutaredoxin Grx3	1.16
SPCC645.14c	chaperone activator Sti1 (predicted)	1.16
SPAPB8E5.10	conserved fungal protein%2C with meiosis specific splicing	1.16
SPAC22G7.03	sequence orphan	1.16
SPAC23H4.18c	RING-box protein 1	1.16
SPBC4C3.05c	DNA-directed RNA polymerase I complex large subunit Nuc1	1.16
SPBC30D10.05c	sepiapterin reductase (predicted)	1.16
SPCC1827.08c	F-box protein Pof7	1.16
SPBC16A3.03c	mitochondrial PPR repeat protein Ppr7	1.15
SPCC550.14	vigilin (predicted)	1.15
SPAC23D3.04c	glycerol-3-phosphate dehydrogenase Gpd2	1.14
SPAC26A3.05	clathrin heavy chain Chc1 (predicted)	1.14
SPAC16A10.06c	Smc5-6 complex non-SMC subunit 2	1.14
SPBC1703.03c	armadillo repeat protein%2C involved in ribosomal large subunit biogenesis (predicted)	1.14
SPAC15E1.08	NatA N-acetyltransferase complex catalytic subunit Naa10 (predicted)	1.14
SPBP35G2.09	U1 snRNP-associated protein Usp103 (predicted)	1.13
SPBC405.05	sequence orphan	1.13

SPBC25B2.04c	mitochondrial GTPase involved in translation Mtg1 (predicted)	1.13
SPAC27D7.05c	anaphase-promoting complex subunit Apc14	1.13
SPCC4G3.06c	mitochondrial ribosomal protein subunit L4 (predicted)	1.13
SPCC794.07	dihydrolipoamide S-acetyltransferase E2%2C Lat1 (predicted)	1.13
SPAC26A3.08	Sm snRNP core protein Smb1	1.13
SPBC32F12.03c	glutathione peroxidase Gpx1	1.12
SPBC800.09	G2/M transition checkpoint protein Sum2	1.12
SPBC14F5.03c	karyopherin Kap123	1.12
SPAC25B8.17	ER signal peptide peptidase (predited)	1.12
SPBC8D2.06	cytoplasmic isoleucine-tRNA ligase Irs1 (predicted)	1.11
SPBC21C3.06	sequence orphan	1.11
SPCC74.05	60S ribosomal protein L27 (predicted)	1.11
SPAC25G10.09c	actin cortical patch component%2C with EF hand and WH2 motif Panl (predicted)	1.11
SPAC16E8.18	sequence orphan	1.11
SPBC651.12c	sequence orphan%2C localizing to double strand breaks Dbl7	1.11
SPCC1682.10	19S proteasome regulatory subunit Rpn8 (predicted)	1.11
SPBC1604.05	glucose-6-phosphate isomerase (predicted)	1.11
SPAC1782.09c	Cdc14-related protein phosphatase Clp1/Flp1	1.10
SPCC31H12.08c	CCR4-Not complex subunit Ccr4 (predicted)	1.10
SPCC23B6.04c	sec14 cytosolic factor family (predicted)	1.10
SPAC26A3.12c	5'-3' exoribonuclease Dhp1	1.10
SPBC337.14	DNA-directed RNA polymerase II complex subunit Rpb4	1.09
SPAC977.12	L-asparaginase (predicted)	1.09
SPAC17A5.15c	glutamate-tRNA ligase (predicted)	1.09
SPAC17G8.06c	dihydroxy-acid dehydratase (predicted)	1.09
SPAC1F7.05	ribonucleoside reductase large subunit Cdc22	1.09
SPAC4G9.11c	cytosine-mismatch binding protein 1	1.08
SPBC1105.09	ubiquitin conjugating enzyme Ubc15	1.08
SPCC5E4.05c	mitochondrial serine hydrolase (predicted)	1.08
SPBC337.04	serine/threonine protein kinase Ppk27 (predicted)	1.08
SPBC11C11.08	SR family protein%2C human SRFS2 ortholog Srp1	1.08
SPBC1604.20c	kinesin-like protein Tea2	1.08
SPAC23G3.11	19S proteasome regulatory subunit Rpn6 (predicted)	1.07
SPAC8C9.11	transcriptional repressor protein BolA domain (predicted)	1.07
SPBC646.10c	U3 snoRNP protein Nop56 (predicted)	1.07
SPAC4F8.10c	SM22/transgelin-like actin modulating protein Stg1	1.07
SPAC26F1.14c	apoptosis-inducing factor homolog Aif1 (predicted)	1.07
SPBC3E7.12c	chitin synthase regulatory factor Cfh4 (predicted)	1.07
SPBC23G7.12c	19S proteasome regulatory subunit Rpt6 (predicted)	1.07
SPBP23A10.07	DNA-directed RNA polymerase I complex subunit Rpa2	1.07
SPAC1687.12c	ubiquinone biosynthesis protein Coq4 (predicted)	1.06
SPBC29A3.15c	mitochondrial ribosomal protein subunit	1.06

	S23 (predicted)	
SPCC1672.05c	cytoplasmic tyrosine-tRNA ligase Yrs1 (predicted)	1.06
SPCC1739.01	zf-CCCH type zinc finger protein	1.06
SPAC1687.01	DNA-directed RNA polymerase I and III subunit Rpc19	1.06
SPAC13G6.11c	mevalonate kinase Erg12 (predicted)	1.06
SPBC215.09c	acetyl-CoA C-acetyltransferase Erg10 (predicted)	1.06
SPBC17G9.11c	pyruvate carboxylase Pyr1	1.06
SPCC70.08c	methyltransferase (predicted)	1.05
SPCC777.08c	TORC2 subunit Bit61	1.05
SPAC26F1.13c	cytoplasmic leucine-tRNA ligase Lrs1 (predicted)	1.05
SPAC17G6.15c	MTC tricarboxylate transporter (predicted)	1.05
SPBC336.02	18S rRNA dimethylase (predicted)	1.05
SPCC285.12	U6 snRNP-associated protein Lsm7 (predicted)	1.05
SPBC215.06c	human LYAR homolog	1.05
SPBC14C8.06	ARP2/3 actin-organizing complex subunit Sop2	1.05
SPAC4F10.12	CENP-L homolog Fta1	1.04
SPAC56F8.08	UBA domain protein Mud1	1.04
SPCC320.11c	RNA-binding protein involved in ribosome biogenesis (predicted)	1.04
SPAC26F1.03	pyruvate dehydrogenase e1 component alpha subunit Pda1 (predicted)	1.03
SPBC1683.06c	uridine ribohydrolase (predicted)	1.03
SPCC663.15c	conserved fungal protein	1.03
SPAC3C7.08c	AAA family ATPase Elf1	1.03
SPAC4A8.11c	fatty acid synthase alpha subunit Lsd1	1.03
SPBC646.11	chaperonin-containing T-complex zeta	1.03
	subunit Cct6	
SPBC21H7.07c	imidazoleglycerol-phosphate dehydratase His5	1.02
SPAPJ691.03	mitochondrial inner membrane organizing system protein (predicted)	1.02
SPCC338.10c	cytochrome c oxidase subunit V (predicted)	1.02
SPAC1783.06c	autophagy associated ubiquitin-like modifier Atg12	1.02
SPCC584.04	translation release factor class II eRF3	1.01
SPBC800.11	inosine-uridine preferring nucleoside hydrolase (predicted)	1.01
SPBC1773.02c	thioredoxin peroxidase (predicted)	1.01
SPBC887.01	acireductone dioxygenase family (predicted)	1.01
SPCP1E11.11	Puf family RNA-binding protein Puf6 (predicted)	1.01
SPCC613.10	ubiquinol-cytochrome-c reductase complex core protein Qcr2 (predicted)	1.01
SPBC17D11.05	translation initiation factor eIF3a	1.00
SPBC25D12.05	tRNA (guanine-N2-)-methyltransferase	1.00
SPBC21B10.02	sequence orphan	1.00
SPBC800.06	ribosome biogenesis protein Brx1 (predicted)	1.00
SPBP23A10.15c	mitochondrial processing peptidase (MPP) complex beta subunit Qcr1 (predicted)	1.00
SPAC1006.09	MAP kinase kinase kinase Win1	1.00
SPBC428.16c	Rheb GTPase Rhb1	0.99
SPAC20G4.04c	checkpoint clamp complex protein Hus1	0.99
SPAC13G6.14	diadenosine 5'%2C5'''-p1%2Cp6-hexaphosphate hydrolase Aps1	0.99
SPAP7G5.02c	GMP synthase	0.99
SPAC12B10.02c	endoplasmic reticulum resident protein	0.99

	required for packaging into COPII vesicles (predicted)	
SPAC227.18	saccharopine dehydrogenase Lys3	0.99
SPCC16C4.05	RNase P and RNase MRP subunit (predicted)	0.98
SPCC1223.15c	DASH complex subunit Spc19	0.98
SPBC18E5.02c	serine palmitoyltransferase complex subunit (predicted)	0.98
SPAC23C11.12	anaphase-promoting complex subunit Hcn1	0.98
SPAC20G8.06	CCR4-Not complex subunit Not1 (predicted)	0.98
SPBC646.09c	eIF3e subunit Int6	0.98
SPCC777.09c	acetylornithine aminotransferase	0.98
SPAC3G9.09c	translation initiation factor eIF2 alpha subunit	0.98
SPAC1556.07	phosphomannomutase Pmm1	0.98
SPAC1556.04c	cytidine deaminase Ccd1 (predicted)	0.98
SPAC16C9.03	export adaptor Nmd3 (predicted)	0.98
SPAC1F7.08	iron transport multicopper oxidase Fio1	0.98
SPAC1071.12c	protein tyrosine phosphatase Stp1	0.97
SPCC1442.07c	ubiquitin/metalloprotease fusion protein (predicted)	0.97
SPAC1B3.01c	uracil phosphoribosyltransferase (predicted)	0.97
SPCC1840.03	karyopherin Sal3	0.97
SPBC337.15c	ubiquinone biosynthesis protein Coq7	0.97
SPAC13G6.13	sequence orphan	0.97
SPBC1861.07	elongin C (predicted)	0.97
SPCC24B10.14c	xrcc4 like factor%2C cernunnon	0.97
SPAC21E11.07	iron-sulfur cluster biogenesis protein (predicted)	0.97
SPBC4B4.12c	sequence orphan	0.96
SPBC32F12.10	phosphoglucomutase (predicted)	0.96
SPAC15E1.02c	DUF1761 family protein	0.96
SPBC26H8.08c	GTPase Grn1	0.96
SPBP4H10.15	aconitate hydratase/mitochondrial ribosomal protein subunit L49%2C fusion protein (predicted)	0.96
SPBC28F2.12	RNA polymerase II large subunit Rpb1	0.96
SPAC323.02c	20S proteasome complex subunit alpha 5%2C Pup2 (predicted)	0.96
SPAC5H10.09c	3-methyl-2-oxobutanoatehydroxymethyltransferase (predicted)	0.96
SPAC23H4.07c	signal recognition particle receptor beta subunit Srp102 (predicted)	0.96
SPAC24H6.10c	phospho-2-dehydro-3-deoxyheptonate aldolase (predicted)	0.96
SPBC8D2.20c	COPII-coated vesicle component Sec31 (predicted)	0.95
SPBC582.08	alanine aminotransferase (predicted)	0.95
SPBC1709.02c	cytoplasmic valine-tRNA ligase Vrs1/Vas1	0.95
SPBC16G5.04	mitochondrial ribosomal protein subunit L13 (predicted)	0.95
SPAC922.06	3-oxoacyl-	0.95
SPBP8B7.22	HDEL receptor (predicted)	0.95
SPAC1F8.04c	hydrolase (predicted)	0.95
SPCC622.12c	NADP-specific glutamate dehydrogenase Gdh1 (predicted)	0.95
SPAC9E9.17c	dubious	0.95
SPAC22A12.03c	COP9/signalosome complex subunit Csn4	0.95
SPCC1281.03c	ER membrane protein complex subunit 4 (predicted)	0.95
SPAC31G5.05c	ribulose phosphate 3-epimerase (predicted)	0.95
SPCC645.13	transcription elongation regulator	0.94

	(predicted)	
SPCC777.15	tRNA dihydrouridine synthase Dus4 (predicted)	0.94
SPAC1F8.06	cell surface glycoprotein	0.94
SPAC23A1.20	conserved gene with no initiator methionine	0.94
SPCC1223.07c	cytoplasmic aspartate-tRNA ligase Drs1 (predicted)	0.94
SPCC645.04	Smc5-6 complex non-SMC subunit Nse3	0.94
SPAC18B11.02c	tRNA pseudouridine synthase (predicted)	0.94
SPBC3D6.03c	mitochondrial 3'-tRNA processing endonuclease Trz2	0.94
SPAC23D3.07	20S proteasome complex subunit beta 2 (predicted)	0.94
SPAC57A10.03	cyclophilin family peptidyl-prolyl cis-trans isomerase Cyp1	0.94
SPBC646.07c	enoyl reductase (predicted)	0.93
SPAC27F1.03c	ubiquitin C-terminal hydrolase Uch1	0.93
SPCC1494.08c	conserved fungal protein	0.93
SPAC56F8.05c	BAR domain protein (predicted)	0.93
SPAC15E1.10	PI31 proteasome inhibitor (predicted)	0.93
SPAC23D3.09	SWI/SNF and RSC complex subunit Arp42	0.93
SPCC1020.06c	transaldolase (predicted)	0.93
SPBC3E7.09	Sad1-UNC-like protein involved protein folding in the ER (predicted)	0.93
SPCC1322.13	phosphoribosylaminoimidazole carboxylase Ade6	0.93
SPAC644.17c	mitochondrial ribosomal protein subunit L9 (predicted)	0.93
SPBC4F6.13c	WD repeat/BOP1NT protein (predicted)	0.93
SPBC428.19c	U3 snoRNP protein Utp15 (predicted)	0.92
SPBC651.02	bis(5'-adenosyl)-triphosphatase (predicted)	0.92
SPAC589.03c	sequence orphan	0.92
SPAC22A12.06c	serine hydrolase-like	0.92
SPAC7D4.09c	3-oxo-5-alpha-steroid 4-dehydrogenase (predicted)	0.92
SPBC428.05c	argininosuccinate synthase (predicted)	0.92
SPBC1773.10c	cytoplasmic asparagine-tRNA ligase Nrs1 (predicted)	0.92
SPAC521.03	short chain dehydrogenase (predicted)	0.92
SPAC31A2.03	mitochondrial ribosomal protein subunit L11 (predicted)	0.92
SPAC13G7.11	mitochondrial respiratory complex assembly protein (predicted)	0.91
SPCC569.01c	cell surface glycoprotein (predicted)%2C DUF1773 family protein 5	0.91
SPBP35G2.14	RNA-binding protein	0.91
SPCC550.15c	ribosome biogenesis protein (predicted)	0.91
SPCC330.09	rRNA processing protein Enp2 (predicted)	0.91
SPCC330.13	DNA-directed RNA polymerase III complex subunit Rpc37 (predicted)	0.91
SPAC25H1.06	CAF assembly factor (CAF-1) complex subunit C%2C Pcf3	0.91
SPAC18G6.04c	serine hydroxymethyltransferase Shm2 (predicted)	0.91
SPBC3B8.03	saccharopine dehydrogenase (predicted)	0.91
SPCC191.09c	glutathione S-transferase Gst1	0.91
SPAC19G12.10c	vacuolar carboxypeptidase Y	0.91
SPBC1711.13	histidinol dehydrogenase His2 (predicted)	0.91
SPBC119.11c	double-strand-specific ribonuclease Pac1	0.91
SPAC25G10.08	translation initiation factor eIF3b (p84)	0.91
SPCC584.01c	sulfite reductase NADPH flavoprotein subunit (predicted)	0.91
SPBC18E5.10	iron sulfur cluster assembly protein (predicted)	0.91

SPCC1235.07	CENP-Q homolog Fta7	0.91
SPBC21D10.10	bromodomain containing protein 1%2C Bdc1	0.90
SPBC18E5.09c	sequence orphan	0.90
SPBC36.12c	SGT1-like protein Git7	0.90
SPAC19A8.15	tryptophan synthase (predicted)	0.90
SPBC651.06	sequence orphan	0.90
SPBC1711.04	methylenetetrahydrofolate reductase (predicted)	0.90
SPCC1672.12c	ER membrane insertion protein Get4 (predicted)	0.90
SPACUNK4.10	glyoxylate reductase (predicted)	0.89
SPBC3E7.16c	2-isopropylmalate synthase Leu3	0.89
SPAC11G7.03	isocitrate dehydrogenase (NAD+) subunit 1 Idh1	0.89
SPAC19D5.05c	U3 snoRNP-associated protein Imp3 (predicted)	0.89
SPBC17G9.03c	cytoplasmic lysine-tRNA ligase Krs1 (predicted)	0.89
SPBC18E5.13	mitochondrial translation initiation factor (predicted)	0.89
SPAC26F1.10c	tyrosine phosphatase Pyp1	0.89
SPBC1734.13	F1-ATPase gamma subunit (predicted)	0.89
SPAC19D5.11c	DNA replication factor C complex subunit Ctf8 (predicted)	0.89
SPAC6F6.02c	F-box protein Pof5	0.89
SPAC27F1.07	dolichyl-diphospho-oligosaccharide-protein glycosyltransferase Ost1 (predicted)	0.89
SPAC823.10c	mitochondrial carrier with solute carrier repeats (predicted)	0.89
SPBC1604.19c	TRAPP complex subunit Trs85 (predicted)	0.89
SPBC428.11	homocysteine synthase Met17	0.89
SPCC23B6.01c	oxysterol binding protein (predicted)	0.89
SPBC1198.08	dipeptidase Dug1 (predicted)	0.89
SPBC19G7.10c	topoisomerase II-associated deadenylation-dependent mRNA-decapping factor (predicted)	0.89
SPBPJ4664.04	coatomer alpha subunit (predicted)	0.89
SPBP23A10.09	GINS complex subunit Psf1	0.89
SPBC21C3.16c	transcription elongation factor complex subunit Spt4	0.89
SPAC2C4.15c	UBX domain protein Ubx2	0.89
SPAC29A4.17c	mitocondrial FUN14 family protein	0.88
SPBC27.08c	sulfate adenylyltransferase	0.88
SPAC1834.11c	secretory pathway protein Sec18 (predicted)	0.88
SPBC409.16c	recombination protein Saw1 (predicted)	0.88
SPAC19A8.07c	U3 snoRNP-associated protein Imp4 (predicted)	0.88
SPCC970.08	inositol polyphosphate kinase (predicted)	0.88
SPAC23A1.12c	phenylalanine-tRNA ligase beta subunit Frs1 (predicted)	0.88
SPCC1322.02	sequence orphan	0.88
SPBC119.03	human COMT catechol O-methyltransferase homolog 1	0.88
SPAC10F6.03c	CTP synthase Cts1 (predicted)	0.88
SPBC15D4.15	4-nitrophenylphosphatase	0.88
SPAPB1E7.07	glutamate synthase Glt1 (predicted)	0.88
SPAC56E4.04c	acetyl-CoA/biotin carboxylase	0.88
SPAC22E12.13c	ribosomal L24-like protein involved in ribosome biogenesis Rlp24 (predicted)	0.88
SPAC24C9.02c	cytochrome c1 heme lyase (predicted)	0.87
SPAC29A4.15	cytoplasmic serine-tRNA ligase Srs1 (predicted)	0.87

SPAC23D3.16	sequence orphan	0.87
SPAC20G8.04c	mitochondrial electron transfer flavoprotein-ubiquinone oxidoreductase (predicted)	0.87
SPAC19D5.04	HECT-type ubiquitin ligase E3 Ptr1	0.87
SPCC24B10.10c	mitochondrial outer membrane ATPase Msp1/Yta4 (predicted)	0.87
SPCC330.05c	orotidine 5'-phosphate decarboxylase Ura4	0.87
SPAC13G7.04c	membrane anchored protein Mac1	0.87
SPBC2F12.03c	EST1 family nonsense-mediated mRNA decay (NMD) pathway protein Ebs1 (predicted)	0.87
SPCC18.18c	fumarate hydratase (predicted)	0.87
SPCC553.06	oligosaccharyltransferase delta subunit Swp1 (predicted)	0.87
SPBC16E9.16c	Lsd90 protein	0.87
SPBC1711.16	WD repeat protein (predicted)	0.87
SPBC21B10.03c	ataxin-2 homolog	0.87
SPBC23E6.05	ribosomal export complex protein Arx1%2C peptidase family (predicted)	0.87
SPAC9G1.04	mitochondrial inner membrane translocase Oxa101	0.86
SPCC162.07	epsin	0.86
SPBC651.01c	GTP binding protein Nog1 (predicted)	0.86
SPCC1393.12	sequence orphan	0.86
SPAC31A2.08	mitochondrial ribosomal protein subunit L23 (predicted)	0.86
SPBC651.11c	AP-3 adaptor complex subunit Apm3 (predicted)	0.86
SPAC4D7.05	translation initiation factor eIF3i	0.86
SPAC1782.07	ubiquinol-cytochrome-c reductase complex subunit 7	0.86
SPAC14C4.09	glucan endo-1%2C3-alpha-glucosidase Agn1	0.86
SPAC1610.01	splicing factor (unnamed)	0.86
SPAC6F12.10c	phosphoribosylformylglycinamidine synthase Ade3 (predicted)	0.86
SPAC6G10.12c	transcription factor Ace2	0.86
SPAC644.16	RNA-binding protein (predicted)	0.86
SPBC1198.06c	mannan endo-1%2C6-alpha-mannosidase (predicted)	0.86
SPAC1486.05	nucleoporin Nup98 and Nup96	0.86
SPBP8B7.11	ubiquitin protease cofactor Glp1 (predicted)	0.86
SPBP8B7.25	cyclophilin family peptidyl-prolyl cis-trans isomerase Cyp4 (predicted)	0.86
SPBC146.14c	coatomer beta subunit (predicted)	0.85
SPAC3F10.06c	initiator methionine tRNA 2'-O-ribosyl phosphate transferase (predicted)	0.85
SPAC19D5.06c	Dhp1p-interacting protein Din1	0.85
SPAC17H9.03c	RAD51D-like protein 1	0.85
SPAC222.16c	COP9/signalosome complex subunit Csn3 (predicted)	0.85
SPBC2A9.09	phosducin family protein (predicted)	0.85
SPBC16A3.09c	Cdc48-Ufd1-Npl4 complex subunit Ufd1 (predicted)	0.85
SPCC1322.15	60S ribosomal protein L34	0.85
SPAPB8E5.02c	19S proteasome regulatory subunit Rpn502	0.85
SPAP8A3.09c	protein phosphatase regulatory subunit Paa1	0.85
SPCC126.08c	lectin family glycoprotein receptor (predicted)	0.85
SPBC16E9.12c	poly(A) binding protein Pab2	0.85
SPAC4G8.08	mitochondrial iron ion transporter (predicted)	0.85

SPCP20C8.02c	S. pombe specific UPF0321 family protein 1	0.85
SPBP35G2.07	acetolactate synthase catalytic subunit	0.84
SPAC24C9.06c	aconitate hydratase (predicted)	0.84
SPCC188.02	protein phosphatase regulatory subunit Par1	0.84
SPAC8C9.14	transcription factor Prr1	0.84
SPBC27B12.10c	mitochondrial TOM complex subunit Tom7 (predicted)	0.84
SPAC57A7.12	heat shock protein Pdr13 (predicted)	0.84
SPBC146.07	U2AF large subunit (U2AF-59)	0.84
SPBC14F5.09c	adenylosuccinate lyase Ade8	0.84
SPCC191.02c	acetyl-CoA ligase (predicted)	0.84
SPAC343.09	UBX domain protein Ubx3%2C Cdc48 cofactor	0.84
SPBC12C2.05c	diacylglycerol binding protein Bzz1 (predicted)	0.84
SPAC26A3.01	aspartic protease Sxa1	0.84
SPAC227.17c	conserved protein	0.84
SPAC8C9.15c	translation initiation factor eIF2B epsilon subunit (predicted)	0.84
SPCC1183.07	U3 snoRNP-associated protein Rrp5 (predicted)	0.83
SPAC1782.08c	exonuclease Rex3 (predicted)	0.83
SPCC1450.02	Swr1 complex bromodomain subunit Brf1	0.83
SPAC4A8.04	vacuolar serine protease Isp6	0.83
SPAC30C2.05	cornichon family protein Erv14 (predicted)	0.83
SPCC338.14	adenosine kinase (predicted)	0.83
SPAC4F10.10c	mannosyltransferase complex subunit%2C Anp family Mnn9 (predicted)	0.83
SPBC106.06	chaperonin-containing T-complex delta subunit Cct4	0.83
SPBC29A3.18	cytochrome c1 Cyt1 (predicted)	0.83
SPBC2G5.03	cytosolic thiouridylase subunit Ctu1	0.83
SPCC188.14	sequence orphan	0.83
SPAC1002.17c	uracil phosphoribosyltransferase (predicted)	0.83
SPAC1782.04	mitochondrial mRNA processing protein Cox24/Pet20 (predicted)	0.83
SPAC9E9.15	CIA30 protein (predicted)	0.83
SPBC947.03c	NatC N-acetyltransferase non catalytic Sm-like domain subunit Naa38 (predicted)	0.83
SPAC22F8.08	COPII cargo receptor Sec24/Sfb2 subunit	0.83
SPAC12G12.01c	ubiquitin-protein ligase E3	0.83
SPAC19G12.15c	trehalose-6-phosphate phosphatase Tpp1	0.83
SPBC29A10.01	NADPH-cytochrome p450 reductase	0.83
SPBC1773.05c	hexitol dehydrogenase (predicted)	0.82
SPAC22E12.09c	kexin	0.82
SPCC1840.10	U6 snRNP-associated protein Lsm8 (predicted)	0.82
SPAC23D3.08	U1 snRNP-associated protein Usp108	0.82
SPAC56F8.10	methylenetetrahydrofolate reductase Met9	0.82
SPBC11B10.02c	histidinol-phosphate aminotransferase imidazole acetol phosphate transaminase His3	0.82
SPCC1450.03	ribonucleoprotein (RNP) complex (predicted)	0.82
SPAC806.07	nucleoside diphosphate kinase Ndk1	0.82
SPAC1556.03	serine/threonine protein phosphatase Azr1	0.82
SPCC364.07	D-3 phosphoglycerate dehydrogenase (predicted)	0.82
SPBC36.10	mitochondrial intermembrane space protein sorting protein (predicted)	0.82
SPBC800.12c	ubiquitin family protein (predicted)	0.82
SPAPYUG7.05	delta-1-pyrroline-5-carboxylate reductase (predicted)	0.82

SPAC23A1.07	ubiquitin-protein ligase E3 (predicted)	0.82
SPAC8C9.05	D-Tyr-tRNA deacylase (predicted)	0.82
SPAC22H10.13	metallothionein Zym1	0.82
SPAPYUG7.03c	medial ring protein Mid2	0.82
SPCC1919.09	translation initiation factor eIF6	0.82
SPAC1B3.02c	transcription elongation factor%2C Elf1 family (predicted)	0.82
SPCC14G10.03c	proteasome maturation factor Ump1 (predicted)	0.82
SPBC24C6.04	delta-1-pyrroline-5-carboxylate dehydrogenase (predicted)	0.82
SPBC887.19	Man5GlcNac2-PP-Dol translocation protein Rft1 (predicted)	0.81
SPBC18E5.11c	enhancer of mRNA decapping Edc3	0.81
SPAPB8E5.07c	rRNA processing protein Rrp12 (predicted)	0.81
SPBP23A10.03c	mitochondrial ACN9 family protein (predicted)	0.81
SPCC1259.16	sequence orphan	0.81
SPBP8B7.08c	leucine carboxyl methyltransferase Ppm1 (predicted)	0.81
SPAC1F7.07c	iron permease Fip1	0.81
SPBC887.08	sequence orphan	0.81
SPBC146.12	monooxygenase Coq6 (predicted)	0.81
SPCC1259.09c	pyruvate dehydrogenase protein x component%2C Pdx1 (predicted)	0.81
SPBC106.12c	THO complex subunit (predicted)	0.81
SPAC17H9.07	signal recognition particle subunit Srp21 (predicted)	0.81
SPCC18B5.11c	replication checkpoint kinase Cds1	0.81
SPAC18G6.07c	rRNA (pseudouridine) methyltransferase Mra1	0.81
SPBC646.14c	origin recognition complex subunit Orc5	0.81
SPBC947.02	AP-1 adaptor complex subunit beta subunit Apl2	0.81
SPBC776.09	ATP-dependent RNA helicase Ste13	0.81
SPAC1F8.05	sequence orphan	0.81
SPCC1682.15	PX/PXA domain protein	0.81
SPBC4C3.07	translation initiation factor eIF3f	0.80
SPBC336.03	Ras1 guanyl-nucleotide exchange factor Efc25	0.80
SPCC16C4.10	6-phosphogluconolactonase (predicted)	0.80
SPAPYUG7.06	PPPDE peptidase family (predicted)	0.80
SPAC12G12.02	rRNA processing protein Efg1 (predicted)	0.80
SPBC4.05	ubiquitin protein ligase E3 component human N-recognin 7 homolog Mlo2	0.80
SPBC16E9.09c	COPII vesicle coat component Erp5/Erp6 (predicted)	0.80
SPAC2F3.02	ER protein translocation subcomplex subunit Sec72 (predicted)	0.80
SPCC1223.08c	dihydrofolate reductase/ serine hydrolase family fusion protein Dfr1	0.80
SPBC28F2.09	transcription factor TFIIA complex large subunit Toa1 (predicted)	0.80
SPBC337.05c	chaperonin-containing T-complex theta subunit Cct8	0.80
SPAC22A12.16	ATP-citrate synthase subunit 2 (predicted)	0.80
SPAC9E9.10c	CENP-B homolog Cbh1	0.79
SPBC691.04	mitochondrial ATP-dependent RNA helicase Mss116 (predicted)	0.79
SPAC3F10.03	mitochondrial and cytoplasmic glycine-tRNA ligase Grs1 (predicted)	0.79
SPBC16H5.02	6-phosphofructokinase (predicted)	0.79
SPAC222.12c	F1-ATPase beta subunit Atp2	0.79
SPAC11G7.02	HECT-type ubiquitin-protein ligase E3	0.79

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SPAC31G5.14	glycine decarboxylase T subunit (predicted)	0.79
SPAC57A10.14	SAGA complex subunit Sgf11	0.79
SPAC23H4.15	ribosome biogenesis protein Tsr1 (predicted)	0.79
SPAC56F8.07	conserved eukaryotic ER membrane protein	0.79
SPAC57A10.06	sequence orphan	0.79
SPAC16E8.01	cytoskeletal protein binding protein Sla1 family%2C Shd1 (predicted)	0.79
SPCC1442.16c	NADPH quinone oxidoreductase/ARE-binding protein (predicted)	0.79
SPAC19G12.04	ureidoglycolate hydrolase (predicted)	0.79
SPAC1420.01c	DUF1752 family protein%2C involved in regulation of transcription (predicted)	0.79
SPBC8E4.04	alditol NADP+ 1-oxidoreductase activity (predicted)	0.79
SPCC613.08	CDK regulator%2C involved in ribosome export (predicted)	0.79
SPBC428.13c	Sid2-Mob1 kinase complex regulatory subunit Mob1	0.79
SPAC1002.01	conserved fungal protein	0.78
SPCC1322.14c	vacuolar transporter chaperone (VTC) complex subunit (predicted)	0.78
SPCC1442.06	20S proteasome complex subunit alpha 2%2C Pre8 (predicted)	0.78
SPAC22E12.08	RNA polymerase I upstream activation factor complex subunit Rrn10	0.78
SPAC637.07	translation initiation factor eIF3d Moe1	0.78
SPBC1347.02	FKBP-type peptidyl-prolyl cis-trans isomerase (predicted)	0.78
SPCC306.09c	adenylyl cyclase-associated protein Cap1	0.78
SPBC2D10.03c	DUF866 domain protein	0.78
SPAC23D3.03c	GTPase activating protein (predicted)	0.78
SPCPJ732.03	sequence orphan	0.78
SPAC19B12.11c	zinc finger protein%2C human ZNF593 ortholog	0.78
SPBC365.14c	UDP-glucose 4-epimerase Uge1	0.78
SPAC26A3.04	60S ribosomal protein L20 (predicted)	0.78
SPAC57A7.10c	coatomer gamma subunit Sec21 (predicted)	0.78
SPBC887.10	response regulator Mcs4	0.78
SPBC1604.21c	ubiquitin activating enzyme E1	0.78
SPAC977.16c	dihydroxyacetone kinase Dak2	0.78
SPAC1B3.06c	UbiE family methyltransferase (predicted)	0.77
SPAC25H1.08c	ribosome biogenesis protein Sqt1 (predicted)	0.77
SPAC23A1.17	WIP family cytoskeletal protein (predicted)	0.77
SPBC36B7.06c	sequence orphan	0.77
SPBC3E7.14	Sm snRNP core protein Smf1	0.77
SPBC646.16	20S proteasome complex subunit alpha 1 (predicted)	0.77
SPCC737.02c	ubiquinol-cytochrome-c reductase complex subunit 6 (predicted)	0.77
SPBC215.11c	aldo/keto reductase%2C unknown biological role	0.77
SPBC1826.01c	TATA-binding protein associated factor Mot1 (predicted)	0.77
SPAC4A8.16c	translation initiation factor eIF3c	0.77
SPBC17D11.06	DNA primase large subunit Spp2	0.77
SPAC17C9.03	translation initiation factor eIF4G	0.77
SPAC23G3.06	U3 snoRNP protein Nop58 (predicted)	0.77
SPAC1834.10c	sequence orphan	0.77
SPAC11D3.09	agmatinase (predicted)	0.77
SPBC354.10	RNAPII degradation factor Def1 (predicted)	0.77

SPBC1604.08c	importin alpha	0.77
SPBC17D1.06	ATP-dependent RNA helicase Dbp3 (predicted)	0.77
SPAC5H10.01	DUF1445 family protein	0.76
SPBC11B10.06	SWIM domain containing-Srs2 interacting protein 1	0.76
SPAC4A8.06c	esterase/lipase (predicted)	0.76
SPBC2G2.03c	translocon beta subunit Sbh1 (predicted)	0.76
SPAC3A11.07	NADH dehydrogenase (predicted)	0.76
SPCC1682.05c	signal recognition particle subunit (predicted)	0.76
SPAC2C4.10c	SIP/FAR complex subunit%2C Csc4	0.76
SPAC4A8.13c	20S proteasome complex subunit beta 5	0.76
SPBC23E6.04c	U3 snoRNP-associated protein Utp10 (predicted)	0.76
SPAPYUK71.03c	synaptotagmin family C2 domain protein%2C Syn1	0.76
SPAC821.08c	sleepy homolog Slp1	0.76
SPCC4B3.10c	inositol 1%2C3%2C4%2C5%2C6-pentakisphosphate (IP5) kinase	0.76
SPCC1884.01	sequence orphan	0.76
SPAC607.05	19S proteasome regulatory subunit Rpn9	0.76
SPCC162.09c	3-hydroxy-3-methylglutaryl-CoA reductase Hmg1	0.76
SPBC1734.05c	DNAJ protein Spf31 (predicted)	0.76
SPBC660.13c	DNA replication factor A subunit Ssb1	0.76
SPBC16E9.13	serine/threonine protein kinase Ksp1 (predicted)	0.75
SPCP31B10.02	mitochondrial conserved eukaryotic protein (predicted)	0.75
SPAC186.03	L-asparaginase (predicted)	0.75
SPBC16H5.10c	ATP-dependent RNA helicase Prp43	0.75
SPAC23G3.09	transcription factor TFIID complex subunit Taf4 (predicted)	0.75
SPAPJ696.02	actin cortical patch component Lsb4 (predicted)	0.75
SPAC18G6.06	U3 snoRNP-associated protein Utp11 (predicted)	0.75
SPBC36B7.03	ER protein translocation subcomplex subunit Sec63 (predicted)	0.75
SPBC36.08c	Golgi transport complex subunit Cog2 (predicted)	0.75
SPAC1093.02	pyridoxamine 5'-phosphate oxidase (predicted)	0.75
SPAC29A4.16	halotolerence protein 4	0.75
SPBC1711.09c	SNARE associated Golgi protein (predicted)	0.75
SPACUNK4.11c	nuclear exosome-associated RNA binding protein Mpp6	0.75
SPAC9G1.02	MAP kinase kinase kinase Wis4	0.75
SPBC1105.17	centromere-specific histone H3 CENP-A	0.75
SPBPB2B2.09c	2-dehydropantoate 2-reductase (predicted)	0.75
SPBC418.01c	imidazoleglycerol-phosphate synthase (predicted)	0.75
SPAC24C9.10c	mitochondrial ribosomal protein subunit S2 (predicted)	0.75
SPCC1223.14	chorismate synthase (predicted)	0.75
SPAC1002.09c	dihydrolipoamide dehydrogenase Dld1	0.75
SPAC21E11.08	serine palmitoyltransferase Lcb2 (predicted)	0.74
SPAC31A2.10	Ran GTPase binding protein (predicted)	0.74
SPBC1604.10	mediator complex subunit Srb7	0.74
SPBC56F2.11	homoserine O-acetyltransferase Met6	0.74
SPCP31B10.03c	mediator complex subunit Med31	0.74

SPBC1711.05	nucleocytoplasmic transport chaperone Srp40 (predicted)	0.74
SPAC9E9.06c	threonine synthase (predicted)	0.74
SPBC577.10	20S proteasome complex subunit beta 7 (predicted)	0.74
SPAC2F7.14c	exosome subunit Rrp4	0.74
SPBC3B8.05	diphthamide biosynthesis protein Dph1 (predicted)	0.74
SPAC25G10.05c	ATP phosphoribosyltransferase	0.74
SPBC12C2.09c	Haemolysin-III family protein (predicted)	0.74
SPAC694.02	DEAD/DEAH box helicase	0.74
SPBC1105.02c	homocitrate synthase	0.74
SPBC651.03c	GTPase activating protein Gyp10	0.74
SPAC4A8.12c	protein phosphatase regulatory subunit Sds22	0.74
SPCC1840.11	exosome subunit Csl4	0.74
SPAC16.02c	mRNA export factor Srp2	0.73
SPBC1A4.08c	chaperonin-containing T-complex gamma subunit Cct3	0.73
SPAC1635.01	mitochondrial outer membrane voltage-dependent anion-selective channel (predicted)	0.73
SPCC16A11.06c	pig-B (predicted)	0.73
SPBC21D10.11c	mitochondrial cysteine desulfurase Nfs1 (predicted)	0.73
SPAC977.15	dienelactone hydrolase family	0.73
SPAC23H4.11c	centromere localized protein Cnl2	0.73
SPBC713.03	mitochondrial D-lactate dehydrogenase%2C cytochrome (predicted)	0.73
SPAC3H1.14	cytoplasmic vesicle protein%2C Vid24 family (predicted)	0.73
SPAC20G4.07c	C-24(28) sterol reductase Sts1	0.73
SPAC22E12.11c	histone lysine methyltransferase Set3	0.73
SPAC57A10.12c	dihydroorotate dehydrogenase Ura3	0.73
SPAC1687.09	ENTH/VHS domain protein (predicted)	0.73
SPBC215.08c	arginine specific carbamoyl-phosphate synthase Arg4 (predicted)	0.73
SPBC1198.03c	conserved fungal protein	0.73
SPCC1442.05c	mitochondrial protein	0.73
SPBC29A10.12	DUF1014 family protein%2C HMG-box clan member	0.73
SPAC2F3.03c	DNA-directed RNA polymerase I complex subunit Rpa49 (predicted)	0.72
SPBC660.17c	sequence orphan	0.72
SPCC285.17	RNA polymerase I upstream activation factor complex subunit Spp27	0.72
SPCC191.05c	nucleoside 2-deoxyribosyltransferase (predicted)	0.72
SPCC1827.05c	nucleolar RNA-binding protein NIFK (predicted)	0.72
SPAC6G9.13c	bouquet formation protein Bqt1	0.72
SPBC1861.04c	RNA-binding protein Prp24 (predicted)	0.72
SPCC63.06	human WDR89 family WD repeat protein	0.72
SPAC2F3.04c	mitochondrial single-stranded DNA binding protein Rim1	0.72
SPBC1A4.01	anaphase-promoting complex subunit Apc10	0.72
SPCC70.09c	conserved fungal protein	0.72
SPBC1683.02	adenine/adenosine deaminase family (predicted)	0.72
SPAC13G7.06	phosphoadenosine phosphosulfate reductase	0.72
SPBC146.01	mediator complex subunit Med15	0.72
SPBC17G9.09	translation initiation factor eIF2 gamma	0.72

	subunit (predicted)	
SPAC3C7.11c	calnexin Cnx1	0.72
SPBC31E1.02c	P-type ATPase%2C calcium transporting Pmr1	0.72
SPCC569.02c	S. pombe specific UPF0321 family protein 2	0.71
SPBC16E9.05	sterol 24-C-methyltransferase Erg6	0.71
SPAC22H10.12c	GDP dissociation inhibitor Gdi1 (predicted)	0.71
SPCC63.12c	20S proteasome complex subunit beta 3%2C Pup3 (predicted)	0.71
SPCC1795.03	UDP-galactose transporter Gms1	0.71
SPBC21C3.15c	aldehyde dehydrogenase (predicted)	0.71
SPAC1834.02	pentafunctional aromatic polypeptide Aro1 (predicted)	0.71
SPBC3H7.03c	2-oxoglutarate dehydrogenase (lipoamide) (e1 component of oxoglutarate dehydrogenase complex) (predicted)	0.71
SPCC1281.01	alpha-1%2C4-glucan synthase Ags1	0.71
SPBC14F5.08	mediator complex subunit Med7	0.71
SPBC337.12	human ZC3H3 homolog	0.71
SPAC1F5.02	protein disulfide isomerase (predicted)	0.71
SPBC14F5.01	sequence orphan	0.71
SPAC23C11.11	serine/threonine protein kinase Cka1	0.71
SPAC6G10.04c	20S proteasome complex subunit alpha 6 subunit Pre5 (predicted)	0.71
SPBC14C8.04	acetolactate synthase regulatory unit (predicted)	0.71
SPBC19F8.02	nuclear distribution protein NUDC homolog	0.71
SPCC1672.08c	transcription factor TFIIE beta subunit%2C TFIIEB%2C Tfa2	0.71
SPAC20G8.09c	ribosome biogenesis ATPase (predicted)	0.71
SPAC2C4.09	DUF1640 family protein	0.71
SPCC320.08	membrane transporter (predicted)	0.71
SPBC12D12.02c	DNA polymerase delta subunit Cdm1	0.71
SPAC6F12.16c	ATP-dependent RNA helicase%2C TRAMP complex subunit Mtr4	0.71
SPCC645.12c	sequence orphan	0.71
SPAC1782.06c	prohibitin Phb1 (predicted)	0.71
SPAC977.14c	aldo/keto reductase%2C unknown biological role	0.70
SPAC767.01c	dynamin family protein Vps1	0.70
SPAC3G9.06	cytoplasmic phenylalanine-tRNA ligase alpha subunit Frs2 (predicted)	0.70
SPCC4F11.03c	sequence orphan	0.70
SPCC1682.04	centrin	0.70
SPBC30D10.17c	cell wall biosynthesis/ cell cycle regulator (predicted)	0.70
SPBC2D10.12	Rad23 homolog Rhp23	0.70
SPCC1442.04c	meiotic recombination protein (predicted)	0.70
SPAC27D7.07c	Sm snRNP core protein Smd1	0.70
SPCC1672.10	kinetochore protein Mis16	0.70
SPAC589.06c	pho88 family protein (predicted)	0.70
SPBP4G3.03	PI31 proteasome regulator related	0.70
SPBC30D10.13c	pyruvate dehydrogenase e1 component beta subunit Pdb1	0.70
SPAC19G12.03	chitin deacetylase Cda1	0.70
SPCC18.03	shuttle craft like transcriptional regulator (predicted)	0.70
SPBC23G7.07c	U3-containing 90S preribosome complex subunit Cms1 (predicted)	0.70
SPAC57A10.09c	High-mobility group non-histone chromatin protein (predicted)	0.70
SPAC1F7.10	hydantoin racemase family (predicted)	0.70

SPAC1142.03c	Swi5 complex subunit Swi2	0.70
SPCC645.07	RhoGEF for Rho1%2C Rgf1	0.70
SPAC57A7.15c	sequence orphan	0.70
SPBC146.13c	myosin type I	0.70
SPAC607.07c	sequence orphan	0.70
SPBC19F5.04	aspartate kinase (predicted)	0.70
SPAC4F10.13c	GYF domain protein	0.70
SPAC6G10.08	isocitrate dehydrogenase Idp1 (predicted)	0.70
SPBC25H2.02	cytoplasmic threonine-tRNA ligase Trs1 (predicted)	0.70
SPAC22G7.06c	carbamoyl-phosphate synthase (glutamine hydrolyzing)%2C aspartate carbamoyltransferase Ura1	0.69
SPAC1805.06c	porphobilinogen synthase Hem2 (predicted)	0.69
SPBC12C2.06	cytoplasmic ATP-dependent RNA helicase Dbp5 (predicted)	0.69
SPBC25B2.07c	mitochondria microtubule binder Mmb1	0.69
SPBC8D2.19	serine/threonine protein kinase%2C meiotic Mde3	0.69
SPBC31E1.06	GTP binding protein Bms1 (predicted)	0.69
SPAC19A8.04	C-22 sterol desaturase Erg5	0.69
SPAPB8E5.09	AAA family ATPase Rvb1	0.69
SPAC29A4.04c	pseudouridylate synthase Cbf5 (predicted)	0.69
SPBC405.01	phosphoribosylamine-glycine ligase/phosphoribosylformylglycinamidine cyclo-ligase	0.69
SPBC1A4.02c	3-isopropylmalate dehydrogenase Leu1	0.69
SPAC15E1.09	glutaredoxin Grx2	0.69
SPCC794.11c	ENTH/VHS domain protein Ent3 (predicted)	0.69
SPAC1399.05c	transcription factor%2C zf-fungal binuclear cluster type	0.69
SPCC1281.02c	splicing factor Spf30 (predicted)	0.69
SPCC18.06c	CCR4-Not complex CAF1 family ribonuclease subunit Caf1	0.69
SPCC330.20	conserved fungal protein	0.69
SPCC645.08c	RNA-binding protein Snd1	0.69
SPAC2G11.15c	rRNA methyltransferase Tgs1 (predicted)	0.69
SPBC1604.03c	conserved fungal protein	0.69
SPCC1827.03c	acetyl-CoA ligase (predicted)	0.69
SPAC12B10.09	S-adenosylmethionine transporter (predicted)	0.69
SPAC14C4.06c	poly(A) binding protein Nab2 (predicted)	0.69
SPBC16E9.06c	BolA domain UV induced protein Uvi31	0.69
SPCC1393.13	DUF89 family protein	0.69
SPAC13C5.04	amidotransferase (predicted)	0.68
SPAC664.03	RNA polymerase II associated Paf1 complex (predicted)	0.68
SPAC144.09c	RNA polymerase III transcription factor TFIIIA	0.68
SPBC1734.04	mannosyltransferase complex subunit%2C Anp family (predicted)	0.68
SPBC13G1.12	ESCRT III complex subunit Did2 (predicted)	0.68
SPCC736.04c	alpha-1%2C2-galactosyltransferase Gma12	0.68
SPBC21C3.08c	ornithine transaminase Car2	0.68
SPBC17G9.12c	hydrolase (predicted)	0.68
SPAC30D11.02c	sequence orphan	0.68
SPAC19B12.09	signal recognition particle subunit Srp14	0.68
SPBC2D10.11c	nucleosome assembly protein Nap2 (predicted)	0.68
SPBC13G1.16	dubious	0.68
SPBC83.19c	sequence orphan	0.68
SPBC1105.06	mediator complex subunit Pmc4	0.68

SPAPB21F2.03	ribosome biogenesis protein Slx9 (predicted)	0.68
SPAC26A3.06	rRNA (guanine) methyltransferase (predicted)	0.68
SPAC31G5.04	homoisocitrate dehydrogenase Lys12	0.68
SPAC23A1.02c	phosphoprotein phosphatase (predicted)	0.68
SPCC4B3.16	TIP41-like type 2a phosphatase regulator Tip41	0.68
SPBC14C8.14c	DNA polymerase phi	0.68
SPCC338.05c	ubiquitin conjugating enzyme Mms2	0.68
SPCC965.04c	mitochondrial inner membrane i-AAA protease complex subunit Yme1 (predicted)	0.68
SPAC31G5.18c	silencing defective protein Sde2	0.68
SPAC23D3.17	conserved fungal protein	0.68
SPAC17H9.04c	RNA-binding protein	0.68
SPCC4B3.03c	mitochondrial morphology protein (predicted)	0.68
SPAC688.03c	human AMMECR1 homolog	0.68
SPAC343.14c	translation initiation factor eIF2B beta subunit (predicted)	0.68
SPAC23A1.03	adenine phosphoribosyltransferase (APRT) (predicted)	0.68
SPCC4G3.13c	CUE domain protein Cue1/4 family involved in ER associated protein catabolism (predicted)	0.68
SPAC3F10.16c	GTP binding protein%2C HSR1-related (predicted)	0.68
SPBC1711.07	WD repeat protein Rrb1 (predicted)	0.68
SPAC343.16	homoaconitate hydratase Lys2	0.67
SPBC839.07	Cdc25 family phosphatase Ibp1	0.67
SPBC530.15c	spermidine family transporter (predicted)	0.67
SPAC20G8.03	MFS myo-inositol transporter	0.67
SPBC800.14c	DUF1772 family protein	0.67
SPAC2C4.04c	conserved eukaryotic protein	0.67
SPBC16A3.04	mitochondrial ribosomal protein subunit Rsm25 (predicted)	0.67
SPAC12B10.11	glucan glucosidase Exg2%2C unknown specificity	0.67
SPAC23G3.01	RNA polymerase II complex subunit Rpb2	0.67
SPAC31A2.04c	20S proteasome complex subunit beta 4 (predicted)	0.67
SPAC12B10.15c	ribonuclease H2 complex subunit (predicted)	0.67
SPCC1442.17c	MVB sorting pathway protein (predicted)	0.67
SPAC2F3.09	5-aminolevulinate synthase (predicted)	0.67
SPCC31H12.07	COPII cargo receptor subunit Sec23a (predicted)	0.67
SPAC926.09c	fatty acid synthase beta subunit Fas1	0.67
SPAC823.06	transcription factor TFIID complex subunit Taf3 (predicted)	0.67
SPBC342.04	19S proteasome regulatory subunit Rpn13a	0.67
SPBC18E5.07	DUF3210 family protein	0.67
SPBC2A9.04c	sir antagonist	0.67
SPAC1071.04c	signal peptidase subunit Spc2 (predicted)	0.67
SPAC10F6.04	RCC domain protein Ats1 (predicted)	0.67
SPAC17C9.01c	anaphase-promoting complex subunit Apc3	0.66
SPCC132.02	Sir2 family histone deacetylase Hst2	0.66
SPBC25B2.09c	mitochondrial and cytoplasmic arginine-tRNA ligase Rrs1/Mrs1 (predicted)	0.66
SPBC119.05c	Wiskott-Aldrich syndrome homolog binding protein Lsb1 (predicted)	0.66
SPCC613.09	tRNA-splicing endonuclease subunit Sen54 (predicted)	0.66
SPCC4B3.08	Lsk1 complex gamma subunit (predicted)	0.66

SPAC31G5.13	19S proteasome regulatory subunit Rpn11	0.66
SPAC1805.05	serine/threonine protein kinase Cki3	0.66
SPBC1271.12	oxysterol binding protein (predicted)	0.66
SPCC1672.07	U3 snoRNP-associated protein Utp21 (predicted)	0.66
SPBC9B6.08	clathrin light chain	0.66
SPBC25H2.12c	chaperonin-containing T-complex eta subunit Cct7	0.66
SPAC23C4.15	DNA-directed RNA polymerase I%2C II and III subunit Rpb5	0.66
SPAC5H10.11	alpha-1%2C2-galactosyltransferase Gmh1 (predicted)	0.66
SPAC8F11.02c	diphthamide biosynthesis protein Dph3 (predicted)	0.66
SPAC26A3.17c	N-methyltransferase (predicted)	0.66
SPCC1259.15c	ubiquitin conjugating enzyme E2-C%2C Ubc11	0.66
SPCC1450.11c	serine/threonine protein kinase Cek1	0.66
SPAC1610.02c	mitochondrial ribosomal protein subunit L1 (predicted)	0.66
SPAC56E4.03	aromatic aminotransferase (predicted)	0.66
SPBC83.13	mitochondrial tricarboxylic acid transporter (predicted)	0.66
SPAPJ695.02	sequence orphan	0.66
SPAC2F7.03c	DYRK family protein kinase Pom1	0.66
SPBC17A3.06	phosphoprotein phosphatase (predicted)	0.66
SPBC1718.03	DNA-directed RNA polymerase I complex subunit Ker1	0.66
SPCC18.12c	rRNA processing protein Utp23 (predicted)	0.66
SPAC4A8.03c	protein phosphatase 2C Ptc4	0.66
SPBC3D6.06c	ribose-phosphate pyrophosphokinase Prs5 (predicted)	0.66
SPAC1F7.02c	ATP-dependent RNA helicase Has1 (predicted)	0.65
SPBC83.07	Lid2 complex subunit%2C histone demethylase H3-K36 specific Jmj3	0.65
SPAC222.04c	Ino80 complex subunit Ies6	0.65
SPBC106.14c	SDA1 family protein (predicted)	0.65
SPAC11G7.01	sequence orphan	0.65
SPCC757.12	alpha-amylase homolog (predicted)	0.65
SPAC1B3.09c	Noc2p-Noc3p complex subunit Noc2 family (predicted)	0.65
SPAC23G3.10c	SWI/SNF and RSC complex subunit Ssr3	0.65
SPAC25B8.01	cytochrome P450 regulator Dap1	0.65
SPBC26H8.07c	tubulin beta Nda3	0.65
SPBC21B10.14	mitochondrial ribosomal protein Ymr1 (predicted)	0.65
SPAC17H9.14c	protein disulfide isomerase	0.65
SPAC1805.17	importin family nuclear export receptor Crm1	0.65
SPBC3B9.03	signal recognition particle receptor alpha subunit Srp101 (predicted)	0.65
SPBP4H10.11c	long-chain-fatty-acid-CoA ligase	0.65
SPAC227.05	prefoldin subunit 4 (predicted)	0.65
SPBP18G5.03	Tor complex Tor2 interacting protein 1	0.65
SPBC1677.03c	mitochondrial threonine ammonia-lyase (predicted)	0.65
SPBC1271.01c	F-box protein Pof13	0.65
SPBC13G1.01c	mitochondrial ribosomal protein subunit S4 (predicted)	0.65
SPCC1672.03c	guanine deaminase (predicted)	0.65
SPAC664.11	mitochondrial heat shock protein Hsp70	0.65
SPBC26H8.12	cytochrome c heme lyase (predicted)	0.65
SPCPB16A4.03c	bifunctional IMP	0.65

	cyclohydrolase/phosphoribosylaminoimidazolecarboxamideformyltransferase	
SPAC926.06c	leucine-rich repeat protein%2C unknown	0.65
SPBC119.10	asparagine synthetase	0.65
SPBC13G1.04c	alkB homolog/2-OG-Fe(II) oxygenase family Abh1 (predicted)	0.65
SPAC30C2.08	conserved fungal protein	0.64
SPAC1751.02c	mitochondrial ribosomal protein subunit S19 (predicted)	0.64
SPBC1718.06	mitochondrial dynamin family GTPase Msp1	0.64
SPCC18.10	pyridoxine-pyridoxal-pyridoxamine kinase (predicted)	0.64
SPBC16E9.03c	mitochondrial inner membrane protein involved in respiratory chain complex IV assembly Coa1 (predicted)	0.64
SPAC29A4.07	mediator complex subunit Srb6	0.64
SPBPB21E7.01c	enolase (predicted)	0.64
SPBC119.08	MAP kinase Pmk1	0.64
SPBC18H10.17c	mitochondrial recombinase Mhr1 (predicted)	0.64
SPBC119.14	Rad22 homolog Rti1	0.64
SPAC3H8.08c	transcription factor (predicted)	0.64
SPAC13G7.12c	choline kinase (predicted)	0.64
SPAC4H3.09	mitochondrial type II fatty acid synthase component (predicted)	0.64
SPACUNK12.02c	calcium/calmodulin-dependent protein kinase Cmk1	0.64
SPAC13A11.06	pyruvate decarboxylase (predicted)	0.64
SPAC11D3.06	MatE family transporter (predicted)	0.64
SPBC530.05	transcription factor (predicted)	0.64
SPAC6C3.08	proteasome regulatory particle%2C gankyrin (predicted)	0.64
SPAC9.13c	splicing factor Cwf16	0.63
SPCC4B3.17	ubiquinol cytochrome-c reductase assembly protein Cbp3 (predicted)	0.63
SPAC13C5.05c	N-acetylglucosamine-phosphate mutase (predicted)	0.63
SPAC19G12.16c	conserved fungal protein Adg2	0.63
SPBC1778.01c	zuotin (predicted)	0.63
SPBC3B9.02c	splicing factor Cwf28	0.63
SPAC15A10.11	UBR ubiquitin ligase Ubr11	0.63
SPAC1565.05	sequence orphan	0.63
SPCC1281.07c	glutathione S-transferase (predicted)	0.63
SPBC19F5.05c	pescadillo-family BRCT domain protein (predicted)	0.63
SPCC1259.08	conserved fungal protein%2C DUF2457 family	0.63
SPBC36.07	elongator subunit Elp1 (predicted)	0.63
SPAC977.17	MIP water channel (predicted)	0.63
SPAC7D4.03c	conserved fungal family	0.63
SPBC365.08c	Der1-like (degradation in the ER) family (predicted)	0.63
SPBC887.18c	SAGA complex subunit Hfi1	0.63
SPBC1773.07c	Ran GTPase binding protein Sbp1	0.63
SPBC17D1.04	upstream activation factor complex subunit Acr1	0.63
SPCC830.08c	ER membrane protein DP1/Yop1	0.63
SPAC10F6.14c	ABC1 kinase family protein (predicted)	0.63
SPAC222.15	Tat binding protein 1(TBP-1)-interacting protein (TBPIP) homolog (predicted)	0.63
SPAC9.02c	polyamine N-acetyltransferase (predicted)	0.62
SPBC2G5.05	transketolase (predicted)	0.62
SPCC1259.10	mitochondrial metallopeptidase predicted to	0.62

	be involved in tRNA threonylcarbamoyladenosine modification Pgp1	
SPAPB1A10.13	sequence orphan	0.62
SPBC2D10.07c	mitochondrial inner membrane peptidase complex catalytic subunit (predicted)	0.62
SPAC23C4.13	SNARE Bet1 (predicted)	0.62
SPAC144.04c	ornithine decarboxylase Spe1 (predicted)	0.62
SPAC22E12.04	superoxide dismutase copper chaperone Ccs1	0.62
SPBC14C8.13	SRR1 family protein	0.62
SPAC12G12.09	conserved fungal protein	0.62
SPBP8B7.10c	U3 snoRNP-associated protein Utp16 (predicted)	0.62
SPAC10F6.01c	sulfite reductase Sir1	0.62
SPAC3A12.16c	TIM23 translocase complex subunit Tim17 (predicted)	0.62
SPBC3B8.09	U3 snoRNP-associated protein Utp3 (predicted)	0.62
SPCC338.07c	NatA N-acetyltransferase complex regulatory subunit Naa15 (predicted)	0.62
SPBC409.09c	kinetochore protein Mis13	0.62
SPBC1347.04	TIM22 inner membrane protein import complex subunit Tim54 (predicted)	0.62
SPAC57A7.09	human RNF family homolog	0.62
SPBC18H10.02	long-chain-fatty-acid-CoA ligase Lcf1	0.62
SPBC23G7.10c	NADH-dependent flavin oxidoreductase (predicted)	0.62
SPAPJ696.01c	retromer complex subunit Vps17	0.62
SPBC1604.13c	mitochondrial ribosomal protein subunit L32 (predicted)	0.62
SPBC1539.09c	anthranilate synthase component II%2C multifunctional enzyme (predicted)	0.62
SPBC337.16	phosphatidyl-N-methylethanolamine N-methyltransferase (predicted)	0.62
SPBP8B7.02	sequence orphan	0.62
SPBC1711.08	chaperone activator Aha1 (predicted)	0.62
SPCC622.15c	sequence orphan	0.62
SPAC19B12.03	1%2C3-beta-glucan synthase subunit Bgs3	0.61
SPBC4.01	tetraspan protein Dni2 (predicted)	0.61
SPAC688.11	Huntingtin-interacting protein homolog	0.61
SPBP16F5.04	ubiquitin conjugating enzyme Ubc7/UbcP3	0.61
SPAC57A10.10c	La protein homolog	0.61
SPCC757.03c	ThiJ domain protein	0.61
SPCC162.03	short chain dehydrogenase (predicted)	0.61
SPBC1703.13c	mitochondrial inorganic phosphate transporter (predicted)	0.61
SPAC17H9.12c	mitochondrial cytochrome c-heme linkage protein Cyc2 (predicted)	0.61
SPBC651.07	sequence orphan	0.61
SPAC20H4.03c	transcription elongation factor TFIIS	0.61
SPBC36.11	sequence orphan	0.61
SPAC1F12.07	phosphoserine aminotransferase (predicted)	0.61
SPAC3H1.05	CAAX prenyl protease (predicted)	0.61
SPBC660.12c	Ergothioneine biosynthesis protein Egt2	0.61
SPAC29B12.10c	glutathione transporter Pgt1	0.61
SPCPB16A4.02c	conserved fungal protein	0.61
SPAC19A8.09	ER to Golgi transport protein Yos1 (predicted)	0.61
SPAC10F6.05c	ubiquitin conjugating enzyme Ubc6 (predicted)	0.61
SPCC16C4.07	RNA-binding protein Scw1	0.61
SPBP22H7.09c	CENP-N%2C kinetochore protein Mis15	0.61
SPBC119.01	19S proteasome regulatory subunit Rpn3	0.61

SPAC1B3.04c	mitochondrial GTPase involved in translation Guf1 (predicted)	0.61
SPBC1711.03	ER membrane protein complex subunit Aim27 (predicted)	0.61
SPCC14G10.04	sequence orphan	0.61
SPCC4G3.17	HD domain metal dependent phosphohydrolase (predicted)	0.61
SPAC25B8.09	trans-aconitate 3-methyltransferase (predicted)	0.61
SPAC22A12.02c	sequence orphan	0.61
SPAC2F3.06c	karyopherin Kap104	0.61
SPAC4F8.12c	U5 snRNP complex subunit Spp42	0.61
SPAC4D7.08c	amidophosphoribosyltransferase Ade4	0.61
SPAC1F5.03c	FAD-dependent oxidoreductase involved in late endosome to Golgi transport (predicted)	0.61
SPCC16C4.11	Pho85/PhoA-like cyclin-dependent kinase Pef1	0.61
SPBC27B12.13	mitochondrial TOM complex subunit Tom40 (predicted)	0.61
SPAC23C4.07	meiotically upregulated gene Mug22	0.61
SPCC1450.05c	mediator complex subunit Med19/Rox3	0.61
SPBC1709.14	peptide N-glycanase (predicted)	0.61
SPBP8B7.13	Vac7 ortholog (predicted)	0.61
SPBC17G9.06c	siderophore-iron biosynthesis protein (predicted)	0.60
SPBC13E7.04	F1-ATPase delta subunit (predicted)	0.60
SPCP1E11.08	ribosome biogenesis protein Nsa2 (predicted)	0.60
SPBC244.02c	U3 snoRNP-associated protein Utp6 (predicted)	0.60
SPAC2E1P3.01	dehydrogenase (predicted)	0.60
SPCC285.06c	wtf element Wtf17	0.60
SPAC6B12.07c	ubiquitin-protein ligase E3 (predicted)	0.60
SPAC3H1.03	mouse transcriptional regulator%2C HCNGP-like (predicted)	0.60
SPAC23H4.12	MRG family Clr6 histone deacetylase complex subunit Alp13	0.60
SPBC17G9.02c	RNA polymerase II accessory factor%2C Cdc73 family (predicted)	0.60
SPAC1486.01	manganese superoxide dismutase (predicted)	0.60
SPAC20G8.10c	beclin family protein%2C involved in autophagy	0.60
SPAC144.02	Ino80 complex subunit Iec1	0.60
SPAC977.11	CRCB domain protein	0.60
SPBC839.04	60S ribosomal protein L8 (predicted)	0.60
SPBC1718.05	TRAPP complex subunit Trs31 (predicted)	0.60
SPBC839.17c	FKBP12 peptidyl-prolyl cis-trans isomerase Fkh1	0.60
SPBC211.05	splicing factor 3B	0.60
SPAC10F6.07c	sequence orphan	0.60
SPAPB1E7.02c	DNA polymerase alpha accessory factor Mcl1	0.60
SPBC215.10	haloacid dehalogenase-like hydrolase	0.60
SPAC1834.09	variant protein kinase 19 family protein	0.60
SPAP7G5.04c	aminoadipate-semialdehyde dehydrogenase	0.60
SPAC222.09	RNA-binding protein Seb1	0.60
SPBC947.10	Golgi Dsc E3 ligase complex subunit Dsc1	0.60
SPAC513.03	M-factor precursor Mfm2	0.60
SPCC962.06c	zinc finger splicing factor Bpb1	0.60
SPBC23E6.06c	3%2C4-dihydroxy-2-butanone 4-phosphate synthase (predicted)	0.60
SPAC222.18	Srp1 family splicing factor (predicted)	0.60

SPAC1F7.12	aldose reductase ARK13 family YakC	0.59
SPBP8B7.07c	histone lysine methyltransferase Set6 (predicted)	0.59
SPAC3G6.02	mRNA export protein Dss1	0.59
SPCC24B10.17	COPII-coated vesicle component Emp24 (predicted)	0.59
SPBC30B4.04c	SWI/SNF complex subunit Sol1	0.59
SPBC409.14c	mitochondrial ribosomal protein subunit S17 (predicted)	0.59
SPAC3G9.04	phosphoric ester hydrolase Ssu72 (predicted)	0.59
SPAC1F12.08	cytidylyltransferase (predicted)	0.59
SPAC16C9.04c	CCR4-Not complex subunit Mot2 (predicted)	0.59
SPAC15A10.04c	EF-1 alpha binding zinc finger protein Zpr1 (predicted)	0.59
SPCC584.05	SNARE binding protein Sec1 (predicted)	0.59
SPAC30C2.06c	mitochondrial inheritance GTPase%2C tubulin-like (predicted)	0.59
SPAC3F10.17	ribosome biogenesis protein Ltv1 (predicted)	0.59
SPBC106.04	adenosine deaminase Ada1 (predicted)	0.59
SPBC2F12.10	mitochondrial ribosomal protein subunit L35 (predicted)	0.59
SPAC29E6.06c	cytoplasmic cysteine-tRNA ligase Crs1 (predicted)	0.59
SPAC3A12.13c	translation initiation factor eIF3j (p35)	0.59
SPAC2C4.08	conserved fungal protein	0.59
SPAC4C5.02c	GTPase Ryh1	0.59
SPBP23A10.06	mitochondrial manganese ion transporter (predicted)	0.59
SPAC1399.03	uracil permease	0.59
SPAC1296.06	NADPH-dependent diflavin oxidoreductase%2C involved in iron-sulfur cluster assembly Tah18 (predicted)	0.59
SPBC13G1.14c	RNA-binding protein (predicted)	0.59
SPAC4G9.09c	N-acetyl-gamma-glutamyl-phosphate reductase/acetylglutamate kinase	0.59
SPAC11D3.01c	conserved fungal protein	0.59
SPCC1753.01c	single-stranded DNA binding protein Ssb2	0.59
SPBC16C6.12c	Las1 pre-rRNA processing protein	0.59
SPAC890.04c	ribosome biogenesis protein Ytm1 (predicted)	0.59
SPBC14C8.05c	glucan-alpha-1%2C4-glucosidase	0.59
SPBC21D10.12	BAR adaptor protein Hob1	0.59
SPCC4B3.09c	mitochondrial ribosomal protein subunit L12 (predicted)	0.58
SPBC1921.03c	mRNA export receptor%2C Tap%2C nucleoporin Mex67	0.58
SPAC644.06c	NIM1 family serine/threonine protein kinase Cdr1/Nim1	0.58
SPBC19C7.07c	tRNA-splicing endonuclease catalytic subunit Sen34 (predicted)	0.58
SPAPB18E9.01	tRNA (guanine) methyltransferase Trm5 (predicted)	0.58
SPCC1450.13c	riboflavin synthase	0.58
SPAC1556.08c	protein kinase activator (predicted)	0.58
SPCC663.05c	histone chaperone Cia1	0.58
SPBC27.06c	mitochondrial membrane protein Mgr2 (predicted)	0.58
SPAC4F10.09c	ribosome biogenesis protein Noc1 (predicted)	0.58
SPCC24B10.20	short chain dehydrogenase (predicted)	0.58
SPAC1002.04c	transcription factor TFIID complex subunit	0.58

	Taf11 (predicted)	
SPBC947.01	ATP-dependent microtubule severing protein (predicted)	0.58
SPBC27B12.12c	CorA family magnesium ion transporter (predicted)	0.58
SPBC23G7.13c	urea transporter (predicted)	0.58
SPAC513.07	flavonol reductase/cinnamoyl-CoA reductase family	0.58
SPCC622.02	dubious	0.58
SPBC216.03	conserved fungal protein	0.58
SPBC24C6.05	coatomer epsilon subunit (predicted)	0.58
SPAC13G7.10	Myb family telomere binding protein (predicted)	0.58
SPAC23G3.07c	SWI/SNF complex subunit Snf30	0.58
SPBC1703.09	sequence orphan	0.58
SPAC22F8.06	20S proteasome complex subunit beta 6	0.58
SPBC19G7.17	translocon subunit Sec61 homolog (predicted)	0.58
SPAC4D7.02c	glycerophosphoryl diester phosphodiesterase (predicted)	0.58
SPBC4.07c	19S proteasome regulatory subunit Rpt2	0.58
SPBC354.07c	oxysterol binding protein (predicted)	0.58
SPBC21C3.14c	sequence orphan	0.58
SPAC26H5.09c	gfo/idh/mocA family oxidoreductase (predicted)	0.58
SPBC146.08c	translation initiation factor eIF1A-like (predicted)	0.57
SPCC4G3.04c	C-methyltransferase (predicted)	0.57
SPAC25A8.03c	DUF185 protein%2C mitochondrial	0.57
SPAC1071.06	SWI/SNF and RSC complex subunit Arp9	0.57
SPBC646.12c	GTPase activating protein Gap1	0.57
SPAC29A4.20	elongator complex%2C histone acetyltransferase subunit Elp3 (predicted)	0.57
SPAC1D4.08	CDP-diacylglycerol--inositol 3-phosphatidyltransferase Pis1 (predicted)	0.57
SPCC24B10.04	sequence orphan	0.57
SPAC17G8.08c	human TMEM165 homolog	0.57
SPCC1906.01	mannose-1-phosphate guanyltransferase Mpg1	0.57
SPBC8E4.03	agmatinase 2 (predicted)	0.57
SPBC530.08	membrane-tethered transcription factor (predicted)	0.57
SPAC3G9.08	ING family homolog Png1	0.57
SPBC887.22	signal peptidase complex subunit Spc1 (predicted)	0.57
SPAC22H12.01c	sequence orphan	0.57
SPBC18H10.03	translation initiation factor eIF3g	0.57
SPAC4G8.06c	tRNA methyltransferase Trm12 (predicted)	0.57
SPBC1539.03c	argininosuccinate lyase (predicted)	0.57
SPAC22A12.11	dihydroxyacetone kinase Dak1	0.57
SPAC23A1.18c	mitochondrial ribosomal protein subunit L51-b (predicted)	0.57
SPAPJ760.03c	sequence orphan	0.57
SPACUNK4.16c	alpha%2Calpha-trehalose-phosphate synthase (predicted)	0.57
SPCC126.12	NGG1 interacting factor 3 family%2C implicated in transcription	0.56
SPBC1604.06c	CBF/Mak21 family (predicted)	0.56
SPBP8B7.31	acid phosphatase (predicted)	0.56
SPBC21C3.07c	tRNA (cytosine) methyltransferase (predicted)	0.56
SPBC16C6.07c	19S proteasome regulatory subunit Rpt1 (predicted)	0.56
SPAC17A2.08c	spliceosome complex disassembly protein	0.56

	Ntr2 (predicted)	
SPBC577.11	DUF3074 family protein	0.56
SPCC645.02	mitochondrial matrix PGP phosphatase involved in cardiolipin biosynthesis Gep4 (predicted)	0.56
SPAC6F6.03c	ribosome export GTPase (predicted)	0.56
SPAC227.06	Rab GTPase binding (predicted)	0.56
SPBC409.06	ubiquitin C-terminal hydrolase Uch2	0.56
SPAC18G6.11c	ribosomal DNA (rDNA) transcription factor Rrn3	0.56
SPBC646.13	PP2A-type phosphatase inhibitor Sds23/Moc1	0.56
SPBC23G7.11	DNA-3-methyladenine glycosidase Mag2	0.56
SPBP35G2.12	ADP-ribose diphosphatase%2C NudF subfamily (predicted)	0.56
SPAC17C9.08	mitochondrial endodeoxyribonuclease Pnu1	0.56
SPCC338.11c	protein-lysine N-methyltransferase Rrg1 (predicted)	0.56
SPBP8B7.26	sequence orphan	0.56
SPAC1F8.03c	siderophore-iron transporter Str3	0.56
SPBC3H7.15	serine/threonine protein kinase Hhp1	0.56
SPCC4B3.05c	uroporphyrinogen decarboxylase Hem12 (predicted)	0.56
SPBC119.09c	ORMDL family protein (predicted)	0.56
SPBC31F10.16	ChAPs family protein (predicted)	0.56
SPCC622.03c	hypothetical protein	0.55
SPBC56F2.08c	RNA-binding protein (predicted)	0.55
SPAC688.13	TatD DNase family Scn1	0.55
SPCC965.14c	cytosine deaminase (predicted)	0.55
SPCP1E11.04c	membrane associated protein Pal1	0.55
SPBC6B1.06c	ubiquitin C-terminal hydrolase Ubp14	0.55
SPAC13G6.05c	TRAPP complex subunit Trs33 (predicted)	0.55
SPAC926.08c	Brix domain protein Rpf2 (predicted)	0.55
SPCC777.07	alpha-1%2C2-mannosyltransferase Omh3 (predicted)	0.55
SPBC28F2.05c	xylose and arabinose reductase (predicted)	0.55
SPAC4D7.13	U1 snRNP-associated protein Usp104	0.55
SPAC1B1.02c	NAD/NADH kinase (predicted)	0.55
SPCC285.13c	nucleoporin Nup60	0.55
SPBC651.08c	DNA-directed RNA polymerase III complex large subunit Rpc1 (predicted)	0.55
SPAC959.03c	U3 snoRNP-associated protein Utp7 (predicted)	0.55
SPAC6B12.13	protein phosphatase inhibitor (predicted)	0.55
SPAC7D4.13c	sequence orphan	0.55
SPBC1105.16c	RNase P subunit Rpr2 (predicted)	0.55
SPAC3F10.05c	T5orf172 family protein	0.55
SPBC4F6.18c	ADP-ribosylation factor%2C Arf family Arf1	0.55
SPAC26H5.05	IPT/TIG ankyrin repeat containing transcription regulator of fatty acid biosynthesis (predicted)	0.55
SPCC1494.03	armadillo repeat containing%2C Zfs1 target number 1	0.55
SPBC26H8.10	3'-5' exoribonuclease subunit Dis3 (predicted)	0.55
SPAC1A6.06c	sequence orphan Meu31	0.55
SPBC17D1.02	diphthamide biosynthesis protein (predicted)	0.55
SPBC31F10.12	RNA-binding protein Tma20 (predicted)	0.55
SPBC1198.01	glutathione-dependent formaldehyde dehydrogenase (predicted)	0.55
SPBC28F2.04c	splicing factor Cwf7	0.55
SPAC23C11.14	zinc ion transporter Zhf1	0.55

SPCC622.21	wtf element Wtf12	0.55
SPBC4.06	acid phosphatase (predicted)	0.55
SPAC3G6.08	mitochondrial sulfhydryl oxidase (predicted)	0.55
SPCC1020.01c	P-type proton ATPase%2C P3-type Pma2	0.54
SPAC637.08	iron-sulfur cluster assembly ATPase Nbp35 (predicted)	0.54
SPAC19A8.13	U1 snRNP-associated protein Usp101 (predicted)	0.54
SPBC16G5.11c	BAG family molecular chaperone regulator Bag101 (predicted)	0.54
SPCC16C4.22	DNA polymerase epsilon Dpb3 (predicted)	0.54
SPAC222.06	nuclear HMG-like acidic protein Mak16 (predicted)	0.54
SPBC1703.07	ATP citrate synthase subunit 1 (predicted)	0.54
SPAC6B12.14c	conserved fungal protein	0.54
SPBC1861.09	serine/threonine protein kinase Ppk22 (predicted)	0.54
SPBC12D12.08c	ubiquitin-like protein modifier Ned8	0.54
SPBP8B7.20c	RNA methyltransferase Nop2 (predicted)	0.54
SPBC29A3.01	copper transporting ATPase Ccc2 (predicted)	0.54
SPAC323.08	ribonuclease MRP complex subunit (predicted)	0.54
SPAC56F8.11	signal peptidase subunit Spc3 (predicted)	0.54
SPCC830.07c	DNAJ domain protein%2C involved in translation initiation Psi1	0.54
SPCC330.02	Rad7 homolog Rhp7	0.54
SPAP14E8.03	SNARE Bos1 (predicted)	0.54
SPBC29A10.09c	CAF1 family ribonuclease (predicted)	0.54
SPAC14C4.12c	clr6 L associated factor 1 Laf1	0.54
SPBC19C2.14	Sm snRNP core protein Smd3	0.54
SPAC186.09	pyruvate decarboxylase (predicted)	0.54
SPBC1289.06c	mitochondrial PPR repeat protein Ppr8	0.54
SPCC1450.16c	triacylglycerol lipase ptl1	0.54
SPBC725.09c	BAR adaptor protein Hob3	0.54
SPBP4H10.21c	GINS complex subunit Sld5	0.54
SPBC18H10.04c	translation initiation factor (predicted)	0.54
SPAC23C4.03	haspin related kinase Hrk1	0.54
SPCC297.03	serine/threonine protein kinase Ssp1	0.54
SPBC2F12.15c	palmitoyltransferase Pfa3 (predicted)	0.54
SPBPB8B6.03	acetamidase (predicted)	0.54
SPAC6G9.02c	RNA-binding protein Nop9 (predicted)	0.53
SPAC1B3.14	V-type ATPase V0 subunit c (proteolipid subunit)	0.53
SPAC1952.04c	conserved fungal protein	0.53
SPBC337.02c	cell surface glycoprotein%2C adhesion molecule (predicted)%2C DUF1773 family protein 6	0.53
SPAC1834.01	translation release factor eRF1	0.53
SPCC550.06c	mitochondrial heat shock protein Hsp10 (predicted)	0.53
SPAC3H8.02	sec14 cytosolic factor family phosphatidylinositol transporter (predicted)	0.53
SPCC16A11.01	plasma membrane protein involved in inositol lipid-mediated signaling (predicted)	0.53
SPAP27G11.02	TPR repeat protein%2C involved in mitochondrial protein turnover (predicted)	0.53
SPAC29A4.22	dubious	0.53
SPAC30D11.04c	nucleoporin Nup124	0.53
SPAC1834.07	kinesin-like protein Klp3	0.53
SPCC4G3.15c	CCR4-Not complex subunit Not2 (predicted)	0.53
SPAC23C11.13c	xanthine phosphoribosyltransferase	0.53

	(predicted)	
SPAC328.07c	heavy metal ion homeostasis protein (predicted)	0.53
SPBC29A3.05	Swr1 complex subunit Vps71	0.53
SPAC22F3.07c	F0-ATPase subunit G (predicted)	0.53
SPBC8D2.17	alpha-1%2C2-galactosyltransferase (predicted)	0.53
SPAC27D7.04	4-alpha-hydroxytetrahydrobiopterin dehydratase (predicted)	0.53
SPBC725.01	aspartate aminotransferase (predicted)	0.52
SPCC1442.09	anthranilate synthase component I (predicted)	0.52
SPBC25H2.04c	TIM22 inner membrane protein import complex subunit Tim22 (predicted)	0.52
SPAC1420.02c	chaperonin-containing T-complex epsilon subunit Cct5	0.52
SPAC4F10.15c	WASp homolog	0.52
SPAC23C4.12	serine/threonine protein kinase Hhp2	0.52
SPAC23H4.17c	cyclin-dependent protein Srb mediator subunit kinase Srb10	0.52
SPAC27D7.06	electron transfer flavoprotein alpha subunit (predicted)	0.52
SPBP8B7.04	sequence orphan	0.52
SPBC3B8.08	Sjogren's syndrome/scleroderma autoantigen 1 family (predicted)	0.52
SPAC630.04c	sequence orphan	0.52
SPBC2D10.10c	fibrillarin%2C rRNA methyltransferase	0.52
SPAC17A5.09c	protein phosphatase regulatory subunit Glc9 (predicted)	0.52
SPAC2C4.11c	RNA-binding protein Rbp28	0.52
SPBC713.04c	U3 snoRNP-associated protein Utp1 (predicted)	0.52
SPAC1F7.14c	mitochondrial conserved protein	0.52
SPCP1E11.10	ankyrin repeat protein%2C unknown biological role	0.52
SPBC1105.18c	peptide release factor (predicted)	0.52
SPBC14C8.03	methionine aminopeptidase Fma2 (predicted)	0.52
SPBC30D10.15	snoRNP assembly factor Naf1 (predicted)	0.52
SPBC582.07c	19S proteasome regulatory subunit Rpn7	0.52
SPCC550.02c	RNA-binding protein Cwf5	0.52
SPAC23C11.08	CCAAT-binding factor complex subunit Php3	0.52
SPBC26H8.13c	Siva family protein (predicted)	0.52
SPBC25B2.03	zf-C3HC4 type zinc finger	0.51
SPAC1039.03	esterase/lipase (predicted)	0.51
SPAC6B12.12	mitochondrial TOM complex subunit Tom70 (predicted)	0.51
SPBC1734.14c	cyclin-dependent protein kinase regulatory subunit Suc1	0.51
SPBC3E7.10	methionine aminopeptidase Fma1 (predicted)	0.51
SPBC947.15c	mitochondrial NADH dehydrogenase (predicted)	0.51
SPAC644.13c	Rab GTPase binding (predicted)	0.51
SPBP8B7.28c	LIM-like protein linking chromatin modification to RNAi%2C Stc1	0.51
SPCC737.03c	integral inner nuclear membrane protein Ima1	0.51
SPBC16E9.18	phosphatidylserine decarboxylase Psd1	0.51
SPCC584.11c	Svf1 family protein Svf1	0.51
SPAC14C4.16	DASH complex subunit Dad3	0.51
SPBC8D2.09c	U2 snRNP-associated protein Msl1 (predicted)	0.51

SPAC4G8.07c	tRNA (m5U54) methyltransferase Trm2 (predicted)	0.51
SPAC4G9.04c	cleavage and polyadenylation specificity factor (predicted)	0.51
SPBP8B7.19	FACT complex subunit Spt16	0.51
SPAC11D3.05	MFS family membrane transporter (predicted)	0.51
SPCC16C4.08c	p21 activated protein kinase inhibitor Skb15	0.51
SPAC227.09	folylpolyglutamate synthase (predicted)	0.51
SPBP8B7.24c	autophagy associated protein Atg8	0.51
SPCC550.11	karyopherin (predicted)	0.51
SPAC4G8.02c	translocon gamma subunit Sss1 (predicted)	0.51
SPAC17G6.16c	mRNA cleavage and polyadenylation specificity factor complex endoribonuclease subunit Ysh1	0.51
SPBC56F2.15	sequence orphan	0.51
SPBP35G2.08c	zinc knuckle TRAMP complex subunit Air1	0.51
SPAC19G12.14	1-phosphatidylinositol-4-phosphate 5-kinase Its3	0.51
SPAC2C4.03c	Sm snRNP core protein Smd2	0.51
SPBC4C3.10c	20S proteasome complex subunit beta 1 Pre3 (predicted)	0.51
SPBC16G5.03	ubiquitin-protein ligase E3 (predicted)	0.51
SPAC10F6.13c	aspartate aminotransferase (predicted)	0.51
SPBC32F12.02	Ski complex subunit Rec14	0.51
SPAC1687.19c	queuine tRNA-ribosyltransferase (predicted)	0.51
SPAC3G9.15c	rRNA processing protein Fcf2 (predicted)	0.51
SPAC186.06	ER unfolded protein response protein (predicted)	0.51
SPBC119.18	mitochondrial distribution and morphology protein Mdm35 (predicted)	0.50
SPCC1753.04	3'(2')%2C5'-bisphosphate nucleotidase/inositol-1%2C4- bisphosphate 1-phosphatase	0.50
SPBC31F10.05	sequence orphan	0.50
SPAC664.12c	mitochondrial succinate dehydrogenase assembly factor 1 (predicted)	0.50
SPBC3E7.15c	sphingosine N-acyltransferase Lac1	0.50
SPBC582.03	G2/M B-type cyclin Cdc13	0.50
SPBC12C2.11	glutamine-fructose-6-phosphate transaminase (predicted)	0.50
SPAC630.03	actin-like protein Arp3	0.50
SPCC1183.02	glutathione S-transferase (predicted)	0.50
SPCC18.11c	Dpy-30 domain protein Sdc1	0.50
SPBC1718.02	linear element associated protein Hop1	0.50
SPCC16C4.09	RNB-like protein	0.50
SPBC13E7.11	mitochondrial rhomboid protease (predicted)	0.50
SPAC23H3.11c	glucosidase (predicted)	0.50
SPBC21B10.09	acetyl-CoA transporter (predicted)	0.50
SPAC26H5.04	vacuolar import and degradation protein Vid28 (predicted)	0.50
SPAC4F8.14c	3-hydroxy-3-methylglutaryl-CoA synthase	0.50
SPAC1B2.03c	GNS1/SUR4 family protein (predicted)	0.50
SPBC3D6.05	phosphatidate cytidylyltransferase Ptp4 (predicted)	0.50
SPCC70.03c	proline dehydrogenase (predicted)	0.50
SPBC16C6.04	double strand break localizing protein Dbl6	0.50
SPBC16A3.15c	tubulin alpha 1	0.50

Systematic name	Description	H4K20 me2
SPBC19C2.15c	phosphoprotein phosphatase (predicted)	1.62
SPAC1250.02	sequence orphan	1.58
SPBC405.05	sequence orphan	1.57
SPAC3A12.04c	RNase P and RNase MRP subunit p30 (predicted)	1.48
SPBC337.04	serine/threonine protein kinase Ppk27 (predicted)	1.46
SPAC5H10.10	NADPH dehydrogenase (predicted)	1.45
SPAC1250.07	TFIIIC subunit Sfc7 (predicted)	1.45
SPBC428.13c	Sid2-Mob1 kinase complex regulatory subunit Mob1	1.40
SPAC589.11	mitochondrial translation release factor (predicted)	1.38
SPBC1289.14	adducin (predicted)	1.37
SPBC21C3.06	sequence orphan	1.31
SPCC757.02c	epimarase (predicted)	1.30
SPAC3A12.03c	ubiquitin-protein ligase E3 Meu34 (predicted)	1.29
SPCP20C8.04	cell surface glycoprotein (predicted)%2C DUF1773 family protein 6	1.27
SPCC757.06	sequence orphan%2C similar to a region of alpha-galactosidase%2C melibiase%2C possible pseudogene	1.24
SPBC409.10	phosphoribosylamidoimidazolesuccinocarboxamide synthase%2C SAICAR synthetase%2C Ade7	1.21
SPBC1773.08c	alpha-1%2C2-mannosyltransferase Omh4 (predicted)	1.21
SPBC428.19c	U3 snoRNP protein Utp15 (predicted)	1.20
SPAC56F8.08	UBA domain protein Mud1	1.19
SPAC25H1.07	ER membrane protein complex subunit Emc1 (predicted)	1.17
SPAC17A5.19	sequence orphan	1.17
SPAC1805.09c	methionyl-tRNA formyltransferase Fmt1 (predicted)	1.16
SPCC24B10.02c	NAD/NADH kinase (predicted)	1.15
SPBC27B12.02	sequence orphan	1.15
SPBC3E7.09	Sad1-UNC-like protein involved protein folding in the ER (predicted)	1.13
SPBC3H7.13	SIP/FAR complex FHA domain subunit Far10/Csc1	1.13
SPCC162.03	short chain dehydrogenase (predicted)	1.11
SPCC663.06c	short chain dehydrogenase (predicted)	1.09
SPAPB1E7.02c	DNA polymerase alpha accessory factor Mcl1	1.08
SPAC977.07c	cell surface glycoprotein%2C adhesion molecule (predicted)	1.08
SPBC3E7.17	dubious	1.07
SPAPB17E12.02	SMN family protein Yip12	1.07
SPBC1703.09	sequence orphan	1.06
SPAC22F3.08c	ATP-dependent RNA helicase Rok1 (predicted)	1.06
SPAC823.09c	threonine aspartase (predicted)	1.06
SPBC24C6.02	ATP-dependent RNA helicase Spb4 (predicted)	1.06
SPCC74.01	SNARE binding protein Sly1 (predicted)	1.05
SPBC216.03	conserved fungal protein	1.04
SPAC212.01c	S. pombe specific DUF999 family protein 2	1.03
SPAC16E8.17c	succinate-CoA ligase alpha subunit (predicted)	1.02
SPAC869.08	protein-L-isoaspartate O-methyltransferase	1.02

	Pcm2 (predicted)	
SPAC637.08	iron-sulfur cluster assembly ATPase Nbp35 (predicted)	1.01
SPAC2G11.05c	BRO1 domain protein Rim20 (predicted)	0.99
SPAC1039.03	esterase/lipase (predicted)	0.99
SPAP27G11.04c	tRNA specific adenosine deaminase subunit Tad3	0.98
SPBC19G7.08c	arrestin family protein	0.98
SPBC839.17c	FKBP12 peptidyl-prolyl cis-trans isomerase Fkh1	0.98
SPBC354.14c	vacuolar protein Vac8 (predicted)	0.97
SPCC584.02	middle-meiotic transcription factor Cuf2	0.97
SPCC663.14c	TRP-like ion channel (predicted)	0.97
SPCC569.02c	S. pombe specific UPF0321 family protein 2	0.96
SPBC16E9.16c	Lsd90 protein	0.96
SPCC191.09c	glutathione S-transferase Gst1	0.96
SPAC6B12.12	mitochondrial TOM complex subunit Tom70 (predicted)	0.96
SPAC5H10.11	alpha-1%2C2-galactosyltransferase Gmh1 (predicted)	0.96
SPAC3C7.02c	meiotic eisosome BAR domain protein Pil2	0.95
SPCC830.10	nucleoside triphosphatase (predicted)	0.95
SPCC1020.01c	P-type proton ATPase%2C P3-type Pma2	0.95
SPAC16A10.08c	sequence orphan	0.95
SPCC63.12c	20S proteasome complex subunit beta 3%2C Pup3 (predicted)	0.94
SPBC216.04c	peptide-methionine (R)-S-oxide reductase MsrB	0.94
SPAC1486.10	transcription factor Thi1	0.93
SPAC3H1.13	serine/threonine protein kinase Ppk13 (predicted)	0.93
SPBC21B10.12	meiotic recombination protein Rec6	0.93
SPBC31F10.12	RNA-binding protein Tma20 (predicted)	0.92
SPAC167.06c	sequence orphan	0.92
SPBC18H10.17c	mitochondrial recombinase Mhr1 (predicted)	0.91
SPCC10H11.02	DNAJ domain protein Cwf23	0.91
SPAC20H4.10	ubiquitin-protein ligase E4 (predicted)	0.90
SPCC1494.08c	conserved fungal protein	0.90
SPAC3A12.17c	cysteine synthase Cys12	0.90
SPAC1610.02c	mitochondrial ribosomal protein subunit L1 (predicted)	0.90
SPCC777.12c	thioredoxin family protein	0.89
SPBC3D6.03c	mitochondrial 3'-tRNA processing endonuclease Trz2	0.88
SPAC17A5.06	transcription factor TFIIH complex ERCC-3 subunit	0.88
SPAC1687.13c	COP9/signalosome complex subunit Csn5	0.88
SPBC8E4.05c	fumarate lyase superfamily	0.88
SPBC83.10	transthyretin superfamily member%2C human ER membrane protein complex subunit 7 ortholog	0.88
SPCPJ732.03	sequence orphan	0.87
SPAC5H10.08c	pantoate-beta-alanine ligase	0.87
SPAC18G6.04c	serine hydroxymethyltransferase Shm2 (predicted)	0.87
SPCC737.08	midasin (predicted) ;SPCC737.08	0.87
SPAC6C3.08	proteasome regulatory particle%2C gankyrin (predicted)	0.87
SPBC577.12	diphthamide synthetase (predicted)	0.87
SPCC16C4.18c	histone H4-like TAF Taf6%2C SAGA complex subunit	0.87
SPAC2F3.12c	thioredoxin fold protein Plp1 (predicted)	0.86

SPBC17D1.02	diphthamide biosynthesis protein (predicted)	0.86
SPAPJ696.01c	retromer complex subunit Vps17	0.86
SPBC19C2.14	Sm snRNP core protein Smd3	0.86
SPAPB1A11.03	cytochrome b2 (L-lactate cytochrome-c oxidoreductase) (predicted)	0.86
SPAC1B1.03c	karyopherin Kap95	0.86
SPBC1734.15	RSC complex subunit Rsc4	0.85
SPBC16H5.09c	alpha-1%2C2-mannosyltransferase Omh2 (predicted)	0.85
SPAC25A8.03c	DUF185 protein%2C mitochondrial	0.85
SPBC23E6.01c	mRNA processing factor	0.85
SPCC16A11.14	RSC complex subunit Sfh1	0.85
SPBC1271.14	glutamate N-acetyltransferase (predicted)	0.85
SPAC869.03c	urea transporter (predicted)	0.85
SPBC30B4.06c	mitochondrial GIDA family tRNA uridine 5-carboxymethylaminomethyl modification enzyme (predicted)	0.84
SPCC645.08c	RNA-binding protein Snd1	0.84
SPAC959.06c	conserved fungal protein	0.84
SPBC17A3.06	phosphoprotein phosphatase (predicted)	0.84
SPBC1271.06c	sequence orphan	0.84
SPAC13G6.08	Cdc20/Fizzy subfamily WD repeat protein	0.84
SPBC336.11	GARP complex subunit Vps52 (predicted)	0.84
SPBC713.03	mitochondrial D-lactate dehydrogenase%2C cytochrome (predicted)	0.84
SPBC27B12.01c	Mdm10/Mdm12/Mmm1 complex subunit Mmm1 (predicted)	0.83
SPAC26H5.12	mitochondrial RNA polymerase Rpo41	0.83
SPAC6G9.05	coenzyme A diphosphatase (predicted)	0.83
SPAC23H3.10	SWI/SNF and RSC complex subunit Ssr2	0.83
SPBP35G2.06c	nucleoporin Nup131	0.83
SPCC777.11	sequence orphan	0.82
SPCC5E4.05c	mitochondrial serine hydrolase (predicted)	0.82
SPAC4D7.02c	glycerophosphoryl diester phosphodiesterase (predicted)	0.82
SPCC16C4.17	meiotically upregulated gene Mug123	0.82
SPBC30B4.08	double-strand siRNA ribonuclease Eri1	0.82
SPBC16C6.12c	Las1 pre-rRNA processing protein	0.82
SPAC1782.01	proteasome complex subunit Ecm29	0.82
SPAC6F6.10c	ARP2/3 actin-organizing complex subunit Arc34	0.81
SPAPB8E5.09	AAA family ATPase Rvb1	0.81
SPAC6F12.17	mRNA cleavage and polyadenylation specificity factor complex subunit Rna14 (predicted)	0.81
SPCC553.08c	GTPase Ria1 (predicted)	0.81
SPBC15D4.10c	nuclear rim protein Amo1	0.81
SPAC167.01	serine/threonine protein kinase%2C sensor for unfolded proteins in the ER Ire1	0.81
SPBC19C2.13c	cytosolic thiouridylase subunit Ctu2	0.80
SPAC13F5.01c	mitochondrial MutS protein Msh1 (predicted)	0.80
SPBC2D10.18	ABC1 kinase family ubiquinone biosynthesis protein Abc1/Coq8	0.80
SPAC15A10.11	UBR ubiquitin ligase Ubr11	0.80
SPCC1020.08	wybutosine biosynthesis protein Tyw1 (predicted)	0.80
SPBC646.16	20S proteasome complex subunit alpha 1 (predicted)	0.80
SPAC637.12c	KAT5 family histone acetyltransferase Mst1	0.79
SPBC2G5.04c	COPII-coated vesicle component Erv41 (predicted)	0.79

SPAC1D4.10	3'-tRNA processing endonuclease tRNAse Z L2 Trz1 (predicted)	0.79
SPBC36.07	elongator subunit Elp1 (predicted)	0.79
SPBC17A3.05c	DNAJ/DUF1977 DNAJB12 homolog (predicted)	0.79
SPBC13G1.02	mannose-1-phosphate guanyltransferase (predicted)	0.79
SPBC21B10.13c	MBF complex negative regulatory component Yox1	0.79
SPAC14C4.16	DASH complex subunit Dad3	0.79
SPAC23D3.13c	guanyl-nucleotide exchange factor (predicted)	0.79
SPAC26F1.09	GTPase activating protein Gyp51 (predicted)	0.79
SPAC4G8.09	mitochondrial leucine-tRNA ligase (predicted)	0.78
SPBC216.06c	replication fork protection complex subunit Swi1	0.78
SPBC19G7.10c	topoisomerase II-associated deadenylation-dependent mRNA-decapping factor (predicted)	0.78
SPAC23D3.02	DNA replication factor C complex subunit Rfc2	0.78
SPCC1620.09c	transcription factor TFIIF complex alpha subunit Tfg1 (predicted)	0.78
SPAC823.05c	SNARE Tlg2 (predicted)	0.78
SPBC215.11c	aldo/keto reductase%2C unknown biological role	0.78
SPCC31H12.07	COPII cargo receptor subunit Sec23a (predicted)	0.78
SPAC688.11	Huntingtin-interacting protein homolog	0.77
SPAC13A11.04c	SAGA complex ubiquitin C-terminal hydrolase Ubp8	0.77
SPBC20F10.08c	RNA polymerase II nuclear import protein Rtp1 (predicted)	0.77
SPCC1682.08c	RNA-binding protein Mcp2	0.77
SPCC777.13	retromer complex subunit Vps35	0.77
SPAC1687.19c	queuine tRNA-ribosyltransferase (predicted)	0.77
SPCC24B10.05	Tim9-Tim10 complex subunit Tim9 (predicted)	0.77
SPAC8C9.15c	translation initiation factor eIF2B epsilon subunit (predicted)	0.77
SPAC343.03	anaphase-promoting complex subunit Apc11	0.77
SPAC31A2.10	Ran GTPase binding protein (predicted)	0.77
SPAC22A12.09c	U2 snRNP subunit Sap114	0.76
SPAC11D3.11c	zinc finger protein%2C truncated	0.76
SPBC582.05c	BRCT domain protein Brc1	0.76
SPCC338.07c	NatA N-acetyltransferase complex regulatory subunit Naa15 (predicted)	0.76
SPBC106.06	chaperonin-containing T-complex delta subunit Cct4	0.75
SPBP4H10.06c	condensin complex subunit Cut14	0.75
SPACUNK4.07c	P-type ATPase%2C calcium transporting Cta4	0.75
SPCC1884.02	NiCoT heavy metal ion transporter Nic1	0.75
SPBC1711.04	methylenetetrahydrofolate reductase (predicted)	0.75
SPCC1906.02c	CUE domain protein Cue3 (predicted)	0.75
SPBC947.06c	spermidine family transporter (predicted)	0.75
SPBPJ4664.01	decaprenyl diphosphate synthase subunit Dps1	0.75
SPCC338.12	proteinase B inhibitor Pbi2 (predicted)	0.75

SPBC29A3.01	copper transporting ATPase Ccc2 (predicted)	0.75
SPBP8B7.17c	phosphomethylpyrimidine kinase (predicted)	0.75
SPAC683.02c	zf-CCHC type zinc finger protein	0.75
SPAC1486.01	manganese superoxide dismutase (predicted)	0.75
SPCC1494.04c	prephenate dehydrogenase	0.75
SPAC821.06	septin Spn2	0.75
SPBC36.08c	Golgi transport complex subunit Cog2 (predicted)	0.74
SPAC12B10.01c	ubiquitin-protein ligase E3 (predicted)	0.74
SPAC1805.03c	tRNA 2'-O-methyltransferase Trm13 (predicted)	0.74
SPAC17A2.06c	WD repeat protein Vps8 (predicted)	0.74
SPCC777.08c	TORC2 subunit Bit61	0.74
SPBC577.14c	ornithine decarboxylase antizyme with +1 programmed ribosomal frameshift Spa1	0.74
SPAC8F11.03	MutS protein homolog 3	0.74
SPCC1620.13	phosphoglycerate mutase family (predicted)	0.74
SPBC211.04c	MCM complex subunit Mcm6	0.74
SPCC553.04	WD repeat containing cyclophilin family peptidyl-prolyl cis-trans isomerase Cyp9 (predicted)	0.74
SPAC11E3.08c	Smc5-6 complex non-SMC subunit Nse6	0.74
SPCC16A11.08	sorting nexin Atg20 (predicted)	0.73
SPAC23A1.19c	RecQ type DNA helicase Hrq1 (predicted)	0.73
SPAC1002.12c	succinate-semialdehyde dehydrogenase	0.73
SPBC16D10.02	tRNA (guanine-N2-)-methyltransferase catalytic subunit Trm11 (predicted)	0.73
SPCC162.06c	vacuolar sorting protein Vps60 (predicted)	0.73
SPCC4B3.12	histone lysine methyltransferase Set9	0.73
SPAC16E8.06c	RNA-binding protein Nop12 (predicted)	0.73
SPAC6F6.12	autophagy associated protein Atg24 (predicted)	0.73
SPBC24C6.11	G10 protein	0.73
SPAC19D5.02c	peroxisomal membrane protein Pex22 (predicted)	0.73
SPCC965.05c	uracil DNA N-glycosylase Thp1	0.73
SPCC737.09c	ATP-binding cassette-type vacuolar membrane transporter Hmt1	0.72
SPBPB21E7.05	sequence orphan	0.72
SPCP1E11.06	AP-1 adaptor complex gamma subunit Apl4	0.72
SPBC31E1.02c	P-type ATPase%2C calcium transporting Pmr1	0.72
SPCC777.02	transcription factor (predicted)	0.72
SPAC15E1.02c	DUF1761 family protein	0.72
SPBC8D2.07c	transcription factor TFIIIC complex subunit Sfc9 (predicted)	0.72
SPBC4.06	acid phosphatase (predicted)	0.72
SPBC216.05	ATR checkpoint kinase Rad3	0.72
SPBC8D2.12c	mitochondrial translational activator of cytochrome C oxidase I (predicted)	0.72
SPAC27D7.14c	RNA polymerase II associated Paf1 complex subunit Tpr1	0.72
SPCC1494.05c	CSN-associated deubiquitinating enzyme Ubp12	0.72
SPAC1556.07	phosphomannomutase Pmm1	0.72
SPBC215.12	U5 snRNP GTPase subunit Cwf10	0.72
SPCC126.12	NGG1 interacting factor 3 family%2C implicated in transcription	0.72
SPAC23C11.16	Polo kinase Plo1	0.72
SPBC25H2.16c	adaptin (predicted)	0.72
SPBC17G9.06c	siderophore-iron biosynthesis protein	0.71

	(predicted)	
SPAC16E8.18c	sequence orphan	0.71
SPAC1952.13	lipin Ned1	0.71
SPAC11D3.13	ThiJ domain protein	0.71
SPAC27E2.05	DNA polymerase delta small subunit Cdc1	0.71
SPCC18.16c	riboflavin kinase Fmn1	0.71
SPBC1A4.09	pseudouridine synthase (predicted)	0.71
SPCC553.03	AAA family ATPase Pex1 (predicted)	0.71
SPAC17G8.03c	DNA polymerase epsilon interactor Dpb3-like	0.71
SPBP22H7.07	WD repeat protein Prp5	0.71
SPBC336.05c	small RNA 2'-O-methyltransferase activity (predicted)	0.71
SPBC609.03	WD repeat protein%2C Iqw1	0.71
SPAC1006.06	RhoGEF Rgf2	0.71
SPCC74.03c	serine/threonine protein kinase Ssp2	0.71
SPAC1006.02	Astra associated protein 1 Asa1	0.70
SPCC24B10.20	short chain dehydrogenase (predicted)	0.70
SPAC18G6.05c	translation elongation regulator Gcn1 (predicted)	0.70
SPBC106.01	dual specificity protein kinase Mph1	0.70
SPBC119.17	mitochondrial metalloendopeptidase (predicted)	0.70
SPBC16C6.02c	chorein homolog (predicted)	0.70
SPCC285.16c	MutS protein homolog	0.70
SPCC1020.07	haloacid dehalogenase-like hydrolase	0.70
SPAC1002.18	DUF1688 family protein	0.70
SPAC1F12.04c	conserved fungal protein	0.70
SPBC11B10.06	SWIM domain containing-Srs2 interacting protein 1	0.70
SPAC1071.03c	sequence orphan	0.70
SPBC106.11c	phospholipase A2%2C PAF family	0.70
	homolog	
SPBC29A10.01	NADPH-cytochrome p450 reductase	0.70
SPBC31F10.11c	complexed with Cdc5 protein Cwf4	0.70
SPAC27F1.09c	U2 snRNP-associated protein Sap155	0.70
SPCC5E4.10c	human leukocyte receptor 1 ortholog	0.69
SPCC16C4.04	sequence orphan	0.69
SPAPB17E12.04c	COP9/signalosome complex subunit Csn2	0.69
SPCC1259.11c	GTPase activating protein Gyp2 (predicted)	0.69
SPBC1105.06	mediator complex subunit Pmc4	0.69
SPBC1A4.10c	mediator complex subunit Pmc1	0.69
SPCC16A11.09c	TIM23 translocase complex subunit Tim23 (predicted)	0.69
SPBC947.09	ThiJ domain protein	0.69
SPBC1734.10c	mRNA processing protein%2C predicted ubiquitin ligase (predicted)	0.69
SPCC1494.07	tRNA 2'-O-methylase subunit Trm72 (predicted)	0.69
SPBP23A10.06	mitochondrial manganese ion transporter (predicted)	0.69
SPBC211.03c	guanyl-nucleotide exchange factor (predicted)	0.69
SPAC1D4.04	chaperonin-containing T-complex beta subunit Cct2	0.69
SPBC1861.09	serine/threonine protein kinase Ppk22 (predicted)	0.69
SPBC3H7.12	RAVE complex subunit Rav2	0.69
SPBC839.02	arrestin Aly1 related%2C implicated in endocytosis	0.69
SPCC569.09	sequence orphan	0.68
SPBC56F2.03	actin-like protein Arp10 (predicted)	0.68
SPAC22F3.04	AMP binding enzyme (predicted)	0.68
SPAC22G7.04	ubiquitin C-terminal hydrolase%2C	0.68

	poly(A)-specific ribonuclease complex subunit Pan2 (predicted)	
SPAC890.06	nucleoporin Nup155	0.68
SPCC31H12.08c	CCR4-Not complex subunit Ccr4 (predicted)	0.68
SPBC1773.05c	hexitol dehydrogenase (predicted)	0.68
SPBC29A10.05	exonuclease I Exo1	0.68
SPAP27G11.12	human HID1 ortholog 1	0.68
SPCC584.03c	Ran GTP-binding protein (predicted)	0.68
SPCC645.05c	myosin II heavy chain	0.68
SPBC2D10.14c	myosin type V	0.68
SPBC25B2.01	elongation factor 1 alpha related protein (predicted)	0.68
SPBC32F12.02	Ski complex subunit Rec14	0.68
SPAC22H10.09	sequence orphan	0.67
SPCC1494.03	armadillo repeat containing%2C Zfs1 target number 1	0.67
SPBC26H8.09c	SWI/SNF complex subunit Snf59	0.67
SPAC11E3.02c	C2 domain protein	0.67
SPBC365.01	sec14 cytosolic factor family (predicted)	0.67
SPCC5E4.04	separase/separin	0.67
SPBC20F10.07	GRAM domain protein	0.67
SPAC56F8.07	conserved eukaryotic ER membrane protein	0.67
SPAC16E8.13	ubiquitin-protein ligase E3 (predicted)	0.67
SPAC13A11.05	peptidase family M17	0.67
SPBP8B7.23	ubiquitin-protein ligase E3 implicated in transcription (predicted)	0.67
SPAC4F10.02	aspartyl aminopeptidase Aap1	0.67
SPBC18A7.01	X-Pro dipeptidase (predicted)	0.67
SPAC9.02c	polyamine N-acetyltransferase (predicted)	0.67
SPAC24B11.10c	chitin synthase regulatory factor-like Cfh1 (predicted)	0.67
SPAC22H10.03c	karyopherin Kap14	0.67
SPAC6G9.10c	ATP-dependent 5' to 3' DNA/RNA helicase Sen1	0.67
SPCC188.12	septin Spn6 (predicted)	0.67
SPBC1198.14c	fructose-1%2C6-bisphosphatase Fbp1	0.66
SPAC3G6.01	ATP-dependent DNA helicase Hrp3	0.66
SPBC36B7.03	ER protein translocation subcomplex subunit Sec63 (predicted)	0.66
SPBC56F2.07c	ribosome biogenesis factor recycling AAA family ATPase (predicted)	0.66
SPBC3E7.01	1-phosphatidylinositol-3-phosphate 5-kinase Fab1	0.66
SPBC776.13	condensin complex non-SMC subunit Cnd1	0.66
SPBC1289.06c	mitochondrial PPR repeat protein Ppr8	0.66
SPAC2F7.16c	phospholipase D%2C Pld1	0.66
SPAC19A8.06	short chain dehydrogenase (predicted)	0.66
SPAC6F6.17	telomere length regulator protein Rif1	0.66
SPAC644.11c	mitochondrial pyruvate dehydrogenase (lipoamide) kinase Pkp1 (predicted)	0.66
SPCC663.12	poly(A) polymerase Cid12	0.66
SPBC31F10.07	cortical component Lsb5 (predicted)	0.66
SPBC25B2.06c	BTB/POZ domain protein Btb2	0.66
SPAC343.14c	translation initiation factor eIF2B beta subunit (predicted)	0.66
SPBC342.02	cytoplasmic glutaminyl-tRNA ligase Qrs1 (predicted)	0.66
SPBC4.05	ubiquitin protein ligase E3 component human N-recognin 7 homolog Mlo2	0.65
SPCC1919.02	pig-X (predicted)	0.65
SPBC26H8.02c	SNAP-25 homologue%2C t-SNARE component Sec9	0.65
SPAC56F8.04c	para-hydroxybenzoate--	0.65

	polyprenyltransferase Ppt1	
SPCC584.14	human ATXN10 ortholog%2C implicated in amino acid biosynthesis	0.65
SPCC306.03c	condensin complex non-SMC subunit Cnd2	0.65
SPAC15E1.04	thymidylate synthase/ flavoprotein fusion protein (predicted)	0.65
SPBC8D2.19	serine/threonine protein kinase%2C meiotic Mde3	0.65
SPAC637.09	ribonuclease H70 (predicted)	0.65
SPAC17A2.07c	sequence orphan	0.65
SPAC22G7.09c	nucleoporin Nup45	0.65
SPBC1347.01c	deoxycytidyl transferase Rev1 (predicted)	0.65
SPAC23G3.01	RNA polymerase II complex subunit Rpb2	0.65
SPBP23A10.08	actin-like protein Arp4	0.65
SPBC8D2.15	mitochondrial lipoic acid synthetase Lip5 (predicted)	0.65
SPAC24C9.11	ribosome small subunit biogenesis protein (predicted)	0.65
SPCC16C4.15	mitochondrial ribosomal protein subunit L2 (predicted)	0.65
SPBC13G1.07	palmitoyltransferase Swf1 (predicted)	0.65
SPBC14F5.09c	adenylosuccinate lyase Ade8	0.65
SPBC691.04	mitochondrial ATP-dependent RNA helicase Mss116 (predicted)	0.65
SPBC1773.14	argininosuccinate lyase	0.64
SPBC651.08c	DNA-directed RNA polymerase III complex large subunit Rpc1 (predicted)	0.64
SPAC1142.06	GET complex ATPase subunit Get3 (predicted)	0.64
SPCC1450.11c	serine/threonine protein kinase Cek1	0.64
SPBC19G7.01c	MutS protein homolog 2	0.64
SPAC19B12.11c	zinc finger protein%2C human ZNF593 ortholog	0.64
SPBPJ4664.06	UDP-glucose-glycoprotein glucosyltransferase Gpt1	0.64
SPCC1672.10	kinetochore protein Mis16	0.64
SPBC30B4.05	karyopherin Kap109	0.64
SPAC2F3.11	exopolyphosphatase (predicted)	0.64
SPCC965.06	potassium channel subunit/aldo-keto reductase (predicted)	0.64
SPBC83.14c	DNA replication factor C complex subunit Rfc5 (predicted)	0.64
SPBC1861.07	elongin C (predicted)	0.64
SPCC162.12	TORC1 subunit Tco89	0.64
SPAC1782.09c	Cdc14-related protein phosphatase Clp1/Flp1	0.64
SPAC24C9.15c	septin Spn5	0.64
SPAP8A3.12c	tripeptidyl-peptidase II Tpp2	0.64
SPAC323.05c	protein methyltransferase Mtq2 (predicted)	0.64
SPAC23D3.06c	nucleoporin Nup146	0.63
SPBC25D12.03c	MCM complex subunit Mcm7	0.63
SPBC1604.19c	TRAPP complex subunit Trs85 (predicted)	0.63
SPBC1703.03c	armadillo repeat protein%2C involved in ribosomal large subunit biogenesis (predicted)	0.63
SPAC12B10.12c	DNA repair protein Rhp41	0.63
SPBC18H10.16	arginine transporter Can1	0.63
SPAC1805.05	serine/threonine protein kinase Cki3	0.63
SPBC29A3.05	Swr1 complex subunit Vps71	0.63
SPBC947.08c	histone promoter control protein Hip4	0.63
SPBC582.08	alanine aminotransferase (predicted)	0.63
SPCC1223.01	ubiquitin-protein ligase E3 (predicted)	0.63
SPBC21H7.04	ATP-dependent RNA helicase Dbp7 (predicted)	0.63

SPCC777.15	tRNA dihydrouridine synthase Dus4 (predicted)	0.63
SPAC6F6.06c	cell polarity factor Rax2	0.63
SPCP31B10.04	conserved fungal protein	0.63
SPBPB21E7.09	L-asparaginase (predicted)	0.63
SPBC3F6.01c	serine/threonine protein phosphatase (predicted)	0.63
SPAC22F3.02	transcription factor Atf31	0.63
SPBC215.01	GTPase activating protein (predicted)	0.63
SPBC29A3.14c	telomerase reverse transcriptase 1 protein Trt1	0.63
SPCC1906.04	wtf element Wtf20	0.63
SPCC188.06c	signal recognition particle subunit Srp54	0.63
SPAC18B11.06	U3 snoRNP-associated protein Lcp5 (predicted)	0.63
SPBC1861.03	NatC N-acetyltransferase complex subunit Mak10 (predicted)	0.63
SPBC354.01	GTP binding protein Gtp1 (predicted)	0.63
SPAC664.10	kinesin-like protein Klp2	0.63
SPBC16C6.06	sorting receptor for vacuolar proteins%2C Vps10	0.63
SPCC417.12	carboxylesterase-lipase family protein	0.63
SPCC126.11c	RNA-binding protein%2C rrm type	0.62
SPCC1620.06c	ribose-phosphate pyrophosphokinase (predicted)	0.62
SPCC188.09c	cell surface glycoprotein%2C adhesion molecule (predicted)	0.62
SPAC23C4.19	transcription elongation factor Spt5	0.62
SPBC8E4.04	alditol NADP+ 1-oxidoreductase activity (predicted)	0.62
SPAC29E6.06c	cytoplasmic cysteine-tRNA ligase Crs1 (predicted)	0.62
SPBC336.04	DNA polymerase delta catalytic subunit Cdc6	0.62
SPBC36.09	U2 snRNP-associated protein sap61	0.62
SPBC839.16	C1-5%2C6%2C7%2C8-tetrahydrofolate (THF) synthase%2C trifunctional enzyme	0.62
SPAC56F8.03	translation initiation factor IF2 (predicted)	0.62
SPAC31G5.18c	silencing defective protein Sde2	0.62
SPAC637.04	cargo-transport protein Ypp1 (predicted)	0.62
SPBC16D10.01c	conserved fungal protein	0.62
SPBC16E9.17c	meiosis-specific cyclin Rem1	0.62
SPCC1259.12c	Ran GTPase binding protein (predicted)	0.62
SPAC630.10	conserved eukaryotic protein%2C DUF3321 family	0.62
SPCC1753.01c	single-stranded DNA binding protein Ssb2	0.62
SPAC13A11.01c	Rho-type GTPase activating protein Rga8	0.62
SPCC613.12c	Rik1-associated factor Raf1	0.62
SPCC10H11.01	ATP-dependent RNA helicase Prp11	0.62
SPBC577.06c	1-phosphatidylinositol 4-kinase Stt4 (predicted)	0.62
SPAC25H1.09	alpha-amylase homolog Mde5	0.62
SPBC21H7.02	SAGA complex/transcription factor TFIID complex subunit Taf10	0.62
SPBC146.11c	meiotically upregulated gene Mug97	0.62
SPBC1709.09	mitochondrial translation termination factor Rrf1	0.61
SPBC651.11c	AP-3 adaptor complex subunit Apm3 (predicted)	0.61
SPAC959.03c	U3 snoRNP-associated protein Utp7 (predicted)	0.61
SPAC343.10	methylenetetrahydrofolate reductase Met11	0.61
SPBC1773.09c	meiotically upregulated gene Mug184	0.61
SPAC1D4.14	THO complex subunit Tho2 (predicted)	0.61

SPAPB8E5.07c	rRNA processing protein Rrp12 (predicted)	0.61
SPBC902.05c	isocitrate dehydrogenase (NAD+) subunit 2	0.61
SPBC660.13c	DNA replication factor A subunit Ssb1	0.61
SPBC28E12.03	Rho-type GTPase activating protein Rga4	0.61
SPCC1322.13	phosphoribosylaminoimidazole carboxylase Ade6	0.61
SPAC22F3.09c	MBF transcription factor complex subunit Res2	0.61
SPBC577.09	ERCC-8 DNA repair homolog	0.61
SPBC582.09	peroxisomal biogenesis factor 11 (predicted)	0.61
SPAPB17E12.03	ubiquitin-protein ligase E3 (predicted)	0.61
SPCC1795.07	mitochondrial ribosomal protein subunit S37 (predicted)	0.61
SPAC1F8.03c	siderophore-iron transporter Str3	0.61
SPAC29A4.18	Clr6 histone deacetylase complex subunit Prw1	0.61
SPCC61.02	SAGA complex subunit Spt3	0.61
SPAC4A8.04	vacuolar serine protease Isp6	0.61
SPAC23G3.08c	ubiquitin C-terminal hydrolase Ubp7	0.61
SPCC285.10c	SPRY domain protein	0.61
SPAC1805.15c	HECT-type ubiquitin-protein ligase Pub2	0.60
SPBC1683.11c	isocitrate lyase (predicted)	0.60
SPCC306.06c	ER membrane protein%2C BIG1 family (predicted)	0.60
SPAC630.09c	GLYK family kinase of unknown specificity (predicted)	0.60
SPAC23C4.14	mannosyltransferase complex subunit Alg1 (predicted)	0.60
SPCC132.01c	nuclear export mediator factor NEMF	0.60
SPBC12D12.06	cyclin CycC%2C Srb mediator subunit Srb11	0.60
SPAC17G6.05c	BRO1 domain protein Bro1 (predicted)	0.60
SPAC821.03c	sequence orphan	0.60
SPAC30D11.14c	RNA-binding protein (predicted)	0.60
SPAC6G10.07	nuclear cap-binding complex large subunit (predicted)	0.60
SPAP7G5.04c	aminoadipate-semialdehyde dehydrogenase	0.60
SPAC25G10.01	RNA-binding protein	0.60
SPBC342.03	sporulation specific 1%2C3-beta-glucanosyltransferase Gas4	0.60
SPAC3G6.09c	trehalose-phosphate synthase Tps2 (predicted)	0.60
SPAC1F12.09	pig-S (predicted)	0.60
SPCC622.12c	NADP-specific glutamate dehydrogenase Gdh1 (predicted)	0.60
SPBC20F10.09	U6 snRNP-associated protein Lsm5 (predicted)	0.60
SPBC336.12c	MBF transcription factor complex subunit Cdc10	0.60
SPCC830.03	polynucleotide kinase Grc3 (predicted)	0.60
SPAC607.05	19S proteasome regulatory subunit Rpn9	0.60
SPBC776.05	membrane transporter (predicted)	0.60
SPAC1610.01	splicing factor (unnamed)	0.60
SPCC1183.06	uracil DNA N-glycosylase Ung1	0.60
SPBC16A3.13	alpha-amylase homolog Aah4	0.59
SPAC22G7.01c	iron responsive transcriptional regulator%2C peptidase family (predicted)	0.59
SPCC895.07	TOG ortholog Alp14	0.59
SPAC6G10.09	alpha glucosidase I Gls1 (predicted)	0.59
SPAC17G6.08	prevacuole/endosomal FYVE tethering component Pep7 (predicted)	0.59
SPCC576.14	diphthine synthase Dph5 (predicted)	0.59
SPBC887.13c	3-oxoacyl-	0.59

SPBC16E9.10c	AAA family ATPase Rix7 (predicted)	0.59
SPBC725.04	oxalyl-CoA decarboxylase (predicted)	0.59
SPCC830.11c	nucleoside-triphosphatase involved in SSU-rRNA maturation (predicted)	0.59
SPAC23D3.03c	GTPase activating protein (predicted)	0.59
SPAC1A6.01c	human thyroid receptor interacting protein homolog%2C transcription coactivator (predicted)	0.59
SPBC1773.06c	alcohol dehydrogenase (predicted)	0.59
SPBC337.05c	chaperonin-containing T-complex theta subunit Cct8	0.59
SPBC1289.04c	Boi family protein	0.59
SPBC1773.15	dipeptide transmembrane transporter Dal5h2 (predicted)	0.59
SPAC22F3.10c	glutamate-cysteine ligase Gcs1	0.59
SPAC3A11.10c	dipeptidyl peptidase (predicted)	0.59
SPBC11G11.07	karyopherin%2C nuclear import receptor Mtr10 (predicted)	0.59
SPBC27.02c	DASH complex subunit Ask1	0.59
SPBC1709.02c	cytoplasmic valine-tRNA ligase Vrs1/Vas1	0.59
SPAC1783.03	Sim4 and Mal2 associated (4 and 2 associated) protein 2	0.59
SPAC6G9.15c	sequence orphan	0.59
SPAC328.06	ubiquitin C-terminal hydrolase Ubp2	0.59
SPCC1442.16c	NADPH quinone oxidoreductase/ARE-binding protein (predicted)	0.59
SPAC1250.03	ubiquitin conjugating enzyme Ubc14 (predicted)	0.59
SPCC1020.12c	xap-5-like protein	0.59
SPBC106.10	cAMP-dependent protein kinase catalytic subunit Pka1	0.59
SPAC4G8.06c	tRNA methyltransferase Trm12 (predicted)	0.59
SPBC16G5.02c	ribokinase (predicted)	0.58
SPBC16D10.04c	DNA replication endonuclease-helicase Dna2	0.58
SPAC3G9.05	GTPase activating protein (predicted)	0.58
SPCC5E4.03c	SAGA complex subunit/TATA-binding protein associated factor/transcription factor TFIID complex subunit Taf5	0.58
SPAC1006.03c	RNA elimination defective protein Red1	0.58
SPAC20G4.07c	C-24(28) sterol reductase Sts1	0.58
SPAPB17E12.07c	tRNA-splicing endonuclease subunit catalytic subunit Sen2 (predicted)	0.58
SPAC1486.02c	Golgi Dsc E3 ligase complex subunit Dsc2	0.58
SPAC23G3.09	transcription factor TFIID complex subunit Taf4 (predicted)	0.58
SPBC342.04	19S proteasome regulatory subunit Rpn13a	0.58
SPAC4F8.01	ESCRT III complex subunit Did4	0.58
SPCC1393.02c	non-specific DNA binding protein Spt2 (predicted)	0.58
SPBC23G7.13c	urea transporter (predicted)	0.58
SPBC16C6.09	protein O-mannosyltransferase Ogm4	0.58
SPAC167.09	GPI-mannosyltransferase II complex subunit Pga1 (predicted)	0.58
SPAC1565.05	sequence orphan	0.58
SPAC4G8.05	serine/threonine protein kinase Ppk14 (predicted)	0.58
SPAC16C9.04c	CCR4-Not complex subunit Mot2 (predicted)	0.58
SPBC8D2.16c	DUF171 family protein	0.58
SPBC1711.17	ATP-dependent RNA helicase Prp16	0.58
SPBC336.09c	RNA polymerase I core factor complex subunit Rrn7	0.58
SPAC1A6.05c	triacylglycerol lipase ptl3	0.58

SPAC2C4.07c	3'-5'-exoribonuclease activity Dis3L2	0.57
SPBC713.02c	ubiquitin C-terminal hydrolase Ubp15	0.57
SPBPB21E7.10	sequence orphan	0.57
SPAC9G1.05	actin cortical patch component Aip1 (predicted)	0.57
SPCC1795.08c	NuA4 histone acetyltransferase complex subunit Vid21	0.57
SPBC6B1.06c	ubiquitin C-terminal hydrolase Ubp14	0.57
SPAC22H10.12c	GDP dissociation inhibitor Gdi1 (predicted)	0.57
SPAC23H3.11c	glucosidase (predicted)	0.57
SPCP1E11.02	Ark1/Prk1 family protein kinase Ppk38	0.57
SPAC343.11c	multi-copy suppressor of Chk1	0.57
SPAC343.16	homoaconitate hydratase Lys2	0.57
SPAC12G12.12	NST UDP-galactose transporter (predicted)	0.57
SPAC29E6.02	U4/U6 x U5 tri-snRNP complex subunit Prp3	0.57
SPAC821.13c	P-type ATPase (predicted)	0.57
SPCC1223.02	4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate synthase Nmt1	0.57
SPAC1006.01	vacuolar serine protease Psp3 (predicted)	0.57
SPBC1709.01	chitin synthase homolog Chs2	0.57
SPAC17A5.11	endonuclease Rec12	0.57
SPAC323.04	mitochondrial ATPase (predicted)	0.57
SPBC428.17c	Wings apart-like homolog Wpl1	0.57
SPCC1020.04c	DNA-directed RNA polymerase I%2C II and III subunit Rpb6	0.57
SPBC3D6.04c	mitotic spindle checkpoint protein Mad1	0.57
SPAC3H1.04c	mitochondrial inner membrane protein Mdm31 (predicted)	0.57
SPBC725.09c	BAR adaptor protein Hob3	0.57
SPBC9B6.09c	mitochondrial peptide-transporting ATPase	0.57
SPAC4F8.12c	U5 snRNP complex subunit Spp42	0.57
SPACUNK4.10	glyoxylate reductase (predicted)	0.57
SPAC2F3.13c	queuine tRNA-ribosyltransferase (predicted)	0.57
SPBC9B6.10	Hsp90 co-chaperone Cdc37	0.56
SPAC26F1.12c	conserved eukaryotic protein	0.56
SPAC2G11.03c	vacuolar sorting protein Vps45	0.56
SPAC29E6.03c	ER to Golgi tethering factor Uso1 (predicted)	0.56
SPAC2C4.15c	UBX domain protein Ubx2	0.56
SPBP23A10.14c	RNA polymerase II transcription elongation factor SpELL	0.56
SPAC1610.04	meiotically upregulated gene Mug99	0.56
SPBC216.07c	phosphatidylinositol kinase Tor2	0.56
SPAC17G6.12	cullin 1	0.56
SPAC30.02c	elongator complex associated protein Kti2 (predicted)	0.56
SPAC890.02c	centrosomal transforming acidic coiled-coil (TACC) protein ortholog Alp7	0.56
SPCC1322.12c	serine/threonine protein kinase Bub1	0.56
SPAC20G4.08	mRNA decapping scaffolding protein	0.56
SPCC663.03	leptomycin efflux transporter Pmd1	0.56
SPAC29A4.20	elongator complex%2C histone acetyltransferase subunit Elp3 (predicted)	0.56
SPCC16A11.17	MCM complex subunit Mcm4/Cdc21	0.56
SPAC13G6.12c	chitin synthase I	0.56
SPBC15C4.06c	ubiquitin-protein ligase E3 (predicted)	0.56
SPBC2G5.02c	CK2 family regulatory subunit (predicted)	0.56
SPCC18B5.07c	nucleoporin Nup61	0.56
SPCC895.05	formin For3	0.56
SPBC16G5.16	transcription factor%2C zf-fungal binuclear cluster type (predicted)	0.56
SPBC24C6.10c	WISH/DIP/SPIN90 ortholog Dip1	0.56

SPBC3D6.13c	ER associated protein disulfide isomerase Pdi2	0.56
SPBC646.17c	meiotic dynein intermediate chain Dic1	0.56
SPAP27G11.03	D123 family protein	0.56
SPCC70.07c	thymidylate kinase Tmp1	0.56
SPBC1734.09	NST UDP-N-acetylglucosamine transporter (predicted)	0.56
SPAPB21F2.02	Dopey family protein (predicted)	0.56
SPCC290.03c	nucleoporin Nup186	0.56
SPAC4A8.02c	conserved protein%2C UPF0047 family	0.56
SPAC21E11.07	iron-sulfur cluster biogenesis protein (predicted)	0.55
SPCC320.07c	RNA-binding protein Mde7	0.55
SPAC3C7.05c	alpha-1%2C6- mannanase (predicted)	0.55
SPAC12B10.14c	pseudokinase Tea5	0.55
SPBC11B10.03	Golgi transport complex subunit Cog8 (predicted)	0.55
SPBC1271.11	mitochondrial carboxylate transporter (predicted)	0.55
SPAC1142.04	Noc complex subunit Noc2 family (predicted)	0.55
SPCC970.10c	ubiquitin-protein ligase E3 Brl2	0.55
SPAC19A8.08	nonsense-mediated decay protein Upf2	0.55
SPBC14F5.08	mediator complex subunit Med7	0.55
SPCC162.08c	nucleoporin nup211	0.55
SPBC30B4.07c	transcription factor TFIIH complex subunit Tfb4	0.55
SPAC23A1.12c	phenylalanine-tRNA ligase beta subunit Frs1 (predicted)	0.55
SPAC1B1.02c	NAD/NADH kinase (predicted)	0.55
SPBC106.12c	THO complex subunit (predicted)	0.55
SPCC1682.03c	meiotically upregulated gene Mug174	0.55
SPBC428.01c	nucleoporin Nup107	0.55
SPAPB1E7.05	glycerophosphoryl diester phosphodiesterase Gde1 (predicted)	0.55
SPBC342.06c	RTT109 family histone lysine acetyltransferase	0.55
SPCC338.04	caffeine induced death protein Cid2	0.55
SPCC895.03c	SUA5/yciO/yrdC family protein Sua5 (predicted)	0.55
SPAC14C4.07	membrane transporter (predicted)	0.55
SPBC18H10.06c	Set1C complex subunit Swd2.1	0.55
SPAC644.16	RNA-binding protein (predicted)	0.55
SPBC3E7.07c	DUF757 family protein	0.55
SPCC584.05	SNARE binding protein Sec1 (predicted)	0.55
SPBC11B10.04c	mitochondrial ribosomal protein subunit S28 (predicted)	0.55
SPAC1565.02c	Rho-type GTPase activating protein (predicted)	0.54
SPAC6F12.02	transcription factor Rst2	0.54
SPCC553.06	oligosaccharyltransferase delta subunit Swp1 (predicted)	0.54
SPBPB21E7.07	enhancer of RNA-mediated gene silencing	0.54
SPBC11G11.04	TRAPP complex subunit Trs20 (predicted)	0.54
SPBC106.07c	N alpha-acetylation related protein Nat2 (predicted)	0.54
SPAC9E9.06c	threonine synthase (predicted)	0.54
SPCC338.13	Golgi transport complex subunit Cog4 (predicted)	0.54
SPAC22E12.03c	ThiJ domain protein	0.54
SPCC132.04c	NAD-dependent glutamate dehydrogenase Gdh2 (predicted)	0.54
SPBC1215.01	SURF-family protein Shy1 (predicted)	0.54
SPCC1840.03	karyopherin Sal3	0.54

SPAC1142.03c	Swi5 complex subunit Swi2	0.54
SPBC1347.09	hexaprenyldihydroxybenzoate methyltransferase%2C Coq3 variant (predicted)	0.54
SPAC2G11.02	ribosome biogenesis protein Urb2 (predicted)	0.54
SPBC3D6.07	pig-A%2C phosphatidylinositol N-acetylglucosaminyltransferase subunit Gpi3 (predicted)	0.54
SPAC15A10.08	alpha-actinin	0.54
SPAC2E1P3.03c	retrotransposable element/transposon Tf2-type	0.54
SPAC17C9.01c	anaphase-promoting complex subunit Apc3	0.54
SPBP4H10.21c	GINS complex subunit Sld5	0.54
SPBC1861.08c	U2 snRNP-associated protein Lea1 (predicted)	0.54
SPAC2G11.14	transcription factor TFIID complex subunit Taf111	0.54
SPAC630.07c	sequence orphan	0.54
SPBC19F5.03	inositol polyphosphate phosphatase (predicted)	0.54
SPBC15D4.15	4-nitrophenylphosphatase	0.54
SPAC17A5.09c	protein phosphatase regulatory subunit Glc9 (predicted)	0.54
SPCC1620.11	nucleoporin Nic96 homolog	0.54
SPBC14F5.07	ER-localized ubiquitin ligase Doa10 (predicted)	0.54
SPAC3A12.05c	TATA-binding protein associated factor Taf2 (predicted)	0.54
SPCC1235.03	SMR domain protein%2C possibly involved in DNA repair	0.54
SPCC24B10.15	RNA endoribonuclease involved in mRNP quality control (predicted)	0.54
SPAC6G10.05c	TRAPP complex subunit Trs120 (predicted)	0.53
SPAC1F5.11c	NuA4 complex phosphatidylinositol pseudokinase complex subunit Tra2 ;SPAC1F5.11c	0.53
SPBC365.02c	protoheme IX farnesyltransferase (predicted)	0.53
SPAC3H1.01c	origin recognition complex subunit Orp3	0.53
SPCC1235.12c	meiotically upregulated gene Mug46	0.53
SPAC458.02c	mRNP complex (predicted)	0.53
SPAC29B12.01	SNF2 family helicase Ino80	0.53
SPAC2C4.12c	tRNA 2'-phosphotransferase Tpt1 (predicted)	0.53
SPAC26H5.02c	DNA replication ATPase (predicted)	0.53
SPCC18B5.10c	TREX complex subunit Tex1 (predicted)	0.53
SPCC790.02	HOPS/CORVET complex subunit%2C ubiquitin-protein ligase E3 (predicted)	0.53
SPAC513.05	alpha-mannosidase (predicted)	0.53
SPAC20G8.09c	ribosome biogenesis ATPase (predicted)	0.53
SPCC18.03	shuttle craft like transcriptional regulator (predicted)	0.53
SPCC1753.05	RNA export factor Rsm1	0.53
SPCC553.07c	DinB translesion DNA repair polymerase%2C pol kappa	0.53
SPAC29B12.02c	histone lysine methyltransferase Set2	0.53
SPBC1347.03	sporulation specific PIL domain protein Meu14	0.53
SPCC1672.07	U3 snoRNP-associated protein Utp21 (predicted)	0.53
SPAC637.11	mitochondrial ATP-dependent RNA helicase Rpm2	0.53

SPBC23E6.03c	protein N-terminal amidase Nta1 (predicted)	0.53
SPCC188.03	condensin complex non-SMC subunit Cnd3	0.53
SPBC1773.02c	thioredoxin peroxidase (predicted)	0.53
SPBC27B12.11c	transcription factor Pho7	0.53
SPBC2A9.03	WD40/YVTN repeat-like	0.53
SPBC354.02c	translocon alpha subunit Sec61	0.53
SPBP22H7.02c	RNA-binding protein Mrd1 (predicted)	0.53
SPCC1450.14c	ER protein folding oxidoreductin Ero1b	0.53
SPCC23B6.03c	ATM checkpoint kinase	0.53
SPAPB17E12.08	N-glycosylation protein (predicted)	0.53
SPCC320.10	signal recognition particle subunit Srp72 (predicted)	0.53
SPBC1604.12	sequence orphan	0.53
SPBC27B12.05	WD repeat protein involved in transcriptional regulation (predicted)	0.53
SPBC31F10.13c	hira protein%2C histone chaperone Hip1	0.53
SPBC31E1.01c	autophagy associated protein Atg2	0.53
SPBC3H7.06c	F-box protein Pof9	0.53
SPBC16D10.10	tRNA specific adenosine deaminase subunit Tad2	0.52
SPAC13G6.06c	glycine cleavage complex subunit P (predicted)	0.52
SPAC23C11.08	CCAAT-binding factor complex subunit Php3	0.52
SPAC869.09	conserved fungal protein	0.52
SPBC27B12.09c	mitochondrial FAD transporter (predicted)	0.52
SPAC15E1.06	retromer complex subunit Vps29	0.52
SPAC4G9.08c	DNA-directed RNA polymerase III complex subunit Rpc2	0.52
SPBC6B1.10	splicing factor Prp17	0.52
SPBC16A3.10	membrane bound O-acyltransferase%2C MBOAT (predicted)	0.52
SPBC800.03	histone deacetylase (class II) Clr3	0.52
SPAC22F3.03c	ATP-dependent DNA helicase Rdh54	0.52
SPBC19F8.02	nuclear distribution protein NUDC homolog	0.52
SPCC1281.05	RSC complex subunit Rsc7	0.52
SPBC15C4.01c	TPR repeat protein Oca3/ ER membrane protein complex Ecm2 (predicted)	0.52
SPBC1778.04	Spo4-Spo6 kinase complex regulatory subunit Spo6	0.52
SPBC16D10.03	metallopeptidase Pgp2	0.52
SPCC188.13c	dicer	0.52
SPCC1259.13	Chk1 protein kinase	0.52
SPCC74.06	histidine kinase Mak3	0.52
SPAC17G8.01c	tRNA ligase Trl1 (predicted)	0.52
SPAC57A7.11	WD repeat protein%2C Raptor homolog Mip1	0.52
SPAC17A2.04c	HSP chaperone complex subunit Cns1 (predicted)	0.52
SPAP7G5.02c	GMP synthase	0.52
SPAC4D7.01c	Sec7 domain protein%2C ARF GEF (predicted)	0.52
SPCC584.01c	sulfite reductase NADPH flavoprotein subunit (predicted)	0.52
SPAC1F5.06	ER heat shock protein Lsh1 (predicted)	0.52
SPAC1610.03c	poly(A) binding protein Crp79	0.52
SPCC550.02c	RNA-binding protein Cwf5	0.52
SPBPB2B2.09c	2-dehydropantoate 2-reductase (predicted)	0.52
SPBC25B2.11	F-box protein Pof2	0.51
SPBC902.04	RNA-binding protein	0.51
SPBC13E7.01	splicing factor Cwf22	0.51
SPBP35G2.05c	serine/threonine protein kinase Cki2	0.51

SPAC6G10.02c	cell end marker Tea3	0.51
SPAC4A8.05c	myosin II heavy chain Myo3	0.51
SPBC11C11.11c	ATP helicase Irc3 (predicted)	0.51
SPBC29A3.02c	phosphoribosyl-AMP cyclohydrolase/phosphoribosyl- ATP pyrophosphohydrolase His7	0.51
SPAC6F12.14	anaphase-promoting complex subunit Apc8	0.51
SPAC824.02	GPI inositol deacylase Bst1 (predicted)	0.51
SPBC29A10.07	nucleoporin Pom152	0.51
SPCC417.11c	glutamate-1-semialdehyde 2%2C1-aminomutase (predicted)	0.51
SPAC24C9.09	mitochondrial threonine-tRNA ligase (predicted)	0.51
SPAC26H5.04	vacuolar import and degradation protein Vid28 (predicted)	0.51
SPAC513.06c	dihydrodiol dehydrogenase (predicted)	0.51
SPCC777.07	alpha-1%2C2-mannosyltransferase Omh3 (predicted)	0.51
SPBC31F10.14c	HIRA interacting protein Hip3	0.51
SPBC215.15	COPII-coated vesicle component Sec13	0.51
SPAP8A3.14c	mitochondrial inner membrane protein Sls1 (predicted)	0.51
SPBC36.05c	histone deacetylase (class I) Clr6	0.51
SPAC1851.02	1-acylglycerol-3-phosphate O-acyltransferase Slc1 (predicted)	0.51
SPAC167.05	Usp (universal stress protein) family protein%2C implicated in meiotic chromosome segregation	0.51
SPBC8D2.05c	spindle pole body protein Sfi1	0.51
SPCC757.03c	ThiJ domain protein	0.51
SPBC1604.02c	mitochondrial PPR repeat protein Ppr1	0.51
SPBC3F6.05	Rho-type GTPase activating protein Rga1	0.51
SPAC11H11.03c	SMR and DUF1771 domain protein (predicted)	0.51
SPBC1539.03c	argininosuccinate lyase (predicted)	0.51
SPAC18B11.03c	N-acetyltransferase (predicted)	0.50
SPBC14C8.15	triglyceride lipase-cholesterol esterase (predicted)	0.50
SPAC23H4.18c	RING-box protein 1	0.50
SPCC645.07	RhoGEF for Rho1%2C Rgf1	0.50
SPAPB1A10.10c	GTPase Ypt71	0.50
SPAC1F5.05c	conserved fungal protein	0.50
SPBC15C4.05	ATP-dependent RNA/DNA helicase (predicted)	0.50
SPAC10F6.11c	autophagy associated protein kinase activator Atg17	0.50
SPAC22E12.14c	serine/threonine protein kinase Sck2	0.50
SPAP27G11.05c	HOPS complex subunit Vps41 (predicted)	0.50
SPAC12B10.08c	mitochondrial tRNA(Ile)-lysidine synthetase family (predicted)	0.50
SPCC1919.11	BAR adaptor protein	0.50
SPBC530.03c	BAG family molecular chaperone regulator Bag102 (predicted)	0.50
SPAC1687.07	conserved fungal protein	0.50
SPAC328.01c	karyopherin (predicted)	0.50
SPAC22A12.07c	protein O-mannosyltransferase Ogm1	0.50
SPCC1682.10	19S proteasome regulatory subunit Rpn8 (predicted)	0.50
SPBC19C7.06	cytoplasmic proline-tRNA ligase Prs1 (predicted)	0.50
SPBC16E9.02c	CUE domain protein	0.50
SPBC1348.07	S. pombe specific DUF999 protein family 6	0.50
SPAC31G5.04	homoisocitrate dehydrogenase Lys12	0.50
SPAC6G9.14	RNA-binding protein (predicted)	0.50

SPBC3H7.01	GDP/GTP exchange factor%2C WD repeat protein Spo14	0.50
SPBC776.16	sequence orphan	0.50
SPCC1494.06c	ATP-dependent RNA helicase Dbp9 (predicted)	0.50
SPCC962.01	C2 domain protein	0.50
SPBC887.09c	leucine-rich repeat protein Lrp1	0.50
SPBC1734.16c	SIN3 family co-repressor Pst3	0.50
SPAC1556.04c	cytidine deaminase Ccd1 (predicted)	0.50
SPBC19C2.10	BAR adaptor protein	0.50
SPBC1306.01c	mitochondrial translation elongation factor G (predicted)	0.50

Systematic name	**Description**	**H4K20 me3**
SPAC1420.04c	cytochrome c oxidase assembly protein Cox1101/ mitochondrial ribosomal protein Rsm22 fusion protein	2.46
SPAC977.01	S. pombe specific 5Tm protein family	2.37
SPAC1B3.10c	SEL1 repeat protein%2C unknown biological role	1.50
SPAC31A2.10	Ran GTPase binding protein (predicted)	1.41
SPCC757.02c	epimarase (predicted)	1.33
SPAC16E8.03	glucosamine-phosphate N-acetyltransferase (predicted)	1.30
SPBC2D10.14c	myosin type V	1.30
SPBC800.02	cell cycle transcriptional repressor Whi5 (predicted)	1.29
SPBC1348.10c	phospholipase (predicted)	1.28
SPBC23E6.01c	mRNA processing factor	1.25
SPBC16E9.16c	Lsd90 protein	1.22
SPAC2F3.12c	thioredoxin fold protein Plp1 (predicted)	1.21
SPAC2G11.05c	BRO1 domain protein Rim20 (predicted)	1.20
SPBP16F5.03c	SAGA complex phosphatidylinositol pseudokinase Tra1	1.19
SPBC12D12.06	cyclin CycC%2C Srb mediator subunit Srb11	1.19
SPAC23G3.02c	ferrichrome synthetase Sib1	1.17
SPCC23B6.03c	ATM checkpoint kinase	1.16
SPBC27B12.05	WD repeat protein involved in transcriptional regulation (predicted)	1.15
SPBC1773.06c	alcohol dehydrogenase (predicted)	1.15
SPAC3C7.05c	alpha-1%2C6- mannanase (predicted)	1.15
SPCC417.12	carboxylesterase-lipase family protein	1.12
SPAC13F5.01c	mitochondrial MutS protein Msh1 (predicted)	1.11
SPAC4D7.01c	Sec7 domain protein%2C ARF GEF (predicted)	1.11
SPCC550.03c	Ski complex RNA helicase Ski2 (predicted)	1.10
SPCC4B3.12	histone lysine methyltransferase Set9	1.10
SPCC1393.05	RNA-silencing factor Ers1	1.10
SPAC22F3.04	AMP binding enzyme (predicted)	1.08
SPBC21.07c	serine/threonine protein kinase Ppk24	1.08
SPCC1259.12c	Ran GTPase binding protein (predicted)	1.07
SPCC757.07c	catalase	1.06
SPBC1773.09c	meiotically upregulated gene Mug184	1.05
SPBC31E1.01c	autophagy associated protein Atg2	1.05
SPCC645.11c	meiotically upregulated gene Mug117	1.04
SPBC19C2.13c	cytosolic thiouridylase subunit Ctu2	1.04
SPAC1F5.11c	NuA4 complex phosphatidylinositol pseudokinase complex subunit Tra2 ;SPAC1F5.11c	1.04
SPCP1E11.02	Ark1/Prk1 family protein kinase Ppk38	1.04
SPBC577.07	ubiquitin C-terminal hydrolase Ubp10	1.04

	(predicted)	
SPBC21C3.01c	chorein homolog (predicted)	1.03
SPCC16A11.04	sorting nexin Snx12 (predicted)	1.02
SPBP35G2.06c	nucleoporin Nup131	1.02
SPBC685.03	sequence orphan	1.02
SPBC16C6.02c	chorein homolog (predicted)	1.01
SPAC3G9.11c	pyruvate decarboxylase (predicted)	1.00
SPBC19F8.07	cyclin-dependent protein kinase/CDK-activating kinase Mcs6	1.00
SPBC27B12.04c	SIP/FAR complex subunit%2C Far11/Csc2	0.99
SPAC6F12.15c	anaphase-promoting complex subunit Cut9	0.99
SPAC1296.03c	serine carboxypeptidase Sxa2	0.99
SPBP8B7.29	para-aminobenzoate synthase (predicted)	0.98
SPBC29A3.14c	telomerase reverse transcriptase 1 protein Trt1	0.98
SPBC25H2.13c	DNA polymerase epsilon catalytic subunit Pol2	0.98
SPAC11E3.05	ubiquitin-protein ligase E3%2C coatamer related complex subunit Sea3 (predicted)	0.97
SPBC13G1.10c	ATP-dependent RNA helicase Slh1 (predicted)	0.97
SPCC417.11c	glutamate-1-semialdehyde 2%2C1-aminomutase (predicted)	0.97
SPAC1B3.20	sequence orphan	0.96
SPBC577.13	inositol-polyphosphate 5-phosphatase%2C synaptojanin homolog 2 (predicted)	0.96
SPAC1002.05c	histone demethylase Jmj2	0.96
SPCC830.04c	sequence orphan	0.95
SPBC29A3.03c	ubiquitin-protein ligase E3 (predicted)	0.95
SPAC2C4.14c	PAK-related kinase Ppk11	0.95
SPCC1020.01c	P-type proton ATPase%2C P3-type Pma2	0.95
SPBC1778.02	telomere binding protein Rap1	0.94
SPCC14G10.02	ribosome biogenesis protein Urb1 (predicted)	0.94
SPCC1884.02	NiCoT heavy metal ion transporter Nic1	0.94
SPAC1039.06	alanine racemase (predicted)	0.93
SPAC16E8.09	RhoGEF Scd1	0.93
SPAC824.05	HOPS/CORVET complex subunit Vps16 (predicted)	0.93
SPAC1527.01	alpha-1%2C3-glucan synthase Mok11	0.92
SPCC18.17c	26S proteasome non-ATPase regulatory subunit (predicted)	0.92
SPBC21B10.12	meiotic recombination protein Rec6	0.92
SPCC1183.01	exocyst complex subunit Sec15 (predicted)	0.91
SPBC15C4.06c	ubiquitin-protein ligase E3 (predicted)	0.91
SPBP35G2.04c	sequence orphan	0.91
SPBC11C11.03	spindle pole body protein Ndc80	0.91
SPAC7D4.11c	secretory pathway protein Sec39 (predicted)	0.91
SPBC24C6.11	G10 protein	0.91
SPBC947.05c	ferric-chelate reductase Frp2 (predicted)	0.90
SPBC947.11c	DNA replication factor C complex subunit Elg1	0.90
SPAC16E8.10c	mitochondrial ribosomal protein subunit S7 (predicted)	0.90
SPBC3B8.11	RNA polymerase I transcription factor subunit Rrn6 (predicted)	0.90
SPAC31G5.15	phosphatidylserine decarboxylase Psd3	0.90
SPAC458.04c	meiotic dynein intermediate light chain Dli1/Dil1	0.89
SPBC1198.12	fizzy-related protein Mfr1	0.89
SPCC417.07c	MT organizer Mto1	0.89
SPCC188.08c	ubiquitin C-terminal hydrolase Ubp5	0.89
SPBC32H8.13c	alpha-1%2C3-glucan synthase Mok12	0.89

SPCC757.04	transcription factor (predicted)	0.89
SPBC1683.11c	isocitrate lyase (predicted)	0.88
SPBC28E12.02	RNA-binding protein	0.88
SPAC1093.06c	dynein heavy chain Dhc1	0.88
SPAC11H11.04	pheromone p-factor receptor	0.88
SPBC8E4.05c	fumarate lyase superfamily	0.88
SPCC306.07c	U3 snoRNP-associated protein Cic1/Utp30 family (predicted)	0.88
SPCC1494.08c	conserved fungal protein	0.87
SPAC23H3.11c	glucosidase (predicted)	0.87
SPCC1259.14c	S. pombe specific UPF0300 family protein 5	0.87
SPBC1773.03c	aminotransferase class-III%2C unknown specificity	0.86
SPBC336.05c	small RNA 2'-O-methyltransferase activity (predicted)	0.86
SPAC11D3.15	5-oxoprolinase (ATP-hydrolizing) (predicted)	0.86
SPBC1861.06c	S. pombe specific UPF0300 family protein 4	0.86
SPBC16H5.13	WD repeat protein%2C human WDR7 ortholog	0.85
SPBC56F2.07c	ribosome biogenesis factor recycling AAA family ATPase (predicted)	0.85
SPBP35G2.10	SHREC complex subunit Mit1	0.85
SPAC1B1.02c	NAD/NADH kinase (predicted)	0.85
SPAC10F6.15	S. pombe specific UPF0300 family protein 1	0.85
SPBC15D4.07c	autophagy associated protein Atg9	0.85
SPBC1773.08c	alpha-1%2C2-mannosyltransferase Omh4 (predicted)	0.84
SPAC3G9.12	CLASP family microtubule-associated protein	0.84
SPAC110.02	cohesin-associated protein Pds5	0.84
SPAC57A10.08c	carboxylic ester hydrolase activity (predicted)	0.84
SPBC16E9.10c	AAA family ATPase Rix7 (predicted)	0.84
SPAC323.06c	NEDD8 activating enzyme (predicted)	0.84
SPAC144.15c	Golgi transport complex subunit Cog1 (predicted)	0.84
SPAC56F8.04c	para-hydroxybenzoate--polyprenyltransferase Ppt1	0.84
SPAC2F3.13c	queuine tRNA-ribosyltransferase (predicted)	0.83
SPAC589.02c	mediator complex subunit Srb9	0.83
SPAC1565.07c	TATA-binding protein (predicted)	0.83
SPBC16A3.11	sister chromatid cohesion protein/DNA polymerase eta Eso1 fusion protein	0.82
SPBP35G2.03c	inner centromere protein%2C shugoshin%2C Sgo1	0.82
SPCC63.04	alpha-1%2C4-glucan synthase Mok14	0.82
SPBC16D10.04c	DNA replication endonuclease-helicase Dna2	0.82
SPAC31A2.16	RhoGEF Gef2	0.82
SPCC132.04c	NAD-dependent glutamate dehydrogenase Gdh2 (predicted)	0.82
SPBC19G7.01c	MutS protein homolog 2	0.81
SPAC16C9.06c	ATP-dependent RNA helicase Upf1	0.81
SPBC1289.16c	copper amine oxidase-like protein Cao2	0.81
SPBPJ4664.01	decaprenyl diphosphate synthase subunit Dps1	0.81
SPCC1281.04	pyridoxal reductase (predicted)	0.81
SPAC513.06c	dihydrodiol dehydrogenase (predicted)	0.81
SPAC23H3.04	conserved fungal protein	0.81

SPAC1805.15c	HECT-type ubiquitin-protein ligase Pub2	0.81
SPBC577.09	ERCC-8 DNA repair homolog	0.81
SPCC306.06c	ER membrane protein%2C BIG1 family (predicted)	0.81
SPCC1223.04c	ribosomal protein lysine methyltransferase Set11	0.81
SPBC19C7.02	N-end-recognizing protein Ubr1	0.81
SPBC577.08c	thioredoxin-like I protein Txl1	0.81
SPBC106.09	anaphase-promoting complex subunit Apc1	0.80
SPBC17D11.08	WD repeat protein%2C DDB1 and CUL4-associated factor 7 (predicted)	0.80
SPAC2C4.15c	UBX domain protein Ubx2	0.80
SPBC56F2.03	actin-like protein Arp10 (predicted)	0.80
SPAC12B10.16c	conserved protein Mug157	0.80
SPBC11C11.04c	tubulin specific chaperone cofactor D%2C Alp1	0.80
SPCC1259.13	Chk1 protein kinase	0.80
SPBP16F5.02	TFIIH complex cyclin Mcs2	0.80
SPAC1296.04	spore wall assembly protein (predicted)	0.80
SPBC336.14c	serine/threonine protein kinase%2C PAN complex subunit%2C Ppk26	0.80
SPCC1620.04c	Cdc20/Fizzy subfamily WD repeat protein	0.80
SPAC18B11.11	GTPase activating protein (predicted)	0.80
SPCC16C4.15	mitochondrial ribosomal protein subunit L2 (predicted)	0.79
SPAC1002.12c	succinate-semialdehyde dehydrogenase	0.79
SPCC1672.10	kinetochore protein Mis16	0.79
SPBC2G2.10c	sequence orphan	0.79
SPAC1006.06	RhoGEF Rgf2	0.79
SPAC6B12.02c	DNA repair protein Mus7/Mms22	0.79
SPAC31A2.05c	adherin%2C cohesin loading factor Mis4	0.79
SPCC1442.01	guanyl-nucleotide exchange factor Ste6	0.78
SPAC3A11.11c	pyridoxal reductase (predicted)	0.78
SPAC1002.19	GTP cyclohydrolase II (predicted)	0.78
SPCC285.03	ATP-dependent RNA helicase Dbp6 (predicted)	0.78
SPAC869.01	amidase (predicted)	0.78
SPCC4G3.07c	PHD finger containing protein Phf1	0.78
SPBC1706.03	mitochondrial dynamin family fusion GTPase protein (predicted)	0.78
SPBC409.12c	telomere cap complex subunit Stn1	0.77
SPAC1782.01	proteasome complex subunit Ecm29	0.77
SPAC23D3.13c	guanyl-nucleotide exchange factor (predicted)	0.77
SPAC144.05	ATP-dependent DNA helicase (predicted)	0.77
SPAC1687.07	conserved fungal protein	0.77
SPAC1D4.10	3'-tRNA processing endonuclease tRNAse Z L2 Trz1 (predicted)	0.77
SPCC188.13c	dicer	0.77
SPBC1348.03	S. pombe specific 5Tm protein family	0.77
SPAC3A12.03c	ubiquitin-protein ligase E3 Meu34 (predicted)	0.77
SPBC36B7.09	eIF2 alpha kinase Gcn2	0.76
SPBP8B7.30c	transcription factor Thi5	0.76
SPBC336.01	DNA helicase I	0.76
SPBC29A3.09c	AAA family ATPase Gcn20 (predicted)	0.76
SPBP8B7.18c	phosphomethylpyrimidine kinase (predicted)	0.76
SPBC1861.05	pseudouridine-metabolizing bifunctional protein (predicted)	0.76
SPAC1F3.02c	MEK kinase (MEKK) Mkh1	0.76
SPAC27E2.09	histidine kinase Mak2	0.76
SPAC688.08	mediator complex subunit Srb8	0.75
SPBC29A10.07	nucleoporin Pom152	0.75

SPAC3C7.02c	meiotic eisosome BAR domain protein Pil2	0.75
SPAC26F1.08c	conserved protein	0.75
SPBC17A3.09c	lipoate-protein ligase A (predicted)	0.74
SPCC320.05	sulphate transporter (predicted)	0.74
SPCC11E10.09c	alpha-amylase homolog (predicted)	0.74
SPAC513.05	alpha-mannosidase (predicted)	0.74
SPBC216.05	ATR checkpoint kinase Rad3	0.74
SPBC577.06c	1-phosphatidylinositol 4-kinase Stt4 (predicted)	0.74
SPBC3D6.03c	mitochondrial 3'-tRNA processing endonuclease Trz2	0.74
SPAC17A5.06	transcription factor TFIIH complex ERCC-3 subunit	0.73
SPAC1687.18c	cohesin loading factor Ssl3	0.73
SPBC146.03c	condensin complex subunit Cut3	0.73
SPAC3A12.05c	TATA-binding protein associated factor Taf2 (predicted)	0.73
SPAC23E2.02	histone demethylase SWIRM2 (predicted)	0.73
SPAC1006.05c	alpha-1%2C6-mannosyltransferase Och1	0.73
SPAC24H6.03	cullin 3	0.73
SPCC11E10.08	silencing protein Rik1	0.72
SPCC777.03c	nifs homolog%2C possible cysteine desulfurase	0.72
SPACUNK4.12c	metallopeptidase (predicted)	0.72
SPAC4G8.09	mitochondrial leucine-tRNA ligase (predicted)	0.72
SPAC22F3.05c	ADP-ribosylation factor Alp41	0.72
SPBC216.06c	replication fork protection complex subunit Swi1	0.72
SPBC23E6.03c	protein N-terminal amidase Nta1 (predicted)	0.72
SPAC806.08c	gamma tubulin complex subunit Mod21	0.72
SPCC5E4.10c	human leukocyte receptor 1 ortholog	0.72
SPAC22F3.02	transcription factor Atf31	0.72
SPAC212.03	hypothetical protein	0.71
SPCC4G3.12c	ubiquitin-protein ligase E3 (predicted)	0.71
SPBC1709.15c	cleavage factor two Cft2/polyadenylation factor CPSF-73 (predicted)	0.71
SPBC16E9.07	sequence orphan	0.71
SPAC23A1.19c	RecQ type DNA helicase Hrq1 (predicted)	0.71
SPBC29A10.15	origin recognition complex subunit Orc1	0.71
SPCC126.06	twinfilin (predicted)	0.70
SPAC25H1.09	alpha-amylase homolog Mde5	0.70
SPBC12D12.05c	mitochondrial carrier%2C calcium binding subfamily (predicted)	0.70
SPAC323.03c	sequence orphan	0.70
SPCC4E9.01c	meiotic cohesin complex subunit Rec11	0.70
SPBC115.02c	AFG1 family mitochondrial ATPase (predicted)	0.70
SPAC16E8.13	ubiquitin-protein ligase E3 (predicted)	0.70
SPAC26H5.12	mitochondrial RNA polymerase Rpo41	0.70
SPBC27B12.06	pig-O (predicted)	0.70
SPCC550.10	aldehyde dehydrogenase Atd3 (predicted)	0.70
SPAC24C9.05c	conserved protein Mug20	0.70
SPBC577.12	diphthamide synthetase (predicted)	0.70
SPBC685.02	mitochondrial single stranded DNA specific 5'-3' exodeoxyribonuclease Exo5 (predicted)	0.70
SPAC3A11.03	methyltransferase (predicted)	0.70
SPBC25H2.03	vacuolar protein involved in phosphoinositide metabolism (predicted)	0.70
SPCC320.07c	RNA-binding protein Mde7	0.69
SPAC19E9.02	serine/threonine protein kinase%2C NIMA related Fin1	0.69

SPCC777.02	transcription factor (predicted)	0.69
SPBC428.01c	nucleoporin Nup107	0.69
SPBC18H10.10c	splicing associated factor Saf4	0.69
SPCC188.12	septin Spn6 (predicted)	0.69
SPBC887.13c	3-oxoacyl-	0.68
SPCC162.12	TORC1 subunit Tco89	0.68
SPAC922.07c	aldehyde dehydrogenase (predicted)	0.68
SPBC24C6.06	G-protein alpha subunit	0.68
SPBC839.16	C1-5%2C6%2C7%2C8-tetrahydrofolate (THF) synthase%2C trifunctional enzyme	0.68
SPAC11D3.11c	zinc finger protein%2C truncated	0.68
SPCC63.11	U5 snRNP-associated protein Prp28 (predicted)	0.68
SPBC1539.05	Golgi transport complex subunit Cog3 (predicted)	0.68
SPCC5E4.06	Smc5-6 complex SMC subunit Smc6	0.68
SPAC23D3.06c	nucleoporin Nup146	0.68
SPAC25G10.07c	kinesin-like protein Cut7	0.68
SPCC553.09c	DNA polymerase alpha B-subunit	0.67
SPAC23C4.05c	LEA domain protein	0.67
SPBC660.10	mitochondrial translation elongation factor G (predicted)	0.67
SPAC6G10.05c	TRAPP complex subunit Trs120 (predicted)	0.67
SPCC757.05c	peptidase family M20 protein	0.67
SPCC338.17c	mitotic cohesin complex%2C non-SMC subunit Rad21 (kleisin)	0.67
SPBC216.03	conserved fungal protein	0.67
SPBC1105.10	RAVE complex subunit Rav1	0.67
SPBC15C4.05	ATP-dependent RNA/DNA helicase (predicted)	0.67
SPCC584.02	middle-meiotic transcription factor Cuf2	0.67
SPBPB21E7.04c	human COMT ortholog 2	0.67
SPBC1604.01	Ergothioneine biosynthesis protein Egt1	0.66
SPBC119.17	mitochondrial metalloendopeptidase (predicted)	0.66
SPAC20G4.03c	eIF2 alpha kinase Hri1	0.66
SPBC2D10.17	cryptic loci regulator Clr1	0.66
SPCC1682.03c	meiotically upregulated gene Mug174	0.66
SPAC144.14	kinesin-like protein Klp8	0.66
SPBC26H8.04c	DEP domain protein	0.66
SPAC19D5.01	tyrosine phosphatase Pyp2	0.66
SPAC1002.18	DUF1688 family protein	0.66
SPCC162.02c	AMP-binding dehydrogenase (predicted)	0.66
SPAC25B8.16	RNase P and RNase MRP subunit (predicted)	0.66
SPBC428.20c	gamma tubulin complex Spc98/GCP3 subunit Alp6	0.66
SPCC970.02	mannan endo-1%2C6-alpha-mannosidase (predicted)	0.66
SPBC776.13	condensin complex non-SMC subunit Cnd1	0.66
SPBC56F2.04	U3 snoRNP protein Utp20 (predicted)	0.66
SPBC1347.12	centractin family actin-like protein Arp1 (predicted)	0.66
SPAC17G6.12	cullin 1	0.65
SPBC24C6.09c	phosphoketolase family protein (predicted)	0.65
SPAC1851.04c	Ypt/Rab-specific guanyl-nucleotide exchange factor (GEF) subunit Ric1	0.65
SPBC1683.13c	transcription factor Cha4 (predicted)	0.65
SPAC4H3.05	ATP-dependent DNA helicase%2C UvrD subfamily	0.65
SPBC428.07	meiotic chromosome segregation protein Meu6	0.65
SPBC336.04	DNA polymerase delta catalytic subunit	0.65

	Cdc6	
SPAC25G10.01	RNA-binding protein	0.65
SPBC1703.04	MutL family protein Mlh1 (predicted)	0.65
SPBC1604.17c	Tel2 interacting protein Tti2%2C predicted ASTRA complex subunit	0.65
SPBC1A4.10c	mediator complex subunit Pmc1	0.64
SPAC24C9.07c	1%2C3-beta-glucan synthase subunit Bgs2	0.64
SPAC16E8.02	DUF962 family protein	0.64
SPAC2G11.12	RecQ type DNA helicase Rqh1	0.64
SPCC1259.11c	GTPase activating protein Gyp2 (predicted)	0.64
SPCC338.16	F-box protein Pof3	0.64
SPBC725.05c	nucleotide pyrophosphatase (predicted)	0.64
SPCC965.10	transcription factor (predicted)	0.64
SPBC16C6.06	sorting receptor for vacuolar proteins%2C Vps10	0.64
SPBC336.11	GARP complex subunit Vps52 (predicted)	0.64
SPBC11C11.11c	ATP helicase Irc3 (predicted)	0.64
SPAC1F3.06c	sporulation protein Spo15	0.64
SPBC4F6.07c	ATP-dependent RNA helicase Mak5 (predicted)	0.64
SPBC1773.17c	glyoxylate reductase (predicted)	0.64
SPAC11E3.11c	guanyl-nucleotide exchange factor Syt22	0.64
SPBC20F10.08c	RNA polymerase II nuclear import protein Rtp1 (predicted)	0.63
SPAPB17E12.03	ubiquitin-protein ligase E3 (predicted)	0.63
SPCC4B3.04c	lysophospholipase (predicted)	0.63
SPAC3G6.01	ATP-dependent DNA helicase Hrp3	0.63
SPCC364.05	CORVET complex subunit%2C GTPase regulator Vps3 (predicted)	0.63
SPBC1709.19c	NifU-like protein (predicted)	0.63
SPAC1556.01c	DNA repair protein Rad50	0.63
SPBC31F10.14c	HIRA interacting protein Hip3	0.63
SPBC16A3.13	alpha-amylase homolog Aah4	0.63
SPBC30D10.10c	phosphatidylinositol kinase Tor1	0.63
SPCC5E4.04	separase/separin	0.63
SPCC16C4.17	meiotically upregulated gene Mug123	0.63
SPAC8F11.03	MutS protein homolog 3	0.63
SPAC11D3.14c	5-oxoprolinase (ATP-hydrolizing) (predicted)	0.62
SPBC1198.13c	transcription factor TFIIF complex beta subunit Tfg2 (predicted)	0.62
SPBC582.10c	ATP-dependent DNA helicase Rhp16b (predicted)	0.62
SPAC6F6.01	calcium channel Cch1	0.62
SPCC1620.11	nucleoporin Nic96 homolog	0.62
SPAC3A11.02	zinc finger protein Cps3	0.62
SPBC16A3.12c	triglyceride lipase-cholesterol esterase (predicted)	0.62
SPBC1734.03	trifunctional dihydropteroatesynthase/2-amino-4-hydroxy-6-hydro xymethyldihydropteridinediphosphokinase/ dihydroneopterin aldolase (predicted)	0.62
SPCC330.11	BTB/POZ domain protein Btb1	0.62
SPAC29E6.01	F-box protein Pof11	0.62
SPBC887.12	P-type ATPase (predicted)	0.62
SPBP22H7.05c	ATPase with bromodomain protein (predicted)	0.62
SPAC823.16c	WD repeat protein involved in autophagy Atg18b	0.61
SPCC645.10	ATP(CTP) tRNA nucleotidyltransferase (predicted)	0.61
SPBC17D1.07c	GTPase regulator Rng2-like (predicted)	0.61
SPAC823.12	HOPs/CORVET complex subunit Vps11 (predicted)	0.61

SPBC18H10.05	WD repeat protein%2C human WDR44 family	0.61
SPAC328.04	AAA family ATPase%2C unknown biological role	0.61
SPBC21H7.06c	inositol metabolism protein Opi10 (predicted)	0.61
SPAC17A5.16	Ubp5 interacting protein Ftp105	0.61
SPCC1795.01c	mitotic spindle checkpoint protein Mad3	0.61
SPBC1A4.09	pseudouridine synthase (predicted)	0.61
SPAC2C4.13	V-type ATPase V0 subunit c'' (predicted)	0.61
SPBC776.05	membrane transporter (predicted)	0.61
SPBC2A9.11c	nuclear export factor (predicted)	0.61
SPAC6F6.17	telomere length regulator protein Rif1	0.61
SPAC3H5.09c	conserved eukaryotic mitochondrial protein (predicted)	0.61
SPAC144.16	sister chromatid cohesion protein (predicted)	0.61
SPCC14G10.01	dephospho-CoA kinase (predicted)	0.61
SPBC902.04	RNA-binding protein	0.60
SPAC959.06c	conserved fungal protein	0.60
SPAC17A5.01	peroxin-6 (predicted)	0.60
SPCC1494.07	tRNA 2'-O-methylase subunit Trm72 (predicted)	0.60
SPAC15E1.07c	meiotic cohesin complex associated protein Moa1	0.60
SPCC1620.10	complexed with Cdc5 protein Cwf26	0.60
SPAPB1A11.03	cytochrome b2 (L-lactate cytochrome-c oxidoreductase) (predicted)	0.60
SPCC1919.05	Ski complex TPR repeat subunit Ski3 (predicted)	0.60
SPCC306.10	wtf element Wtf8	0.60
SPCC736.11	argonaute	0.60
SPBC16A3.10	membrane bound O-acyltransferase%2C MBOAT (predicted)	0.60
SPBC582.05c	BRCT domain protein Brc1	0.60
SPCC1840.08c	protein disulfide isomerase (predicted)	0.60
SPBC21.06c	serine/threonine protein kinase Cdc7	0.60
SPAC13F5.06c	exocyst complex subunit Sec10	0.60
SPAC167.01	serine/threonine protein kinase%2C sensor for unfolded proteins in the ER Ire1	0.60
SPAC3G9.13c	mitochondrial tryptophan-tRNA ligase Msw1 (predicted)	0.59
SPAC2F7.10	palmitoyltransferase Akr1 (predicted)	0.59
SPCC550.09	peroxin Pex32 (predicted)	0.59
SPAC23D3.14c	alpha-amylase homolog Aah2 (predicted)	0.59
SPAC30D11.01c	alpha-glucosidase (predicted)	0.59
SPBC23E6.02	ATP-dependent DNA helicase (predicted)	0.59
SPAC644.11c	mitochondrial pyruvate dehydrogenase (lipoamide) kinase Pkp1 (predicted)	0.59
SPAC13G6.12c	chitin synthase I	0.59
SPBP23A10.13	origin recognition complex subunit Orc4	0.59
SPBC12C2.08	dynamin Dnm1	0.59
SPBC3D6.10	AP-endonuclease Apn2	0.59
SPBC18A7.01	X-Pro dipeptidase (predicted)	0.59
SPAC31G5.07	tetraspan protein Dni1	0.59
SPCC1450.12	PXA domain protein	0.59
SPAC27E2.01	alpha-amylase homolog (predicted)	0.59
SPBC21B10.13c	MBF complex negative regulatory component Yox1	0.58
SPBC115.03	gfo/idh/mocA family oxidoreductase (predicted)	0.58
SPAPB17E12.02	SMN family protein Yip12	0.58
SPAC26H5.04	vacuolar import and degradation protein Vid28 (predicted)	0.58

SPAC15A10.10	Muskelin homolog (predicted)	0.58
SPAC23C11.10	RNA processing protein (predicted)	0.58
SPAC25H1.02	histone demethylase Jmj1 (predicted)	0.58
SPAC17G6.05c	BRO1 domain protein Bro1 (predicted)	0.58
SPBC1683.04	glycosyl hydrolase family 3 (predicted)	0.58
SPAC4A8.05c	myosin II heavy chain Myo3	0.58
SPCC16C4.18c	histone H4-like TAF Taf6%2C SAGA complex subunit	0.58
SPBC14C8.16c	mitochondrial ribosomal protein subunit S35	0.58
SPAC3G6.09c	trehalose-phosphate synthase Tps2 (predicted)	0.58
SPBC3E7.08c	DNA repair nuclease Rad13	0.58
SPCC962.02c	survivin%2C Bir1	0.58
SPBC28E12.06c	beige protein homolog (predicted)	0.58
SPCC830.10	nucleoside triphosphatase (predicted)	0.58
SPAC9G1.09	PAK-related GC kinase Sid1	0.58
SPAC13C5.06c	sequence orphan	0.57
SPAC2E1P5.02c	Rab GTPase binding protein upregulated in meiosis II (predicted)	0.57
SPAC13G7.07	argonaute binding protein 2	0.57
SPBC16G5.17	transcription factor%2C zf-fungal binuclear cluster type (predicted)	0.57
SPCC132.03	sequence orphan	0.57
SPAPB17E12.04c	COP9/signalosome complex subunit Csn2	0.57
SPAC29A4.20	elongator complex%2C histone acetyltransferase subunit Elp3 (predicted)	0.57
SPBC21C3.20c	C2 domain protein Git1	0.57
SPAC6G10.06	FAD-dependent amino acid oxidase involved in late endosome to Golgi transport (predicted)	0.57
SPCC895.07	TOG ortholog Alp14	0.57
SPBC215.11c	aldo/keto reductase%2C unknown biological role	0.57
SPAPB1E7.05	glycerophosphoryl diester phosphodiesterase Gde1 (predicted)	0.57
SPCC18.04	F-box protein Pof6	0.57
SPAC17A5.18c	meiotic recombination protein Rec25	0.57
SPAC20H4.09	ATP-dependent RNA helicase%2C spliceosomal (predicted)	0.56
SPAC1006.02	Astra associated protein 1 Asa1	0.56
SPBC1711.17	ATP-dependent RNA helicase Prp16	0.56
SPBC1347.01c	deoxycytidyl transferase Rev1 (predicted)	0.56
SPAC3A11.06	sorting nexin Mvp1 (predicted)	0.56
SPBC25H2.11c	SAGA complex bromodomain subunit Spt7	0.56
SPAC1783.05	ATP-dependent DNA helicase Hrp1	0.55
SPBC215.02	prefoldin subunit 5 (predicted)	0.55
SPBC3D6.04c	mitotic spindle checkpoint protein Mad1	0.55
SPAC19A8.01c	guanyl-nucleotide exchange factor Sec73 (predicted)	0.55
SPBC725.04	oxalyl-CoA decarboxylase (predicted)	0.55
SPBC16E9.08	prospore membrane protein Mcp4/Mug101	0.55
SPBC31E1.05	RNA export factor%2C cytoplasmic nucleoporin Gle1	0.55
SPBC146.11c	meiotically upregulated gene Mug97	0.55
SPAC15A10.16	actin interacting protein 3 homolog Bud6	0.55
SPCC1223.02	4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate synthase Nmt1	0.54
SPAC23H3.14	LAlv9 family protein%2C involved in post Golgi transport (predicted)	0.54
SPAC6G9.04	sporulation protein Spo7	0.54
SPBC24C6.10c	WISH/DIP/SPIN90 ortholog Dip1	0.54
SPCC18B5.07c	nucleoporin Nup61	0.54
SPAC30D11.08c	Lsd1/2 complex PHD finger containing	0.54

	protein Phf2	
SPCC569.04	sequence orphan	0.54
SPAC824.08	guanosine-diphosphatase Gda1	0.54
SPAC20H4.10	ubiquitin-protein ligase E4 (predicted)	0.54
SPAC10F6.09c	mitotic cohesin complex subunit Psm3	0.54
SPCC338.02	sequence orphan	0.54
SPAC343.04c	WD repeat protein%2C human WDR26 family%2C ubiquitin ligase complex subunit (predicted)	0.54
SPBC27B12.08	Pof6 interacting protein Sip1%2C predicted AP-1 accessory protein	0.54
SPAC1F3.10c	mitochondrial intermediate peptidase Oct1 (predicted)	0.54
SPBC1105.15c	3-hydroxyacyl-ACP dehydratase Htd2 (predicted)	0.54
SPBC17A3.10	peroxisomal ubiquitin-protein ligase E3 (predicted)	0.54
SPAC22G7.04	ubiquitin C-terminal hydrolase%2C poly(A)-specific ribonuclease complex subunit Pan2 (predicted)	0.53
SPBC646.02	complexed with Cdc5 protein Cwf11	0.53
SPAC24C9.15c	septin Spn5	0.53
SPAC6G9.16c	sequence orphan	0.53
SPBC1709.08	cleavage factor one Cft1 (predicted)	0.53
SPAC22F3.09c	MBF transcription factor complex subunit Res2	0.53
SPBC11G11.07	karyopherin%2C nuclear import receptor Mtr10 (predicted)	0.53
SPAC12B10.14c	pseudokinase Tea5	0.53
SPAC3C7.13c	glucose-6-phosphate 1-dehydrogenase (predicted)	0.53
SPBC30B4.06c	mitochondrial GIDA family tRNA uridine 5-carboxymethylaminomethyl modification enzyme (predicted)	0.53
SPAC17A2.01	high-affinity import carrier for pyridoxine%2C pyridoxal%2C and pyridoxamine Bsu1	0.53
SPAC1250.01	ATP-dependent DNA helicase Snf21	0.53
SPAC1687.03c	DNA replication factor C complex subunit Rfc4 (predicted)	0.53
SPAC14C4.05c	LEM domain protein Man1%2C Sad1 interacting factor (predicted)	0.53
SPAC1071.02	Dos2 silencing complex subunit Mms19	0.53
SPBC418.02	NatA N-acetyltransferase complex subunit (predicted)	0.53
SPCC285.06c	wtf element Wtf17	0.53
SPAC10F6.02c	ATP-dependent RNA helicase Prp22	0.53
SPBC32H8.06	TPR repeat protein%2C meiotically spliced	0.53
SPBC29A10.02	meiotic RNA-binding protein 1	0.53
SPAC1687.02	CAAX prenyl protease (predicted)	0.53
SPAC20H4.06c	RNA-binding protein	0.53
SPAC31G5.16c	dolichol-phosphate mannosyltransferase catalytic subunit Dpm1	0.52
SPCC1919.11	BAR adaptor protein	0.52
SPBC1773.05c	hexitol dehydrogenase (predicted)	0.52
SPCC18B5.08c	mitochondrial isoleucine-tRNA ligase (predicted)	0.52
SPBC3D6.09	DNA polymerase epsilon subunit Dpb4	0.52
SPBC18H10.09	zf-CHY type zinc finger protein	0.52
SPBC3E7.01	1-phosphatidylinositol-3-phosphate 5-kinase Fab1	0.52
SPBC14C8.15	triglyceride lipase-cholesterol esterase (predicted)	0.52
SPCC622.13c	Tel Two Interacting protein 1	0.52

SPCC16A11.12c	ubiquitin C-terminal hydrolase Ubp1	0.52
SPAC139.03	transcription factor%2C zf-fungal binuclear cluster type (predicted)	0.52
SPAC20G8.01	ATP-dependent DNA ligase Cdc17	0.52
SPBC691.04	mitochondrial ATP-dependent RNA helicase Mss116 (predicted)	0.52
SPBC1709.07	3-keto sterol reductase (predicted)	0.52
SPBC1685.06	poly(A) polymerase Cid11 (predicted)	0.52
SPBC20F10.05	NRDE-2 family protein (predicted)	0.52
SPAC1952.11c	urease Ure2	0.52
SPCC31H12.02c	membrane transporter (predicted)	0.52
SPBC902.02c	RFC-like complex subunit Ctf18	0.52
SPBC211.04c	MCM complex subunit Mcm6	0.52
SPAC1296.01c	phosphoacetylglucosamine mutase (predicted)	0.51
SPAC8F11.07c	DNA replication protein Cdc24	0.51
SPBC691.05c	membrane transporter (predicted)	0.51
SPAC20G8.08c	SMARCAD1 family ATP-dependent DNA helicase Fft1 (predicted)	0.51
SPAC22F3.03c	ATP-dependent DNA helicase Rdh54	0.51
SPBC1685.14c	Vid27 family protein	0.51
SPAC4A8.02c	conserved protein%2C UPF0047 family	0.51
SPAC5H10.04	NADPH dehydrogenase (predicted)	0.51
SPBC651.10	Smc5-6 complex non-SMC subunit Nse5	0.51
SPBC2D10.06	MBF transcription factor complex subunit Rep1	0.51
SPAC20H4.11c	Rho family GTPase Rho5	0.51
SPBP4H10.20	m7G(5')pppN diphosphatase (predicted)	0.51
SPBC1861.03	NatC N-acetyltransferase complex subunit Mak10 (predicted)	0.51
SPBC409.10	phosphoribosylamidoimidazolesuccinocarboxamide synthase%2C SAICAR synthetase%2C Ade7	0.51
SPBC543.03c	Ku domain protein Pku80	0.51
SPBC839.10	U1 snRNP-associated protein Usp107	0.51
SPCC1753.05	RNA export factor Rsm1	0.51
SPBC1734.07c	TRAPP complex subunit Trs85 (predicted)	0.51
SPBC20F10.07	GRAM domain protein	0.51
SPCC1620.12c	GTPase activating protein (predicted)	0.51
SPBC17A3.08	TatD homolog (predicted)	0.51
SPAC821.13c	P-type ATPase (predicted)	0.51
SPAC1486.04c	medial ring protein Alm1	0.51
SPAC1093.03	inositol polyphosphate phosphatase (predicted)	0.51
SPAC1006.03c	RNA elimination defective protein Red1	0.51
SPAC14C4.03	Cds1/Rad53/Chk2 family protein kinase Mek1	0.51
SPAC2F7.16c	phospholipase D%2C Pld1	0.51
SPCC970.01	DNA repair endonuclease XPF	0.50
SPBPJ4664.06	UDP-glucose-glycoprotein glucosyltransferase Gpt1	0.50
SPBC211.03c	guanyl-nucleotide exchange factor (predicted)	0.50
SPAC23C4.16c	autophagy associated lipase Atg15	0.50
SPBP19A11.07c	human HID1 ortholog 2	0.50
SPCC126.07c	human CTD-binding SR-like protein rA9 homolog (predicted)	0.50
SPAC4H3.03c	glucan 1%2C4-alpha-glucosidase (predicted)	0.50
SPCC285.07c	wtf element Wtf18	0.50

Table S2. GO terms enriched in H4K20me1-associated genes

GO_term	description	fraction in selection	fraction total	# in selec-tion (>0.5)	# total in GO term	enrich-ment	P-value
GO:0000502	proteasome complex	0.024	0.008	28	40	3.10	2.2E-11
GO:0005838	proteasome regulatory particle	0.012	0.004	14	19	3.26	2.8E-07
GO:0071540	eukaryotic translation initiation factor 3 complex, eIF3e	0.008	0.002	9	10	3.99	3.3E-07
GO:0005852	eukaryotic translation initiation factor 3 complex	0.009	0.002	10	12	3.69	7.1E-07
GO:0009116	nucleoside metabolic process	0.02	0.009	23	44	2.32	3.8E-06
GO:0004298	threonine-type endopeptidase activity	0.009	0.003	11	15	3.25	3.8E-06
GO:0006631	fatty acid metabolic process	0.016	0.007	19	34	2.48	5.2E-06
GO:0006085	acetyl-CoA biosynthetic process	0.006	0.002	7	8	3.88	6.6E-06
GO:0016282	eukaryotic 43S preinitiation complex	0.006	0.002	7	8	3.88	6.6E-06
GO:0006084	acetyl-CoA metabolic process	0.014	0.006	16	29	2.44	2.9E-05
GO:0003743	translation initiation factor activity	0.016	0.007	19	37	2.28	2.9E-05
GO:0009085	lysine biosynthetic process	0.005	0.001	6	7	3.80	2.9E-05
GO:0006537	glutamate biosynthetic process	0.006	0.002	7	9	3.45	4.8E-05
GO:0030686	90S preribosome	0.006	0.002	7	9	3.45	4.8E-05
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	0.008	0.003	9	13	3.07	4.8E-05
GO:0008540	proteasome regulatory particle, base subcomplex	0.007	0.002	8	11	3.22	5.2E-05
GO:0006536	glutamate metabolic process	0.012	0.005	14	25	2.48	5.9E-05
GO:0005732	small nucleolar ribonucleoprotein complex	0.02	0.01	23	50	2.04	6.2E-05
GO:0016769	transferase activity, transferring nitrogenous groups	0.012	0.005	14	26	2.39	1.1E-04
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	0.004	0.001	5	6	3.69	1.3E-04
GO:0000103	sulfate assimilation	0.004	0.001	5	6	3.69	1.3E-04
GO:0005967	mitochondrial pyruvate dehydrogenase complex	0.004	0.001	5	6	3.69	1.3E-04
GO:0006613	cotranslational protein targeting to membrane	0.008	0.003	9	14	2.85	1.3E-04
GO:0045047	protein targeting to ER	0.011	0.005	13	24	2.40	1.6E-04
GO:0006188	IMP biosynthetic process	0.007	0.002	8	12	2.95	1.7E-04
GO:0005832	chaperonin-containing T-complex	0.005	0.002	6	8	3.32	1.9E-04
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	0.005	0.002	6	8	3.32	1.9E-04

GO:0006213	pyrimidine nucleoside metabolic process	0.006	0.002	7	10	3.10	1.9E-04
GO:0000054	ribosomal subunit export from nucleus	0.013	0.006	15	30	2.22	2.3E-04
GO:0006633	fatty acid biosynthetic process	0.01	0.004	12	22	2.42	2.3E-04
GO:0009070	serine family amino acid biosynthetic process	0.008	0.003	9	15	2.66	3.2E-04
GO:0030515	snoRNA binding	0.012	0.005	14	28	2.22	3.4E-04
GO:0006144	purine base metabolic process	0.009	0.003	10	18	2.46	4.8E-04
GO:0000243	commitment complex	0.006	0.002	7	11	2.82	5.6E-04
GO:0009082	branched chain family amino acid biosynthetic process	0.006	0.002	7	11	2.82	5.6E-04
GO:0007007	inner mitochondrial membrane organization	0.008	0.003	9	16	2.49	6.9E-04
GO:0005685	U1 snRNP	0.008	0.003	9	16	2.49	6.9E-04
GO:0006206	pyrimidine base metabolic process	0.008	0.003	9	16	2.49	6.9E-04
GO:0008483	transaminase activity	0.01	0.005	12	24	2.22	7.4E-04
GO:0008655	pyrimidine salvage	0.004	0.001	5	7	3.16	7.4E-04
GO:0008541	proteasome regulatory particle, lid subcomplex	0.004	0.001	5	7	3.16	7.4E-04
GO:0016597	amino acid binding	0.004	0.001	5	7	3.16	7.4E-04
GO:0016651	oxidoreductase activity, acting on NADH or NADPH	0.009	0.004	10	19	2.33	9.1E-04
GO:0042176	regulation of protein catabolic process	0.009	0.004	10	19	2.33	9.1E-04
GO:0045039	protein import into mitochondrial inner membrane	0.006	0.002	7	12	2.58	0.0014
GO:0051539	4 iron, 4 sulfur cluster binding	0.009	0.004	10	20	2.22	0.0016
GO:0030684	preribosome	0.009	0.004	11	23	2.12	0.0018
GO:0006189	'de novo' IMP biosynthetic process	0.005	0.002	6	10	2.66	0.0018
GO:0016831	carboxy-lyase activity	0.007	0.003	8	15	2.36	0.0019
GO:0016455	RNA polymerase II transcription mediator activity	0.007	0.003	8	15	2.36	0.0019
GO:0006531	aspartate metabolic process	0.004	0.002	5	8	2.77	0.0024
GO:0006551	leucine metabolic process	0.004	0.002	5	8	2.77	0.0024
GO:0009097	isoleucine biosynthetic process	0.004	0.002	5	8	2.77	0.0024
GO:0030015	CCR4-NOT core complex	0.004	0.002	5	8	2.77	0.0024
GO:0043101	purine salvage	0.004	0.002	5	8	2.77	0.0024
GO:0006568	tryptophan metabolic process	0.006	0.003	7	13	2.39	0.0028
GO:0051170	nuclear import	0.006	0.003	7	13	2.39	0.0028
GO:0010181	FMN binding	0.006	0.003	7	13	2.39	0.0028

GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.008	0.004	9	19	2.10	0.0040
GO:0004725	protein tyrosine phosphatase activity	0.005	0.002	6	11	2.42	0.0041
GO:0000105	histidine biosynthetic process	0.005	0.002	6	11	2.42	0.0041
GO:0016592	mediator complex	0.009	0.004	10	22	2.01	0.0043
GO:0000395	nuclear mRNA 5'-splice site recognition	0.006	0.003	7	14	2.22	0.0053
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	0.006	0.003	7	14	2.22	0.0053
GO:0007021	tubulin complex assembly	0.006	0.003	7	14	2.22	0.0053
GO:0009073	aromatic amino acid family biosynthetic process	0.006	0.003	7	14	2.22	0.0053
GO:0006376	mRNA splice site selection	0.006	0.003	7	14	2.22	0.0053
GO:0006353	transcription termination	0.006	0.003	7	14	2.22	0.0053
GO:0030014	CCR4-NOT complex	0.004	0.002	5	9	2.46	0.0058
GO:0006207	'de novo' pyrimidine base biosynthetic process	0.004	0.002	5	9	2.46	0.0058
GO:0006606	protein import into nucleus	0.005	0.002	6	12	2.22	0.0079
GO:0006740	NADPH regeneration	0.006	0.003	7	15	2.07	0.0091
GO:0051205	protein insertion into membrane	0.006	0.003	7	15	2.07	0.0091
GO:0043021	ribonucleoprotein binding	0.006	0.003	7	15	2.07	0.0091
GO:0003711	transcription elongation regulator activity	0.006	0.003	7	15	2.07	0.0091
GO:0005750	mitochondrial respiratory chain complex III	0.004	0.002	5	10	2.22	0.0118
GO:0000120	RNA polymerase I transcription factor complex	0.004	0.002	5	10	2.22	0.0118
GO:0019856	pyrimidine base biosynthetic process	0.004	0.002	5	10	2.22	0.0118
GO:0006369	termination of RNA polymerase II transcription	0.004	0.002	5	10	2.22	0.0118
GO:0016884	carbon-nitrogen ligase activity, with glutamine as amido-N-donor	0.005	0.003	6	13	2.05	0.0138
GO:0051605	protein maturation by peptide bond cleavage	0.005	0.003	6	13	2.05	0.0138
GO:0043628	ncRNA 3'-end processing	0.004	0.002	5	11	2.01	0.0210
GO:0006526	arginine biosynthetic process	0.004	0.002	5	11	2.01	0.0210
GO:0006098	pentose-phosphate shunt	0.004	0.002	5	11	2.01	0.0210
GO:0042125	protein galactosylation	0.004	0.002	5	11	2.01	0.0210

Table S3. GO terms enriched in H4K20me2-associated genes

GO_term	description	fraction in selection	fraction total	# in selection (>0.5)	# total in GO term	enrichment	P-value
GO:0006298	mismatch repair	0.009	0.002	7	11	4.44	1.9E-05
GO:0005643	nuclear pore	0.024	0.01	18	51	2.46	4.0E-05
GO:0008033	tRNA processing	0.034	0.017	25	87	2.00	1.3E-04
GO:0030983	mismatched DNA binding	0.007	0.002	5	8	4.36	1.9E-04
GO:0032266	phosphatidylinositol-3-phosphate binding	0.007	0.002	5	9	3.87	4.9E-04
GO:0031047	gene silencing by RNA	0.012	0.004	9	23	2.73	6.8E-04
GO:0004843	ubiquitin-specific protease activity	0.014	0.005	10	27	2.58	7.1E-04
GO:0005669	transcription factor TFIID complex	0.009	0.003	7	17	2.87	0.0013
GO:0000032	cell wall mannoprotein biosynthetic process	0.007	0.002	5	11	3.17	0.0021
GO:0035268	protein mannosylation	0.007	0.002	5	11	3.17	0.0021
GO:0031048	chromatin silencing by small RNA	0.008	0.003	6	15	2.79	0.0027
GO:0004221	ubiquitin thiolesterase activity	0.009	0.004	7	19	2.57	0.0030
GO:0048278	vesicle docking	0.008	0.003	6	16	2.61	0.0043
GO:0051285	cell cortex of cell tip	0.012	0.006	9	29	2.16	0.0053
GO:0005099	Ras GTPase activator activity	0.011	0.005	8	25	2.23	0.0058
GO:0003690	double-stranded DNA binding	0.009	0.004	7	21	2.32	0.0062
GO:0032319	regulation of Rho GTPase activity	0.008	0.003	6	17	2.46	0.0064
GO:0006896	Golgi to vacuole transport	0.008	0.003	6	17	2.46	0.0064
GO:0031390	Ctf18 RFC-like complex	0.007	0.003	5	14	2.49	0.0092
GO:0030261	chromosome condensation	0.008	0.004	6	19	2.20	0.0128
GO:0016050	vesicle organization	0.008	0.004	6	19	2.20	0.0128
GO:0071937	barrier septum formation involved in cell cycle cytokinesis	0.008	0.004	6	19	2.20	0.0128
GO:0035023	regulation of Rho protein signal transduction	0.008	0.004	6	19	2.20	0.0128
GO:0015662	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	0.007	0.003	5	15	2.32	0.0135
GO:0031321	ascospore-type prospore formation	0.008	0.004	6	20	2.09	0.0173
GO:0031134	sister chromatid biorientation	0.007	0.003	5	17	2.05	0.0259

Table S4. GO terms enriched in H4K20me3-associated genes

GO_term	description	fraction in selection	fraction total	# in selec-tion (>0.5)	# total in GO term	enrich-ment	P-value
GO:0004386	helicase activity	0.063	0.018	32	92	3.51	1.1E-11
GO:0008026	ATP-dependent helicase activity	0.057	0.016	29	82	3.57	4.9E-11
GO:0008094	DNA-dependent ATPase activity	0.047	0.012	24	61	3.98	1.3E-10
GO:0016462	pyrophosphatase activity	0.132	0.062	67	318	2.13	2.1E-10
GO:0017111	nucleoside-triphosphatase activity	0.124	0.058	63	297	2.14	5.4E-10
GO:0006200	ATP catabolic process	0.09	0.036	46	187	2.49	6.8E-10
GO:0016887	ATPase activity	0.102	0.044	52	227	2.32	9.4E-10
GO:0004003	ATP-dependent DNA helicase activity	0.035	0.008	18	40	4.55	1.1E-09
GO:0003678	DNA helicase activity	0.035	0.008	18	42	4.33	3.0E-09
GO:0042623	ATPase activity, coupled	0.077	0.032	39	167	2.36	5.9E-08
GO:0007062	sister chromatid cohesion	0.024	0.006	12	29	4.18	1.2E-06
GO:0007126	meiosis	0.079	0.038	40	194	2.08	1.5E-06
GO:0006974	response to DNA damage stimulus	0.084	0.042	43	216	2.01	1.7E-06
GO:0008278	cohesin complex	0.012	0.002	6	9	6.74	2.7E-06
GO:0005086	ARF guanyl-nucleotide exchange factor activity	0.01	0.001	5	7	7.22	5.9E-06
GO:0006281	DNA repair	0.065	0.031	33	157	2.12	6.9E-06
GO:0004556	alpha-amylase activity	0.012	0.002	6	10	6.06	8.2E-06
GO:0007064	mitotic sister chromatid cohesion	0.012	0.002	6	12	5.05	4.5E-05
GO:0045143	homologous chromosome segregation	0.016	0.004	8	20	4.04	5.3E-05
GO:0044264	cellular polysaccharide metabolic process	0.033	0.013	17	67	2.56	5.7E-05
GO:0000084	S phase of mitotic cell cycle	0.016	0.004	8	21	3.85	8.4E-05
GO:0006310	DNA recombination	0.045	0.021	23	107	2.17	8.7E-05
GO:0048015	phosphoinositide-mediated signaling	0.014	0.003	7	17	4.16	9.4E-05
GO:0046379	extracellular polysaccharide metabolic process	0.018	0.005	9	26	3.50	1.0E-04
GO:0005657	replication fork	0.031	0.012	16	64	2.53	1.1E-04
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	0.026	0.009	13	48	2.74	1.5E-04
GO:0044247	cellular polysaccharide catabolic process	0.012	0.003	6	14	4.33	1.6E-04

GO:0030437	ascospore formation	0.043	0.02	22	105	2.12	1.8E-04
GO:0016567	protein ubiquitination	0.049	0.024	25	126	2.01	1.9E-04
GO:0043596	nuclear replication fork	0.028	0.011	14	56	2.53	2.4E-04
GO:0000723	telomere maintenance	0.028	0.011	14	56	2.53	2.4E-04
GO:0016577	histone demethylation	0.01	0.002	5	11	4.59	2.7E-04
GO:0003724	RNA helicase activity	0.022	0.008	11	41	2.71	4.2E-04
GO:0007127	meiosis I	0.037	0.018	19	91	2.11	4.5E-04
GO:0005085	guanyl-nucleotide exchange factor activity	0.02	0.007	10	36	2.81	4.8E-04
GO:0070988	demethylation	0.01	0.002	5	12	4.21	5.0E-04
GO:0016798	hydrolase activity, acting on glycosyl bonds	0.028	0.012	14	60	2.36	5.5E-04
GO:0045132	meiotic chromosome segregation	0.028	0.012	14	60	2.36	5.5E-04
GO:0000781	chromosome, telomeric region	0.022	0.008	11	43	2.59	6.7E-04
GO:0006312	mitotic recombination	0.012	0.003	6	17	3.57	7.2E-04
GO:0003774	motor activity	0.012	0.003	6	17	3.57	7.2E-04
GO:0032012	regulation of ARF protein signal transduction	0.01	0.003	5	13	3.89	8.5E-04
GO:0003887	DNA-directed DNA polymerase activity	0.012	0.003	6	18	3.37	0.0011
GO:0008186	RNA-dependent ATPase activity	0.02	0.008	10	40	2.53	0.0013
GO:0004004	ATP-dependent RNA helicase activity	0.02	0.008	10	40	2.53	0.0013
GO:0016298	lipase activity	0.014	0.005	7	24	2.95	0.0015
GO:0007131	reciprocal meiotic recombination	0.024	0.01	12	53	2.29	0.0015
GO:0030476	ascospore wall assembly	0.012	0.004	6	19	3.19	0.0016
GO:0000151	ubiquitin ligase complex	0.026	0.012	13	60	2.19	0.0017
GO:0016042	lipid catabolic process	0.014	0.005	7	25	2.83	0.0021
GO:0000109	nucleotide-excision repair complex	0.012	0.004	6	20	3.03	0.0022
GO:0007088	regulation of mitosis	0.026	0.012	13	63	2.09	0.0028
GO:0048278	vesicle docking	0.01	0.003	5	16	3.16	0.0031
GO:0031933	telomeric heterochromatin	0.01	0.003	5	16	3.16	0.0031
GO:0006301	postreplication repair	0.01	0.003	5	16	3.16	0.0031
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	0.018	0.008	9	39	2.33	0.0037
GO:0051783	regulation of nuclear division	0.026	0.013	13	65	2.02	0.0038

GO:0007031	peroxisome organization	0.012	0.004	6	22	2.76	0.0041
GO:0019932	second-messenger-mediated signaling	0.02	0.009	10	46	2.20	0.0043
GO:0008608	attachment of spindle microtubules to kinetochore	0.014	0.005	7	28	2.53	0.0045
GO:0006289	nucleotide-excision repair	0.014	0.005	7	28	2.53	0.0045
GO:0004091	carboxylesterase activity	0.012	0.005	6	24	2.53	0.0069
GO:0000725	recombinational repair	0.016	0.007	8	36	2.25	0.0070
GO:0030261	chromosome condensation	0.01	0.004	5	19	2.66	0.0080
GO:0040020	regulation of meiosis	0.01	0.004	5	19	2.66	0.0080
GO:0040023	establishment of nucleus localization	0.01	0.004	5	19	2.66	0.0080
GO:0090307	spindle assembly involved in mitosis	0.01	0.004	5	19	2.66	0.0080
GO:0000784	nuclear chromosome, telomeric region	0.01	0.004	5	19	2.66	0.0080
GO:0009250	glucan biosynthetic process	0.014	0.006	7	31	2.28	0.0088
GO:0045005	maintenance of fidelity involved in DNA-dependent DNA replication	0.014	0.006	7	31	2.28	0.0088
GO:0000724	double-strand break repair via homologous recombination	0.014	0.006	7	31	2.28	0.0088
GO:0006302	double-strand break repair	0.018	0.009	9	44	2.07	0.0093
GO:0007533	mating type switching	0.01	0.004	5	20	2.53	0.011
GO:0007531	mating type determination	0.012	0.005	6	26	2.33	0.011
GO:0000792	heterochromatin	0.014	0.006	7	33	2.14	0.013
GO:0035091	phosphoinositide binding	0.014	0.006	7	33	2.14	0.013
GO:0005875	microtubule associated complex	0.01	0.004	5	21	2.41	0.014
GO:0003690	double-stranded DNA binding	0.01	0.004	5	21	2.41	0.014
GO:0010553	negative regulation of gene-specific transcription from RNA polymerase II promoter	0.01	0.004	5	21	2.41	0.014
GO:0016891	endoribonuclease activity, producing 5'-phosphomonoesters	0.01	0.004	5	21	2.41	0.014
GO:0007094	mitotic cell cycle spindle assembly checkpoint	0.012	0.005	6	28	2.17	0.017
GO:0008194	UDP-glycosyltransferase activity	0.012	0.005	6	28	2.17	0.017
GO:0005628	prospore membrane	0.01	0.004	5	22	2.30	0.017
GO:0051445	regulation of meiotic cell cycle	0.01	0.004	5	22	2.30	0.017
GO:0030466	chromatin silencing at silent mating-type cassette	0.014	0.007	7	35	2.02	0.019
GO:0045839	negative regulation of mitosis	0.012	0.006	6	29	2.09	0.020
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	0.012	0.006	6	29	2.09	0.020

GO:0006090	pyruvate metabolic process	0.012	0.006	6	29	2.09	0.020
GO:0031577	spindle checkpoint	0.012	0.006	6	29	2.09	0.020
GO:0031047	gene silencing by RNA	0.01	0.004	5	23	2.20	0.021
GO:0044242	cellular lipid catabolic process	0.01	0.004	5	23	2.20	0.021
GO:0004521	endoribonuclease activity	0.012	0.006	6	30	2.02	0.024
GO:0006887	exocytosis	0.012	0.006	6	30	2.02	0.024
GO:0005777	peroxisome	0.01	0.005	5	24	2.11	0.026
GO:0031261	DNA replication preinitiation complex	0.01	0.005	5	24	2.11	0.026
GO:0016564	transcription repressor activity	0.01	0.005	5	24	2.11	0.026

Table S5 Gene ontology terms enriched in H4K20me3 signal (log2(WT/*set9*Δ)>0.5)

GO_term	**Description**	**Enrichment**[*]	**N° genes**[**]	**P-value**
GO:0016462	pyrophosphatase activity	2.1	67	<0.00001
GO:0017111	nucleoside-triphosphatase activity	2.1	63	<0.00001
GO:0006200	ATP catabolic process	2.5	46	<0.00001
GO:0016887	ATPase activity	2.3	52	<0.00001
GO:0042623	ATPase activity, coupled	2.4	39	<0.00001
GO:0007126	meiosis	2.1	40	<0.00001
GO:0006974	response to DNA damage stimulus	2.0	43	<0.00001
GO:0006281	DNA repair	2.1	33	0.00001
GO:0006310	DNA recombination	2.2	23	0.00009
GO:0030437	ascospore formation	2.1	22	0.00018
GO:0016567	protein ubiquitination	2.0	25	0.00019

[*] Calculated as (genes of GO term in selection/total genes of GO term)/(genes in selection/total protein coding genes).

[**] Genes with H4K20me3 signal (WT–set9Δ) and belonging to the specific GO term.

Table S6. GO terms enriched in genes expressed at same levels as H4K20me3 associated

GO_term	description	fraction in selection	fraction total	# in selec-tion	# total in GO term	enrich-ment	P-value
GO:0034470	ncRNA processing	0.082	0.039	26	250	2.12	4.2E-04
GO:0006396	RNA processing	0.117	0.069	37	447	1.68	1.5E-03
GO:0034660	ncRNA metabolic process	0.085	0.045	27	291	1.89	1.8E-03
GO:0016298	lipase activity	0.019	0.003	6	23	5.53	3.6E-03
GO:0006473	protein amino acid acetylation	0.028	0.008	9	54	3.39	4.3E-03
GO:0016072	rRNA metabolic process	0.057	0.027	18	173	2.12	4.3E-03
GO:0016042	lipid catabolic process	0.019	0.004	6	25	4.88	6.4E-03
GO:0006364	rRNA processing	0.054	0.027	17	172	2.01	9.3E-03
GO:0043543	protein amino acid acylation	0.028	0.010	9	62	2.95	9.9E-03
GO:0042254	ribosome biogenesis	0.066	0.036	21	235	1.82	1.0E-02
GO:0003724	RNA helicase activity	0.022	0.006	7	41	3.62	1.1E-02
GO:0016192	vesicle-mediated transport	0.073	0.042	23	269	1.74	1.1E-02
GO:0016573	histone acetylation	0.022	0.006	7	41	3.47	1.4E-02
GO:0046486	glycerolipid metabolic process	0.032	0.013	10	84	2.42	2.1E-02
GO:0016887	ATPase activity	0.057	0.032	18	217	1.76	2.4E-02
GO:0006400	tRNA modification	0.025	0.009	8	59	2.76	2.4E-02
GO:0022613	ribonucleoprotein complex biogenesis	0.066	0.040	21	258	1.66	2.6E-02
GO:0000123	histone acetyltransferase complex	0.022	0.007	7	37	3.00	2.6E-02
GO:0016570	histone modification	0.035	0.016	11	102	2.19	2.6E-02
GO:0016569	covalent chromatin modification	0.035	0.016	11	102	2.19	2.6E-02
GO:0004091	carboxylesterase activity	0.016	0.004	5	25	4.24	2.7E-02
GO:0044242	cellular lipid catabolic process	0.016	0.004	5	24	4.24	2.7E-02
GO:0006650	glycerophospholipid metabolic process	0.028	0.012	9	77	2.38	3.3E-02
GO:0016791	phosphatase activity	0.025	0.010	8	67	2.53	3.6E-02
GO:0004004	ATP-dependent RNA helicase activity	0.019	0.006	6	40	3.18	3.7E-02
GO:0008186	RNA-dependent ATPase activity	0.019	0.006	6	40	3.18	3.7E-02
GO:0009310	amine catabolic process	0.019	0.006	6	41	2.98	4.8E-02
GO:0046872	metal ion binding	0.136	0.105	43	708	1.29	5.2E-02
GO:0006644	phospholipid metabolic process	0.028	0.013	9	86	2.13	5.8E-02

GO:0032543	mitochondrial translation	0.035	0.018	11	117	1.91	5.9E-02
GO:0006399	tRNA metabolic process	0.038	0.021	12	133	1.84	5.9E-02
GO:0008026	ATP-dependent helicase activity	0.025	0.011	8	76	2.23	6.3E-02
GO:0070035	purine NTP-dependent helicase activity	0.025	0.011	8	76	2.23	6.3E-02
GO:0016879	ligase activity, forming carbon-nitrogen bonds	0.038	0.021	12	142	1.79	6.7E-02
GO:0043169	cation binding	0.136	0.107	43	722	1.26	6.8E-02
GO:0019637	organophosphate metabolic process	0.028	0.014	9	89	2.06	6.8E-02
GO:0043167	ion binding	0.136	0.108	43	724	1.26	7.0E-02
GO:0008033	tRNA processing	0.028	0.014	9	90	2.03	7.2E-02
GO:0009451	RNA modification	0.025	0.012	8	76	2.14	7.7E-02
GO:0016881	acid-amino acid ligase activity	0.032	0.017	10	115	1.84	8.8E-02
GO:0016568	chromatin modification	0.047	0.031	15	197	1.55	1.0E-01

Table S7. ***S. pombe*** **strains used in this study.**

Strain	**Genotype**	**Reference**
Hu0303	*h–, 972*	
Hu0029	*h–, ade6-M210 leu1-32 ura4-D18*	
Hu2549 (=A8894)	*h+ ars1 :prad15 cre-EBD-LEU2, H3.2-lox-HA-hygR-Lox-T7, cdc25-22 (ts), ade6-210, leu1-32*	This study
Hu2653	*h–, leu1-32, ura4-DS/E, ade6-M216, pInv1-H3-HA*	Sadeghi et al 2014
Hu1654 (=YSLS252)	*h–, set9::kanMX*	SL Sanders
Hu2095 (=FYA259)	*h–, spt16-18:kanMX6, leu1-32*	RC Allshire
Hu2640	*h+, ade6-M216, leu1-32, ura4-DS/E, otrR(Sph1)::ura4, htb1-K119R::kanMX6*	SI Grewal
167	*h+, htb1+:kanMX6, spt16-myc::hphMX6*	JC Tanny

Table S8. Sequencing statistics for ChIP-exo samples after Bowtie2 alignment to ASM294v2 assembly of *S. pombe* genome

Sample (time_epitope_replicate)	**total number of reads** ($\times 10^6$)	**aligning exactly 1 time** ($\times 10^6$)	**aligned >1 times** ($\times 10^6$)	**overall alignment rate**	**coverage** (# reads/nucleosome (150bp))
0h_HA_1	17.63	15.56	1.02	94.1%	165.8
2h_HA_1	16.89	14.98	0.94	94.3%	159.2
0h_T7_1	0.36	0.31	0.02	91.4%	3.3
2h_T7_1	13.64	12.03	0.74	93.6%	127.7
0h_HA_2	16.33	14.33	0.95	93.6%	152.8
2h_HA_2	17.78	15.69	1.04	94.1%	167.3
0h_T7_2	3.70	2.99	0.21	86.6%	32.0
2h_T7_2	14.99	13.10	0.70	92.1%	138.0