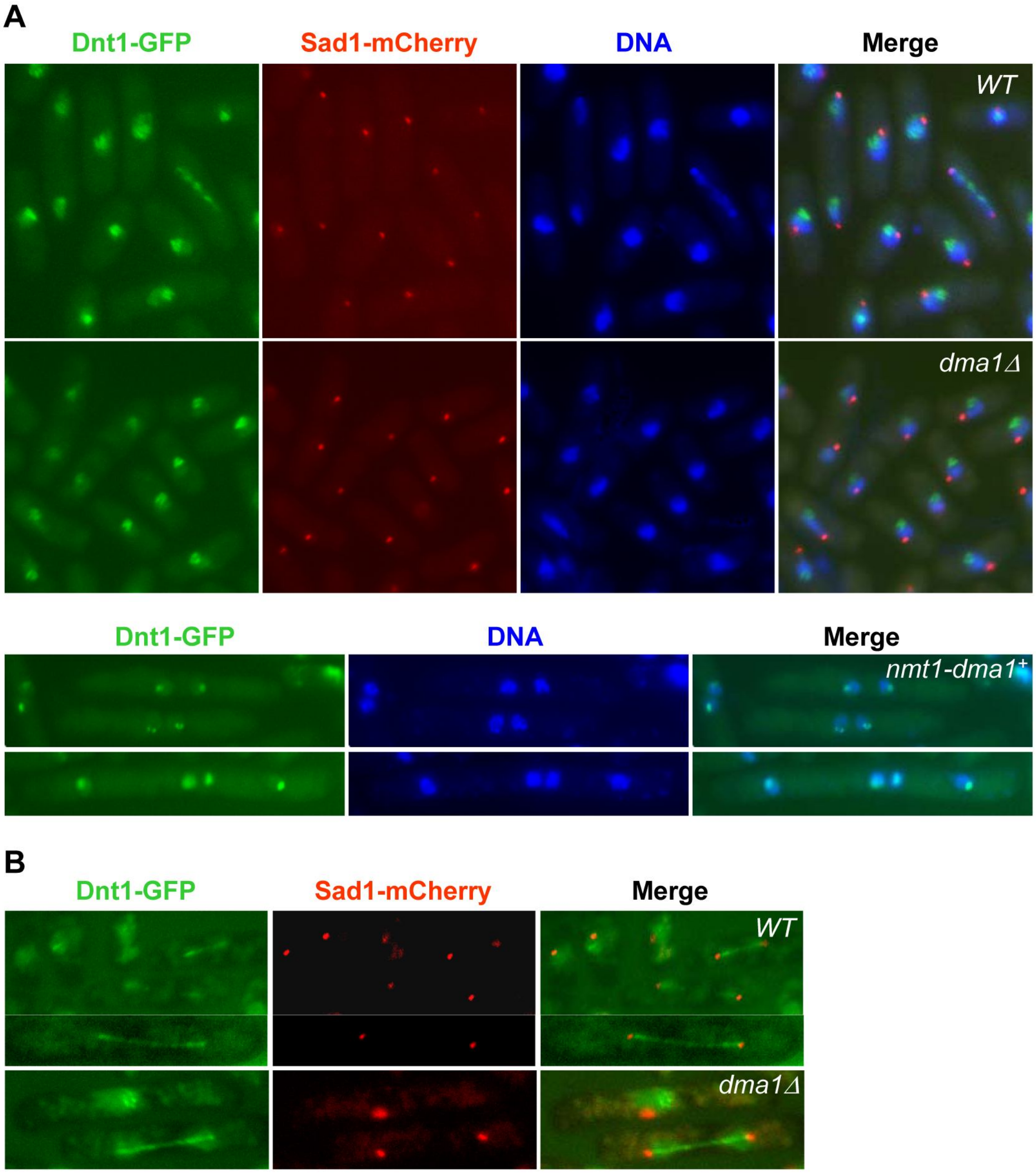
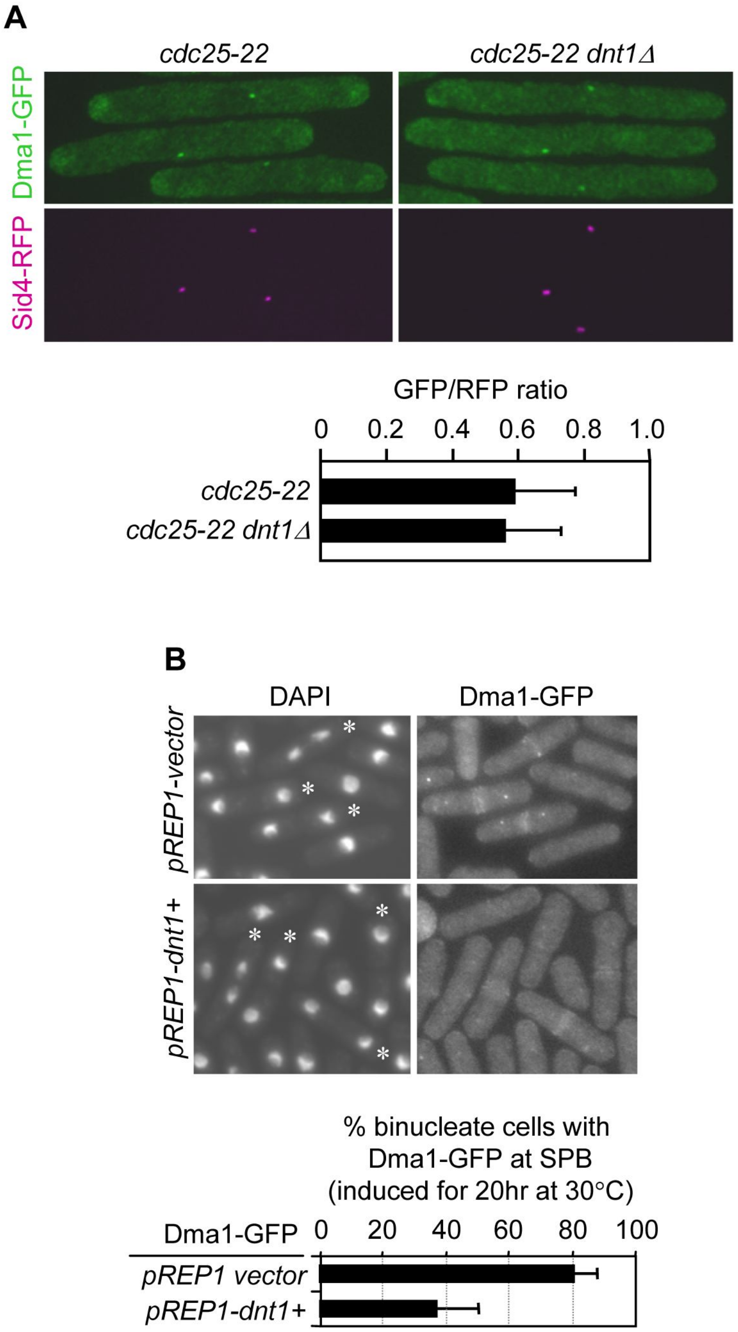
Supplementary figure legends:



Supplementary figure S1. Absence or overexpression of Dma1 does not impair localization of Dnt1 in the nucleolus or on anaphase spindle.

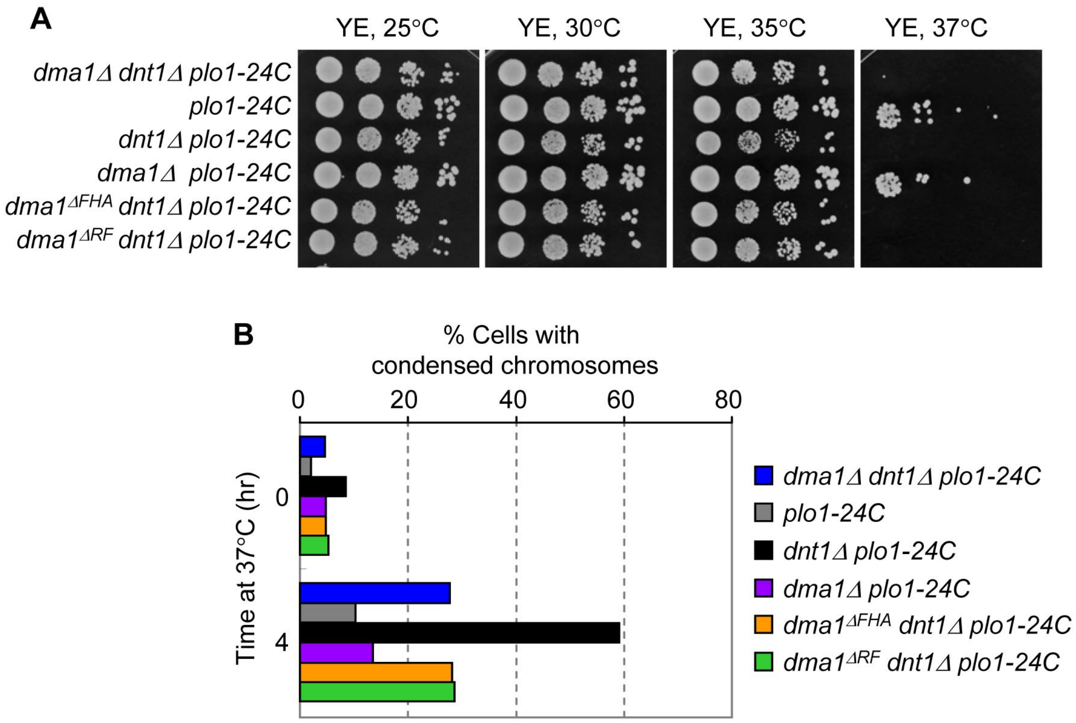
(A) Wild type and *dma1Δ* cells carrying Dnt1-GFP and Sad1-mCherry were grown in liquid YE at 30°C, then collected, fixed with methanol at room temperature, and DAPI stained. For *nmt1-dma1*$^{+}$ cells carrying Dnt1-GFP, overexpression of Dma1 was induced in EMM liquid media without thiamine for 20hr at 30°C. Cells were fixed and stained with DAPI. (B) Examples of anaphase cells with spindles.



Supplementary figure S2. Localization of Dma1-GFP at SPB during G2 is not affected by *dnt1Δ*, and overexpression of *dnt1*$^+$ can drive Dma1-GFP off SPBs in binucleate cells.

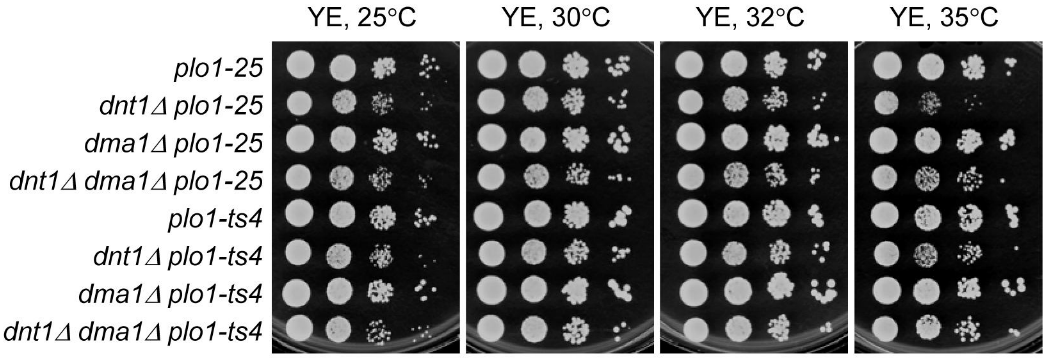
(A) During G2, Dma1-GFP intensity at SPBs is not affected by the absence of *dnt1*$^+$. *cdc25-22* cells were arrested at G2 by incubation at 36°C for 4hr, and then Dma1-GFP and Sid4-RFP intensities were quantitated in *dnt1*$^+$ and *dnt1Δ* cells. Final values are expressed as GFP/RFP ratios. Error bars represent the SEM. 20 cells were measured for each strain and averaged for statistical analysis, $p>0.05$.

(B) Wild type cells carrying Dma1-GFP were transformed with expression plasmids pREP1 (vector) or pREP1-*dnt1*$^+$ and induced for overexpression of *dnt1*$^+$ in EMM liquid media without thiamine for 20hr at 30°C. Cells were collected, fixed and DAPI stained. (Upper) Representative cells are shown. Asterisks indicate binucleate cells. (Lower) Binucleate cells with Dma1-GFP signals at SPBs were scored ($n>150$). Error bars represent the SD from 3 independent experiments.



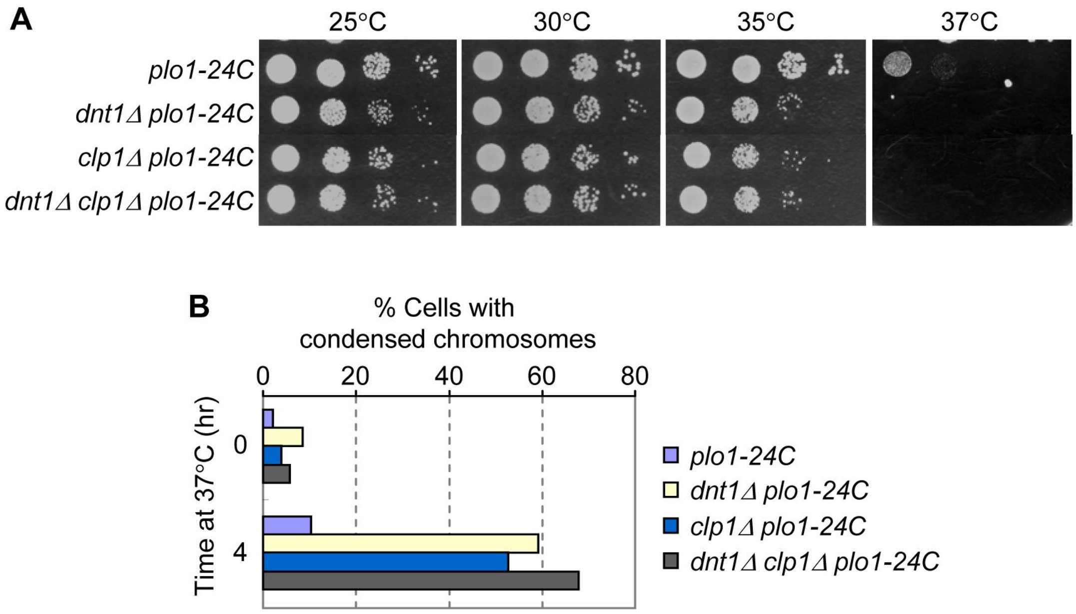
Supplementary figure S3. Negative genetic interaction between *plo1-24C* and *dnt1Δ* can be rescued by disruption of FHA or RF domains in Dma1.

(A) Serial dilutions (10 fold) of the indicated single, double or triple mutant strains were spotted on YE and incubated at the indicated temperatures. (B) Liquid cultures of the indicated strains were grown at 25°C then shifted to 37°C, and the percentages of cells with condensed chromosomes/metaphase arrest were quantified after being fixed and stained with DAPI (n=200).



Supplementary figure S4. The sensitivity of other alleles of *plo1* mutants to deletion of *dnt1*$^+$ can also be alleviated by disruption of Dma1 function.

(A and B) Serial dilutions (10 fold) of the indicated single, double or triple mutant strains were spotted on YE and incubated at the indicated temperatures. All *plo1* mutant alleles show synthetic interactions with *dnt1Δ*.



Supplementary figure S5. Negative genetic interaction between *plo1-24C* and *dnt1Δ* is independent of Clp1.

(A) Growth of serial dilutions (10 fold) of the indicated strains were grown on YE at the indicated temperatures. (B) Quantification of condensed chromosomes/metaphase arrest in liquid cultures at 37°C were performed as in supplementary figure S3B.

Supplementary tables:

Table S1. Yeast strains used in this study.

Strain	Genotype
YDM105	h^- *leu1-32 ura4-D18 ade6-210*
YDM106	h^+ *leu1-32 ura4-D18 ade6-210*
YDM1758	h^- *dma1-3HA-TAP::kanR leu1-32 ura4-D18 ade6-210*
YDM1863	h^+ *dma1-3HA-TAP::kanR mts3-1 leu1-32 ura4-D18*
YDM2460	h^+ *dnt1-3HA-TAP::kanR leu1-32 ura4-D18 ade6-210*
YDM2258	h^- *dma1-3HA-TAP::kanR nda3-KM311 leu1-32 ura4-D18 ade6-21x*
YDM3262	$h^?$ *dma1-3HA-TAP::kanR nda3-KM311 dnt1Δ::ura4*$^+$ *leu1-32 ura4-D18*
YDM3263	$h^?$ *dma1-3HA-TAP::kanR mts3-1 dnt1Δ::ura4*$^+$ *leu1-32 ura4-D18*
YDM919	h^- *dma1-GFP::kanR leu1-32 ura4-D18 ade6-21x*
YDM2420	h^- *dnt1-13myc::kanR leu1-32 ade6-210 ura4-D18*
YDM2421	h^- *dma1-GFP::kanR dnt1-13myc::kanR leu1-32 ade6-21x ura4-D18*
YDM2558	$h^?$ *cdc10-129 dma1-GFP::kanR dnt1-13myc::kanR*
YDM2562	$h^?$ *mts3-1 dma1-GFP::kanR dnt1-13myc::kanR*
YDM2557	$h^?$ *nda3-KM311 dma1-GFP::kanR dnt1-13myc::kanR*
YDM3274	$h^?$ *mts3-1 dma1Δ::kanR dnt1-13myc-kanR leu1-32 ura4-D18*
JY2703	h^+ *nda3-KM311 dnt1-GFP::kanR sad1-mCherry::natMx6 leu1-32 ura4-D18*
JY2734	h^- *mts3-1 dnt1-GFP::kanR sad1-mCherry::natMx6 ura4-D18*
YDM3041	h^- *leu1-32::nmt1-dma1::leu1*$^+$ *dnt1Δ::ura4*$^+$ *ura4-D18 ade6-216*
JY384	h^+ *leu1-32::nmt1-dma1::leu1*$^+$ *dnt1Δ::ura4*$^+$ *cut2-GFP::LEU2*
JY392	h^+ *leu1-32::nmt1-dma1::leu1*$^+$ *dnt1Δ::kanR cdc13-GFP::LEU2 ura4-D18*
YDM1035	h^- *leu1-32::nmt1-dma1::leu1*$^+$ *ade6-216 ura4-D18*
YDM3124	h^- *leu1-32::nmt1-dma1::leu1*$^+$ *dnt1Δ::ura4*$^+$ *mad2Δ::ura4*$^+$ *ura4-D18*
JY368	$h^?$ *leu1-32::nmt1-dma1::leu1*$^+$ *dnt1Δ::kanR bub1Δ::ura4*$^+$
JY699	h^+ *leu1-32::nmt1-dma1*$^{\Delta RF}$*::leu1*$^+$ *ura4-D18 ade6-210*
JY700	h^+ *leu1-32::nmt1-dma1*$^{C210;H212A}$*::leu1*$^+$ *ura4-D18 ade6-210*
JY744	h^- *leu1-32::nmt1-dma1*$^{\Delta RF}$*::leu1*$^+$ *dnt1Δ::ura4*$^+$ *ura4-D18 ade6-210*
JY747	h^+ *leu1-32::nmt1-dma1*$^{C210;H212A}$*::leu1*$^+$ *dnt1Δ::ura4*$^+$ *ura4-D18 ade6-210*
JY2032	h^+ *leu1-32::nmt1-dma1*$^{\Delta FHA}$*::leu1*$^+$ *dnt1Δ::kanR ura4-D18 ade6-210*
JY2034	h^+ *leu1-32::nmt1-dma1*^{R64A}*::leu1*$^+$ *dnt1Δ::kanR ura4-D18 ade6-210*
JY2036	h^+ *leu1-32::nmt1-dma1*^{H88A}*::leu1*$^+$ *dnt1Δ::kanR ura4-D18 ade6-210*
YDM1159	h^- *dma1Δ::ura4 ura4-D18 leu1-32 ade6-21x*
YDM2379	h^- *dnt1Δ::ura4*$^+$ *leu1-32 ura4-D18 ade6-210*
YDM2812	h^+ *dnt1Δ::kanR leu1-32 ura4-D18 ade6-210*
YDM2440	h^+ *dnt1Δ::ura4*$^+$ *dma1Δ::ura4+ leu1-32 ura4-D18 ade6-216*
YDM1010	h^- *alp4-1891 leu1-32*
JY576	h^- *dnt1Δ::kanR alp4-1891 leu1-32 ura4*
JY621	$h^?$ *dma1Δ::ura4*$^+$ *dnt1Δ::kanR alp4-1891 leu1-32 ura4*
YDM1009	h^- *alp6-719 leu1-32*
JY575	h^- *dnt1Δ::kanR alp6-719 leu1-32 ura4*
JY620	$h^?$ *dma1Δ::ura4+ dnt1Δ::kanR alp6-719 leu1-32 ura4*
JY423	h^- *sad1-1 leu1*
JY504	h^- *dnt1Δ::ura4*$^+$ *sad1-1 leu1*
JY727	$h^?$ *dma1Δ::kanR sad1-1 leu1-32 ura4-D18*
JY698	$h^?$ *dma1Δ::kanR dnt1Δ::ura4*$^+$ *sad1-1 leu1-32 ura4-D18*
YDM113	h^+ *plo1-24C leu1-32 ura4-D18 ade6-21x*
YDM3266	h^+ *dnt1Δ::kanR plo1-24C leu1-32 ura4-D18 ade6-21x*

YDM3289	*h*$^{?}$ *dma1Δ::ura4*$^{+}$ *dnt1Δ::kanR plo1-24C*
JY2632	*h*$^{+}$ *dma1*$^{\Delta FHA}$ *ura4-D18 leu1-32 ade6-216*
JY2774	*h*$^{-}$ *dma1*$^{\Delta FHA}$ *dnt1Δ::kanR plo1-24C leu1-32 ura4-D18 ade6-21x*
JY2633	*h*$^{+}$ *dma1*$^{\Delta RF}$ *ura4-D18 leu1-32 ade6-216*
JY2775	*h*$^{+}$ *dma1*$^{\Delta RF}$ *dnt1Δ::kanR plo1-24C leu1-32 ura4-D18 ade6-21x*
YDM3292	*h*$^{?}$ *mad2Δ::ura4*$^{+}$ *plo1-24C*
YDM3333	*h*$^{?}$ *dnt1Δ::kanR mad2Δ::ura4*$^{+}$ *plo1-24C leu1-32 ura4-D18*
YDM412	*h*$^{-}$ *plo1-25 leu1-32*
YDM1411	*h*$^{+}$ *plo1-25 leu1-32 ade6-21x*
YDM3267	*h*$^{-}$ *dnt1Δ::kanR plo1-25 leu1-32*
YDM3290	*h*$^{?}$ *dma1Δ::ura4*$^{+}$ *dnt1Δ::kanR plo1-25*
YDM3303	*h*$^{?}$ *dnt1Δ::ura4*$^{+}$ *plo1-25 mad2Δ::ura4*$^{+}$ *leu1-32 ura4-D18*
YDM1532	*h*$^{+}$ *plo1-ts4::ura4*$^{+}$ *ura4-D18 ade6-21x leu1-32*
YDM3268	*h*$^{?}$ *dnt1Δ::kanR plo1-ts4::ura4*$^{+}$ *ura4-D18 ade6-21x leu1-32*
YDM3291	*h*$^{?}$ *dma1Δ::ura4*$^{+}$ *dnt1Δ::kanR plo1-ts4::ura4*$^{+}$
YDM2825	*h*$^{-}$ *plo1-24C GFP-atb2*$^{+}$*::kanR sad1-mCherry::natMX6 leu1 ura4*
YDM2886	*h*$^{-}$ *dnt1Δ::kanR plo1-24C GFP-atb2*$^{+}$*::kanR sad1-mCherry::natMX6 leu1 ura4*
YDM2785	*h*$^{-}$ *dma1Δ ::ura4+ dnt1Δ::kanR plo1-24C GFP-atb2*$^{+}$*::kanR sad1-mCherry::natMX6 leu1 ura4*
YDM919	*h*$^{-}$ *dma1-GFP::kanR leu1-32 ura4-D18 ade6-21x*
YDM3399	*h*$^{?}$ *dnt1Δ::ura4*$^{+}$ *dma1-GFP::kanR ura4-D18 ade6-21x leu1-32*
YDM918	*h*$^{-}$ *dma1-13myc::kan leu1-32 ura4-D18 ade6-21x*
YDM 3406	*h*$^{?}$ *dnt1Δ::kanR dma1-13myc::kanR ura4-D18 leu1-32*
JY2659	*h*$^{+}$ *dnt1-GFP::kanR sad1-mCherry::natMX6 leu1-32 ura4-D18 ade6-210*
JY2636	*h*$^{?}$ *dma1Δ::ura4*$^{+}$ *dnt1-GFP::kanR sad1-mCherry::natMX6 leu1-32 ura4-D18 ade6-21x*
JY2639	*h*$^{?}$ *leu1-32::nmt1-dma1::leu1*$^{+}$ *dnt1-GFP::kanR ura4-D18 ade6-21x*
KGY8415	*h*$^{-}$ *sid4-HBH::kanR ade6-M210 leu1-32 ura4-D18*
KGY10621	*h*$^{-}$ *dnt1Δ::ura4*$^{+}$ *sid4-HBH::kanR ade6-M21x leu1-32 ura4-D18*
KGY11605	*h*$^{-}$ *dma1-GFP::kanR sid4-RFP::kanR ade6-M210 leu1-32 ura4-D18*
KGY11874	*h*$^{+}$ *dnt1Δ::ura4*$^{+}$ *dma1-GFP::kanR sid4-RFP::kanR ade6-M21x leu1-32 ura4-D18*
KGY11657	*h*$^{-}$ *cdc25-22 dma1-GFP;KanR sid4-RFP:KanR ade6-M210 leu1-32 ura4-D18*
KGY13809	*h*$^{+}$ *cdc25-22 dma1-GFP:kanR sid4-RFP:kanR dnt1::ura4+ ade6-M21x leu1-32 ura4-d18*

Table S2. List of proteins identified by mass spectrometry co-purifying with Dma1-3HA-TAP from mts3-1 arrested cells [Yeast strain used: YDM1972 *h- mts3-1 dma1-3HA-TAP::kanR sid4-GFP::kanR ura4-D18 leu1-32 ade6-21X*]. [1st purification]

Protein Name/Locus	# Unique peptides	Sequence Coverage	Descriptive Name
DMA1, SPAC17G8.10C	58	85.0%	: SPINDLE ASSEMBLY CHECKPOINT COMPONENT; PROTEIN TO PREVENT SEPTUM FORMATION AND PREMATURE EXIT FROM MITOSIS IF SPINDLE FUNCTION IS COMPROMISED:
DNT1, SPBC25D12.02C	47	57.4%	: HYPOTHETICAL PROTEIN; SEQUENCE ORPHAN; SERINE- RICH:
HSP70, SPCC1739.13	28	43.4%	: HEAT SHOCK PROTEIN 70 FAMILY:
GPD1, SPBC32F12.11, TDH1	13	38.4%	: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE:
UBI1, SPAC11G7.04	3	34.4%	: UBIQUITIN FAMILY PROTEIN:
UEP1, SPAC1805.12C, UBI2	3	34.4%	: UBIQUITIN FUSION PROTEIN:
ADH1, SPCC13B11.01, ADH	9	30.9%	: ALCOHOL DEHYDROGENASE I; REDUCING ACETALDEHYDE TO ETHANOL, REGENERATING NAD+:
SKS2, SPBC1709.05, HSC1	10	28.5%	: HEAT SHOCK PROTEIN 70 FAMILY:
SPBC27B12.12C	14	25.8%	: MIT FAMILY METAL ION TRANSPORTER; PUTATIVE INORGANIC CATION TRANSPORTER; SIMILAR TO S. CEREVISIAE ALR1:
EF1-B, SPBC839.15C	14	25.7%	: ELONGATION FACTOR 1 ALPHA-B:
TEF1-E, SPCC794.09C, EF1A-E	14	25.7%	: ELONGATION FACTOR 1-ALPHA-E:
EF1A-B, SPAC23A1.10, TEF1-B, TEF1-D, EF1A-B,	14	25.7%	: ELONGATION FACTOR 1 ALPHA-B/D:
ACT1, SPBC32H8.12C, CPS8, PI012	6	25.6%	: ACTIN:
ANC1, SPBC530.10C	6	23.3%	: ADENINE NUCLEOTIDE CARRIER; MITOCHONDRIAL CARRIER (MCF) FAMILY:
SPAC589.10C	2	22.7%	: UBIQUITIN-LIKE PROTEIN; IDENTICAL TO SPAC6G10.11C.:
UBI4, SPBC337.08C	2	8.9%	: UBIQUITIN FAMILY PROTEIN:
UBI3, SPAC6G10.11C	2	22.7%	: UBIQUITIN FUSION PROTEIN:
SMD3, SPBC19C2.14	2	21.6%	: SMALL NUCLEAR RIBONUCLEOPROTEIN; PUTATIVE PRE- MRNA SPLICING FACTOR; SIMILAR TO S. CEREVISIAE SMD3:
BIP, SPAC22A12.15C	9	20.2%	: 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG; HSP70 FAMILY:
SPBC15D4.08C	2	19.6%	: VERY HYPOTHETICAL PROTEIN:
FBA1, SPBC19C2.07	4	19.3%	: FRUCTOSE-BISPHOSPHATE ALDOLASE; SIMILAR TO S. CEREVISIAE FBA1:
SPAC13G7.02C	12	18.6%	: HEAT SHOCK PROTEIN 70 FAMILY:
RFC4, SPAC1687.03C	2	18.4%	: REPLICATION FACTOR C (ACTIVATOR 1) SUBUNIT; ACTIVATOR OF DNA POLYMERASES:
SPAC2G11.15C, SPAC521.01C	2	17.2%	: PUTATIVE METHYLTRANSFERASE:
SPBC1703.13C	2	16.4%	: MC PHOSPHATE TRANSPORTER:
SPBC13E7.01, SPBC15D4.16	10	15.5%	: CONSERVED PROTEIN; SIMILAR TO S. CEREVISIAE YGR278W CONSERVED PROTEIN; SIMILAR TO S. CEREVISIAE YGR278W:
SPAC24H6.09	6	14.6%	: PUTATIVE GUANINE NUCLEOTIDE EXCHANGE FACTOR; COILED-COIL REGIONS; PREDICTED COILED-COIL REGION:
GPD3, SPBC354.12	7	14.3%	: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE:
HOB3, SPBC725.09C	2	14.0%	: INVOLVED IN CELL CYCLE REGULATION; CYTOKINESIS AND CYTOSKELETAL ORGANIZATION:
DBP2, SPBP8B7.16C	5	13.6%	: DEAD/DEAH BOX HELICASE; PUTATIVE

			PRE-MRNA SPLICING FACTOR; HUMAN P68-LIKE PROTEIN; SIMILAR TO S. CEREVISIAE DPB2; CONTAINS LARGE 3' INTRON LIKE S. CEREVISIAE DBP2:
SPAC821.03C	3	13.0%	: HYPOTHETICAL SERINE-RICH PROTEIN; SEQUENCE ORPHAN:
SPBC660.06	2	12.8%	: HYPOTHETICAL GLYCINE RICH PROTEIN; POMBE SPECIFIC DOMAIN PFAM-B_15930:
SPAC19G12.05	2	12.7%	: MC TRICARBOXYLATE TRANSPORTER:
SPCC970.03	3	12.3%	: PUTATIVE NADH-CYTOCHROME B5 REDUCTASE; SIMILAR TO S. CEREVISIAE CBR1:
SPCC1393.08	2	11.5%	: TRANSCRIPTION FACTOR GATA-TYPE:
SUM3, SPCC1795.11, DED1, SLH3, MOC2	7	11.3%	: DEAD/DEAH BOX HELICASE; ATP-DEPENDENT RNA HELICASE; POSITIVELY INVOLVED IN THE INITIATION OF PROTEIN SYNTHESIS; ESSENTIAL; SUPPRESSOR OF UNCONTROLLED MITOSIS; SUBCELLULAR LOCALIZATION OF GFP FUSION- CYTOPLASM; INTERACTS WITH CHK1; INTERACTS WITH CDC2: O
SPCC1672.05C	2	11.2%	: TYROSYL-TRNA SYNTHETASE CYTOPLASMIC:
SPAP27G11.02	2	11.2%	: HYPOTHETICAL PROTEIN; SIMILAR TO S. CEREVISIAE YKL133C (LOW):
CSX1, SPAC17A2.09C	3	11.1%	: RNA-BINDING PROTEIN; POST-TRANSCRIPTIONAL REGULATOR:
GIT7, SPBC36.12C, SPBC713.01C	2	11.1%	: GLUCOSE INSENSITIVE TRANSCRIPTION:
PYK1, SPAC4H3.10C	5	11.0%	: PYRUVATE KINASE (EC 2.7.1.40):
SPCC24B10.10C	2	10.7%	: PUTATIVE INTRA-MITOCHONDRIAL SORTING PROTEIN, AAA FAMILY OF ATPASE; SIMILAR TO S. CEREVISIAE MPS1:
CWF4, SPBC31F10.11C, SYF3	4	9.8%	: PUTATIVE PRE-MRNA SPLICING FACTOR; 40S SNRNP- CONTAINING COMPLEX; SIMILAR TO S. CEREVISIAE CLF1:
SPBC646.10C	4	9.7%	: PUTATIVE U3 SNORNP COMPONENT; PUTATIVE COMPONENT OF BOX C/D SNORNPS; INVOLVED IN 2'-O-METHYLATION OF RIBOSOMAL RNAS; SIMILAR TO S. CEREVISIAE SIK1:
SPAC323.04	2	9.7%	: PUTATIVE ABC METAL TRANSPORT ATP-BINDING PROTEIN:
LSD1, SPAC4A8.11C, FAS2	11	9.5%	: FATTY ACID SYNTHASE, SUBUNIT ALPHA:
SPAC12G12.06C	2	9.4%	: PUTATIVE RNA 3'-TERMINAL PHOSPHATE CYCLASE:
ALG11, SPCC330.08, GMD3	2	9.3%	: GLYCOSYL TRANSFERASE; INVOLVED IN N-LINKED OLIGOSACCHADRIDE SYNTHESIS:
SSP1, SPAC664.11	5	9.2%	: MITOCHONDRIAL CHAPERONIN; HEAT SHOCK 70 KD PROTEIN; INVOLVED IN MITOCHONDRIAL PROTEIN IMPORT:
SPO4, SPBC21C3.18	2	9.1%	: PROTEIN KINASE; INVOLVED IN MEIOTIC SPINDLE FORMATION:
ADE2, SPAC144.03, MIN10, MIN3	2	9.0%	: ADENYLOSUCCINATE SYNTHETASE:
SPBC19G7.10C	4	8.9%	: TOPOISOMERASE ASSOCIATED YEAST PAT1 HOMOLOG:
FIB, SPBC2D10.10C	3	8.9%	: FIBRILLARIN; PUTATIVE U3 SNORNP COMPONENT; REQUIRED FOR 35S RRNA PROCESSING AND METHYLATION; SIMILAR S. CEREVISIAE NOP1:
SPBC1703.12	2	8.7%	: UBIQUITIN CARBOXYL-TERMINAL HYDROLASE; SIMILAR TO S. CEREVISIAE UBP9:
SPAC637.04	3	8.4%	: HYPOTHETICAL PROTEIN; CONTAINS PFAM-B_33932; CONTAINS PFAM-B_33935; SIMILAR TO S. CEREVISIAE YGR198W NULL LETHAL; CONTAINS 3 TPR DOMAINS:
ARG5, SPBC56F2.09C	2	8.2%	: ARGININE-SPECIFIC CARBAMOYL PHOSPHATE SYNTHASE; SIMILAR TO S. CEREVISIAE CPA1:
KMS1, SPAC3A11.05C	2	8.1%	: MEIOSIS SPECIFIC PROTEIN; MUTANT DISPLAYS DECREASED MEIOTIC RECOMBINATION; PUTATIVE

			SPINDLE POLE BODY COMPONENT:
LEU1, SPBC1A4.02C, SPBC1E8.07C	2	8.1%	: 3-ISOPROPYLMALATE DEHYDROGENASE; SIMILAR TO S. CEREVISIAE LEU2:
SPAC139.02C	3	8.1%	: MC OXALOACETATE TRANSPORTER:
ILV1, SPBP35G2.07	4	7.8%	: ACETOLACTATE SYNTHASE (ACETOHYDROXYACID SYNTHASE); FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS PATHWAY; SIMILAR TO S. CEREVISIAE ILV2:
PRP19, SPAC29A4.08C, CWF8	4	7.8%	: PUTATIVE PRE-MRNA SPLICING FACTOR; WD REPEAT PROTEIN; COMPLEXED WITH CDC5; SIMILAR TO S. CEREVISIAE PRP19:
SPAC821.05	2	7.8%	: PUTATIVE EIF3 P40 EIF/SIGNALOSOME COMPONENT; MOV DOMAIN; NO APPARENT S. CEREVISIAE ORTHOLOG:
ECM2, SPCC550.02C, CWF5	2	7.6%	: PUTATIVE PRE-MRNA SPLICING FACTOR; 40S SNRNP- CONTAINING COMPLEX; RNA-BINDING PROTEIN; SIMILAR TO S. CEREVISIAE ECM2:
GAR2, SPAC140.02	3	7.4%	: GAR2 PROTEIN:
SPAC664.03	2	7.4%	: PUTATIVE DNA-DIRECTED RNA POLYMERASE II REGULATOR:
SPAC2E1P3.04	2	7.2%	: PEROXISOMAL COPPER AMINE OXIDASE; NO APPARENT S. CEREVISIAE ORTHOLOG:
HSP60, SPAC12G12.04, MCP60	2	7.2%	: PUATIVE MITOCHONDRIAL CHAPERONIN 60; PUTATIVE SUCCINATE DEHYDROGENASE ASSEMBLY; HEAT SHOCK PROTEIN 60:
SPBC16E9.11C	3	7.1%	: UBIQUITIN--PROTEIN LIGASE:
SPBC11B10.01, PI010, SPBC32H8.14	2	7.0%	: GLYCOSYL TRANSFERASE:
SPAC15A10.06	2	6.7%	: CPA1 SODIUM ION/PROTON ANTIPORTER:
ITR1, SPAC4F8.15, SPAC7D4.01	2	6.6%	: MFS MYO-INOSITOL TRANSPORTER:
SPAC13G7.05	2	6.5%	: ACYL-COA-STEROL ACYLTRANSFERASE; SIMILAR TO S. CEREVISIAE ARE2:
CLR6, SPBC36.05C	2	6.4%	: HISTONE DEACETYLASE; RPD3-LIKE (CLASS 1); SIMILAR TO S. CEREVISIAE RPD3: O59702;
SPBP22H7.02C, PI029	2	6.2%	: RNA-BINDING PROTEIN; 5 RRM RNA RECOGNITION MOTIFS:
SPAC13G7.04C	2	6.2%	: HYPOTHETICAL PROTEIN; SIMILAR TO S. CEREVISIAE TOS7; CONTAINS PFAM-B_7111; CONTAINS 3 PREDICTED TRANSMEMBRANE HELICES; PREDICTED N-TERMINAL SIGNAL SEQUENCE; POSSIBLY FUNGAL SPECIFIC:
SNU66, SPAC167.03C	2	6.2%	: PUTATIVE PRE-MRNA SPLICING FACTOR; PUTATIVE U4/U6.U5 SNRNP COMPONENT; PREDICTED COILED-COIL; SIMILAR TO S. CEREVISIAE SNU66:
SPCC1682.03C	3	6.2%	: HYPOTHETICAL PROTEIN; SEQUENCE ORPHAN:
SPBC25H2.11C	2	6.1%	: BROMODOMAIN PROTEIN; PUTATIVE TRANSCRIPTIONAL ACTIVATOR; PUTATIVE SAGA COMPLEX ; SIMILAR TO S. CEREVISIAE SPT7:
DIS1, SPCC736.14	2	6.1%	: MICROTUBULE AND SPINDLE POLE BODY ASSOCIATED PROTEIN P93DIS1:
SPBC106.14C	3	6.1%	: POSSIBLY REQUIRED FOR ACTIN CYTOSKELETAL ORGANISATION; SIMILAR TO S. CEREVISIAE SDA1:
SPAC25B8.11	2	6.1%	: PUTATIVE TRANSCRIPTIONAL REGULATOR; ZINC FINGER PROTEIN; SIMILAR TO S. CEREVISIAE DAL81 AN ACTIVATOR FOR ALLANTOIN, 4-AMINOBUTYRIC ACID (GABA), AND UREA CATABOLIC GENES; FUNGAL BINUCLEAR CLUSTER DOMAIN:
BPB1, SPCC962.06C, SF1	2	6.1%	: ZINC FINGER PROTEIN; ZF-CCHC TYPE (ZINC KNUCKLE); PUTATIVE TRANSCRIPTION OR SPLICING FACTOR:
SPBC18E5.02C, SPBC29A3.20C	2	6.1%	: PUTATIVE SERINE PALMITOYLTRANSFERASE PUTATIVE SERINE PALMITOYLTRANSFERASE SUBUNIT:
SWI4, SPAC8F11.03	2	6.0%	: MATING-TYPE SWITCHING PROTEIN; SIMILAR TO S. CEREVISIAE MSH3:

SPBC20F10.05	3	6.0%	: HYPOTHETICAL PROTEIN; SEQUENCE ORPHAN:
POB1, SPBC1289.04C	2	6.0%	: REQUIRED FOR CELL POLARITY; REQUIRED FOR ELONGATION; SIMILAR TO S. CEREVISIAE BOI1 AND BOI2; ESSENTIAL; CONTAINS PH DOMAIN; CONTAINS SAM DOMAIN:
SPBC691.02C, PI034	2	6.0%	: PUTATIVE ENDOPLASMIC RETICULUM TO GOLGI TRANSPORT PROTEIN; SIMILAR TO S. CEREVISIAE TIP20:
HMG1, SPCC162.09C	3	5.9%	:3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE: O74425;Q10283;
SPAC4G9.05	2	5.9%	: RNA-BINDING PROTEIN; PUMILIO FAMILY: Q10238;
SPCC757.12	2	5.8%	: PUTATIVE ALPHA-AMYLASE; NO APPARENT S. CEREVISIAE ORTHOLOG:
URA1, SPAC22G7.06C	7	5.7%	: CONTAINS GLUTAMINE-DEPENDENT CARBAMOYL- PHOSPHATESYNTHASE; CONTAINS ASPARTATE CARBAMOYL TRANSFERASE; SIMILAR TO S. CEREVISIAE URA2:
MTS4, SPBP19A11.03C	3	5.7%	: 26S PROTEASOME REGULATORY SUBUNIT:
SPCC4B3.03C	2	5.7%	: POSSIBLY REQUIRED FOR NORMAL MITOCHONDRIAL STRUCTURE; SIMILAR TO S. CEREVISIAE AMI3:
SPCC1223.13	2	5.6%	: HYPOTHETICAL PROTEIN; SEQUENCE ORPHAN:
SPBC16G5.15C	2	5.6%	: FORK HEAD NUCLEAR SIGNALLING DOMAIN PROTEIN:
SPAC630.05	2	5.5%	: TBC DOMAIN PROTEIN; PUTATIVE GTPASE ACTIVATING PROTEIN OF RAB-LIKE GTPASE:
PMA1, SPAC1071.10C	2	5.4%	: P-TYPE PROTON ATPASE:
LEU2, SPAC9E9.03	2	5.4%	: PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE:
SPCC417.08	4	5.3%	: PUTATIVE ELONGATION FACTOR 3:
EFT2-1, SPAC513.01C, SPAPYUK71.04C	3	5.3%	: ELONGATION FACTOR 2:
EFT2-2, SPCP31B10.07	3	5.3%	: ELONGATION FACTOR 2:
SPAC29A4.20	2	5.3%	: PUTATIVE SUBUNIT OF ELONGATOR/RNAPII HOLOENZYME; PUTATIVE HISTONE ACETYLTRANSFERASE; SIMILAR TO S. CEREVISIAE ELP3:
SPAC1F8.07C	2	5.2%	: PUTATIVE PYRUVATE DECARBOXYLASE:
SPAC4A8.08C	2	5.1%	: PUTATIVE VALYL-TRNA SYNTHETASE, MITOCHONDRIAL:
SPBC12C2.08	2	5.1%	: DYNAMIN FAMILY; CONTAINS DYNAMIN GTPASE EFFECTOR DOMAIN; MORPHOLOGY AND CORTICAL LOCALIZATION OF MITOCHONDRIA; SIMILAR TO S. CEREVISIAE DNM1:
SPBC2D10.17	2	4.8%	: ZINC FINGER PROTEIN; ZF-C2H2 TYPE; PREDICTED COILED-COIL REGION:
SPBC28F2.08C	2	4.8%	: SEL 1 REPEAT PROTEIN; LOW SIMILAR TO S. CEREVISIAE HRD3; PREDICTED N-TERMINAL SIGNAL SEQUENCE; CONTAINS 1 PREDICTED TRANSMEMBRANE HELIX; NO APPARENT S. CEREVISIAE ORTHOLOG:
PFK1, SPBC16H5.02	3	4.7%	: 6-PHOSPHOFRUCTOKINASE BETA SUBUNIT; SIMILAR TO S. CEREVISIAE PFK2:
APC5, SPAC959.09C, SPAP32A8.01C	2	4.6%	: PUTATIVE ANAPHASE-PROMOTING COMPLEX (APC); REQUIRED FOR CYCLIN DEGRADATION; REQUIRED FOR METAPHASE- ANAPHASE TRANSITION:
SPBC31F10.13C	2	4.4%	: WD REPEAT PROTEIN; PUTATIVE HIRA PROTEIN; HISTONE TRANSCRIPTION REGULATOR:
CDC5, SPAC644.12	2	4.4%	: CELL DIVISION CONTROL PROTEIN; TRANSCRIPTIONAL REGULATOR; MYB FAMILY DNA-BINDING PROTEIN; ESSENTIAL; REQUIRED FOR PRE-MRNA SPLICING; REQUIRED FOR G2/M PHASE PROGRESSION AND NUCLEAR DIVISION; FUNCTIONAL HOMOLOG OF S. CEREVISIAE CEF1:
TIF471, SPAC17C9.03	3	4.3%	: PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR EIF4G:
SPCC23B6.04C	2	4.3%	: CONSERVED CRAL/TRIO DOMAIN PROTEIN;

			SEC14 CYTOSOLIC FACTOR FAMILY; POSSIBLY INVOLVED IN LIPID MOVEMENT BETWEEN MEMBRANES BY SIMILAR TO S. CEREVISIAE PDR16:
STE6, SPCC1442.01, SPCC1450.17	2	4.2%	: GUANINE-NUCLEOTIDE RELEASING FACTOR; INVOLVED IN CONJUGATION:
SPAC20H4.01, SPAC631.03	2	4.1%	: HYPOTHETICAL PROTEIN; SIMILAR TO S. CEREVISIAE YDR398W NULL LETHAL:
SPAC1250.01, SPAC29A4.21	2	4.0%	: PUTATIVE CHROMATIN REMODELING COMPLEX COMPONENT; PUTATIVE TRANSCRIPTIONAL ACTIVATOR COMPLEX; SNF2 FAMILY HELICASE; CONTAINS BROMODOMAIN; SIMILAR TO S. CEREVISIAE STH1:
SPAPB8E5.07C	2	4.0%	: CONSERVED PROTEIN; SIMILAR TO S. CEREVISIAE YPL012W NULL LETHAL; CONTAINS PFAM-B_17883:
CWF10, SPBC215.12, SPEF2, SNU114	2	4.0%	: PUTATIVE PRE-MRNA SPLICING FACTOR; SIMILAR TO S. CEREVISIAE SNU114; SIMILAR TO HUMAN U5 SNRNP GTPASE-U5 SNRNP-SPECIFIC RIBOSOMAL TRANSLOCASE EF-2:
MAM1, SPBC25B2.02C, SPBC2G5.09C	3	3.9%	: ABC EFFLUX TRANSPORTER; PUTATIVE MATING FACTOR ABC EFFLUX TRANSPORTER - PUTATIVE MATING FACTOR:
SPAC25G10.08	2	3.9%	: EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT:
SPAC4F10.16C	2	3.7%	: P-TYPE CALCIUM ATPASE:
SPBC56F2.04	3	3.4%	: SIMILAR TO HUMAN DRIM, A PROTEIN DIFFERENTIALLY PRODUCED IN METASTATIC AND NONMETASTATIC HUMAN BREAST CARCINOMA CELLS; SIMIALR TO S. CEREVISIAE YBL004W:
SPBC839.08C	2	3.4%	: POSSIBLY REQUIRED FOR GLYCOSYLPHOSPHATIDYLINOSITOL (GPI) ANCHOR SYNTHESIS:
SPBC18H10.16	2	3.3%	: CCC NA-K-CL TRANSPORTER:
SPCC1259.02C	2	3.3%	: CONSERVED PROTEIN; CONTAINS 5 TRANSMEMBRANE HELICES; CONTAINS PFAM_B-1571; CONTAINS M20 PEPTIDASE; PREDICTED N-TERMINAL SIGNAL SEQUENCE:
PST1, SPBC12C2.10C, SPBC21D10.01C	3	3.2%	: CHROMATIN REMODELING FACTOR, SIN3 FAMILY COREPRESSOR:
SPCC576.05	2	3.2%	: PUTATIVE LEUCINE PERMEASE TRANSCRIPTIONAL REGULATOR:
FAS1, SPAC926.09C	5	3.1%	: FATTY ACID SYNTHASE, SUBUNIT BETA:
RGA2, SPAC26A3.09C	2	3.1%	: GTPASE ACTIVATOR; RHOGAP DOMAIN; SIMILAR TO S. CEREVISIAE BEM3:
SPAC56F8.03	2	3.1%	: PUTATIVE TRANSLATION INITIATION FACTOR IF-2; SIMILAR TO S. CEREVISIAE FUN12:
SPAC23C11.09	2	3.1%	: ALANYL-TRNA SYNTHETASE, CYTOPLASMIC:
SPCC330.11	2	3.0%	: BTB DOMAIN AND ANKARYIN REPEAT CONTAINING PROTEIN.:
SPAC328.06	2	3.0%	: UBIQUITIN CARBOXYL-TERMINAL HYDROLASE; SIMILAR TO S. CEREVISIAE UBP2:
SPAC167.01	2	3.0%	: PUTATIVE SERINE/THREONINE PROTEIN KINASE:
SPBC146.13C	2	2.8%	: PUTATIVE MYOSIN I PROTEIN:
CDC12, SPAC1F5.04C	2	2.7%	: REQUIRED FOR ACTIN RING ASSEMBLY:
SPAC2G11.02	2	2.7%	: HYPOTHETICAL PROTEIN; SIMILAR TO S. POMBE CUT1:
SPBC646.02	2	2.7%	: HYPOTHETICAL PROTEIN; AQUARIUS ORTHOLOG; POSSIBLY INVOLVED IN PTGS; NO APPARENT S. CEREVISIAE ORTHOLOG:
SYF1, SPBC211.02C, CWF3	2	2.7%	: PUTATIVE PRE-MRNA SPLICING FACTOR; SIMILAR TO S. CEREVISIAE SYF1:
SPBC29A10.10C	2	2.6%	: TRNA-SPLICING ENDONUCLEASE POSITIVE EFFECTOR:
SPAC24B11.12C	2	2.6%	: P-TYPE CALCIUM ATPASE:
RGA1, SPBC3F6.05	2	2.6%	: GTPASE ACTIVATOR; RHOGAP DOMAIN; LIM DOMAIN; INVOLVED IN ACTIN CYTOSKELETAL ORGANIZATION; INVOLVED IN FORMATION OF

			CELL WALL AND SEPTUM; SIMILAR TO S. CEREVISIAE LRG1:
SPBP19A11.04C	3	2.5%	: PUTATIVE TRANSCRIPTIONAL ACTIVATOR; LEUCINE ZIPPER:
RPB2, SPAC23G3.01, SPAC521.06	2	2.5%	: DNA-DIRECTED RNA POLYMERASE II 138 KD POLYPEPTIDE:
MAK1, SPAC1834.08	2	2.4%	: PUTATIVE SENSORY TRANSDUCTION HISTIDINE KINASE:
SPAC3F10.11C	2	2.4%	: ABC MULTIDRUG OR METAL ION EFFLUX TRANSPORTER:
ADE3, SPAC6F12.10C, MIN11	2	2.4%	: PUTATIVE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE; SUBCELLULAR LOCALIZATION OF GFP FUSION- CYTOPLASM:
SPAC212.11	5	2.3%	: DNA HELICASE POSSIBLY PSEUDO (PARTIAL):
RAD3, SPBC216.05	2	2.2%	: ATR (ATM) CHECKPOINT KINASE; SIMILAR TO S. CEREVISIAE MEC1:
SPBC1826.01C, SPBC25B2.12.C, SPBC25B2.12C,	2	2.2%	: TRANSCRIPTIONAL ACCESSORY PROTEIN (TAF) INVOLVED IN RNA POLYMERASE II TRANSCRIPTIONAL REPRESSION THROUGH INTERACTION WITH TATA-BINDING PROTEIN (TBP), SNF2P FAMILY OF DNA HELICASES:
SPCC1183.07	2	2.2%	: PUTATIVE RRNA BIOGENESIS PROTEIN; RRP5 HOMOLOG; MULTIPLE S1 RNA BINDING DOMAIN PROTEIN:
MYO51, SPBC2D10.14C	2	2.2%	: CLASS V MYOSIN; CYTOKINETIC ACTIN RING COMPONENT:
SPBC947.10	2	2.2%	: ZINC FINGER PROTEIN; ZF-C3HC4 TYPE (RING FINGER):
SPAPB8E5.09	2	2.2%	: PUTATIVE 3' TO 5' DNA/RNA HELICASE; POSSIBLY INVOLVED IN RIBOSOMAL RNA PROCESSING; SIMILAR TO S. CEREVISIAE RVB1:
SPBC31E1.06, SPBC800.01	2	2.1%	: POSSIBLY INVOLVED IN CELL POLARITY BY SIMILARITY TO YEAST BMS1:
ALM1, SPAC1486.04C	2	1.9%	: COILED-COIL PROTEIN; ASSOCIATES WITH THE MEDIAL REGION DURING MITOSIS; ABNORMAL LONG MORPHOLOGY PROTEIN:
MOK12, SPBC32H8.13C	2	1.8%	: ALPHA GLUCAN SYNTHASE:
SPAC167.07C, SPAC57A7.03C	2	1.8%	: PUTATIVE UBIQUITIN TRANSFERASE PUTATIVE UBIQUITIN LIGASE:
SPAC19D5.04	2	1.6%	: PUTATIVE UBIQUITIN LIGASE:
MOK13, SPBC16D10.05	2	1.4%	: ALPHA-GLUCAN SYNTHASE:
BFR1, SPCC18B5.01C, HBA2, SPCPJ732.04C	2	1.2%	: MFS BREFELDIN A EFFLUX TRANSPORTER:
SPAC23E2.02	2	1.2%	: HYPOTHETICAL PROTEIN; SIMILAR TO S. POMBE SPBC146.09C; CONTAINS PFAM AMINO_OXIDASE DOMAIN; PUTATIVE HMG BOX DOMAIN; GFP FUSION NUCLEAR:
SPP42, SPAC4F8.12C, CWF6	2	0.9%	: U5 SNRNA-ASSOCIATED SPLICING FACTOR; PRE-MRNA SPLICING FACTOR; SIMILAR TO S. CEREVISIAE PRP8:
BGS4, SPCC1840.02C	2	0.9%	: PUTATIVE 1,3-BETA-GLUCAN SYNTHASE SUBUNIT; CELL WALL SYNTHESIS:
VPS13A, SPBC21C3.01C, SPBC31F10.18C	2	0.6%	: PUTATIVE VACUOLAR SORTING PROTEIN:

Table S3. List of proteins identified by mass spectrometry co-purifying with Dma1-3HA-TAP from mts3-1 arrested cells [Yeast strain used: YDM1972 *h- mts3-1 dma1-3HA-TAP::kanR sid4-GFP::kanR ura4-D18 leu1-32 ade6-21X*]. [2nd purification]

Protein Name/Locus	#Unique peptides	Sequence Coverage	Descriptive Name
DMA1, SPAC17G8.10C	24	46.4%	: SPINDLE ASSEMBLY CHECKPOINT COMPONENT; PROTEIN TO PREVENT SEPTUM FORMATION AND PREMATURE EXIT FROM MITOSIS IF SPINDLE FUNCTION IS COMPROMISED: Q10322;
RPL23-1, SPAC3G9.03	3	34.5%	: 60S RIBOSOMAL PROTEIN L23: O42867;
RPL23-2, SPCC1322.11	3	34.5%	: 60S RIBOSOMAL PROTEIN L23: O42867;
RPL31, SPAC890.08	5	34.5%	: 60S RIBOSOMAL PROTEIN L31: O14384;Q9URX6;
HSP70, SPCC1739.13	14	31.7%	: HEAT SHOCK PROTEIN 70 FAMILY: O59855;
ACT1, SPBC32H8.12C, CPS8, PI012	5	30.7%	: ACTIN: P10989;Q10288;
RPS29, SPBC1685.09	2	30.4%	: 40S RIBOSOMAL PROTEIN S29: O74329;
RPL25A, SPBC106.18	6	29.8%	: 60S RIBOSOMAL PROTEIN L25: Q10330;
RPL25B, SPBC4F6.04, RPL23A-2	6	29.8%	: 60S RIBOSOMAL PROTEIN L25: O74391;
RPS7, SPAC18G6.14C	3	29.7%	: 40S RIBOSOMAL PROTEIN S7: Q10101;
RPS23, SPAC23C11.02C	3	28.7%	: 40S RIBOSOMAL PROTEIN S23: P79057;
RPS23-2, SPBP4H10.13	3	28.7%	: 40S RIBOSOMAL PROTEIN S23: P79057;
RPL37A-1, SPBC800.04C, RPL43-1	2	28.7%	: 60S RIBOSOMAL PROTEIN L37A/L43A: Q9HGL8;
RPL37A-2, SPBC83.02C, RPL43-2	2	28.7%	: 60S RIBOSOMAL PROTEIN L37A/L43: O13673;O94686;
GPD1, SPBC32F12.11, TDH1	8	28.3%	: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE: P78958;
RPL35, SPCC613.05C	3	27.9%	: 60S RIBOSOMAL PROTEIN L35: O74904;
DNT1, SPBC25D12.02C	9	24.2%	: HYPOTHETICAL PROTEIN; SEQUENCE ORPHAN; SERINE- RICH: O74354;
EF1-B, SPBC839.15C	8	23.9%	: ELONGATION FACTOR 1 ALPHA-B: ;N0ACC;
TEF1-E, SPCC794.09C, EF1A-E	8	23.9%	: ELONGATION FACTOR 1-ALPHA-E: O59818;P50522;
EF1A-B, SPAC23A1.10, TEF1-B, TEF1-D, EF1A-B,	8	23.9%	: ELONGATION FACTOR 1 ALPHA-B/D: P78764;Q10119;
RPL13, SPAC664.05	2	23.6%	: 60S RIBOSOMAL PROTEIN L13: O74175;
HSP16, SPBC3E7.02C	2	22.4%	: HEAT SHOCK PROTEIN 16: O14368;
SPAC13G7.02C	10	21.0%	: HEAT SHOCK PROTEIN 70 FAMILY: Q10265;
RPS30-1, SPAC19B12.04	2	19.7%	: 40S RIBOSOMAL PROTEIN S30: O14314;O42952;
RPS30-2, SPBC19G7.03C, YSPRS30	2	19.7%	: 40S RIBOSOMAL PROTEIN S30: O14314;O42952;
GPD3, SPBC354.12	4	19.1%	: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE: O43026;
RPS17-1, SPBC839.05C	2	18.3%	: 40S RIBOSOMAL PROTEIN S17: ;N0ACC;
RPL17, SPBC2F12.04	2	18.2%	: 60S RIBOSOMAL PROTEIN L17: O14339;O59794;
RPL26, SPBC29B5.03C	2	17.5%	: 60S RIBOSOMAL PROTEIN L26: P78946;
RPS14-1, SPAC3H5.05C	2	17.3%	: 40S RIBOSOMAL PROTEIN S14: O14150;
RPS14-2,	2	17.3%	: 40S RIBOSOMAL PROTEIN S14: O14150;

SPBC18H10.13			
RPS5, SPAC8C9.08	2	17.2%	: 40S RIBOSOMAL PROTEIN S5: O14277;
RPS5-2, SPAC328.10C	2	17.2%	: 40S RIBOSOMAL PROTEIN S5: Q9P3T6;
RPL28-1, SPBC776.11	3	16.9%	: 60S RIBOSOMAL PROTEIN LL28B 27A: P57728;
RPL28-2, SPCC5E4.07	3	16.9%	: 60S RIBOSOMAL PROTEIN L27A.2/L28A: P36585;
RPS13, SPAC6F6.07C	2	16.6%	: 40S RIBOSOMAL PROTEIN S13: P28189;
RPS18-1, SPBC16D10.11C	2	15.8%	: 40S RIBOSOMAL PROTEIN S18: O94754;
RPS18-2, SPCC1259.01C, SPCC825.06C	2	15.8%	: RIBOSOMAL PROTEIN SUBUNIT S18 40S RIBOSOMAL PROTEIN S18: O94754; Q9USH4;
RPL8-1, SPAC1F7.13C, RPK5A, RPL2-1, SPAC21E1	4	15.0%	: 60S RIBOSOMAL PROTEIN L2A: P08093;P14067;P36593;Q9UU31;
RPL8-3, SPBC839.04, RPK5-B, RPKD4	4	15.0%	: 60S RIBOSOMAL PROTEIN L8: P08093;P14067;P36593;Q9UU31;
RPL8-2, SPBC2F12.07C, RPK37, RPK5B	4	15.0%	: 60S RIBOSOMAL PROTEIN L8 OR L2: P08093;P14067;P36593;Q9UU31;
RPL44, SPAC1687.06C, RPL28	2	14.9%	: 60S RIBOSOMAL PROTEIN L28/L44; NO APPARENT S. CEREVISIAE ORTHOLOG: O14069;P36585;
RAD25, SPAC17A2.13C	3	14.8%	: DNA DAMAGE CHECKPOINT PROTEIN; 14-3-3 PROTEIN; SIMILAR TO S. CEREVISIAE BMH2: P42657;
RPT3, SPCC576.10C	2	8.2%	: 19S PROTEASOME REGULATORY SUBUNIT: O74894;
RPT6, SPBC23G7.12C, LET1	2	7.7%	: 19S PROTEASOME REGULATORY SUBUNIT: P41836;
HSP60, SPAC12G12.04, MCP60	3	7.4%	: PUATIVE MITOCHONDRIAL CHAPERONIN 60; PUTATIVE SUCCINATE DEHYDROGENASE ASSEMBLY; HEAT SHOCK PROTEIN 60: Q09864;Q10285;
SPBC83.08	2	7.1%	: PUTATIVE 3' TO 5' DNA/RNA HELICASE; POSSIBLY INVOLVED IN RIBOSOMAL RNA PROCESSING; POSSIBLY PROTEIN FOR SNORNA ACCUMULATION; POSSIBLY REQUIRED FOR THE PRODUCTION OF SNORNAS; SIMILAR TO S. CEREVISIAE RVB1: O94692;
SPBC800.13	2	6.7%	: SERINE RICH HYPOTHETICAL POSSIBLY NUCLEAR; SEQUENCE ORPHAN; HAS LOW SIMILAR TO HISTONE LIKE TRANSCRIPTION FACTORS, AND A DEAD BOX HELICASE- BELOW THRESHOLD; SUBCELLULAR LOCALIZATION OF GFP FUSION-NUCLEUS: Q9HGK9;
PMA1, SPAC1071.10C	4	6.5%	: P-TYPE PROTON ATPASE: P09627;
RPT6, SPBC23G7.12C, LET1	2	7.7%	: 19S PROTEASOME REGULATORY SUBUNIT: P41836;
RPT4, SPCC1682.16, SPCC306.01	2	6.4%	: 19S PROTEASOME REGULATORY SUBUNIT: O74445;Q9Y7R2;
SPAC10F6.01C, SPAC4C5.05C	3	4.3%	: PUTATIVE SULPHITE REDUCTASE; POSSIBLY INVOLVED IN SULPHATE ASSIMILATION; CELL WALL ORGANISATION AND BIOGENESIS; SIMILAR TO S. CEREVISIAE MET5 PUTATIVE FERREDOXIN OXIDOREDUCTASE: O14167;
EFT2-1, SPAC513.01C, SPAPYUK71.04C	2	4.3%	: ELONGATION FACTOR 2: O14460;Q9USG7;Q9USZ9;Q9UT64;

EFT2-2, SPCP31B10.07	2	4.3%	: ELONGATION FACTOR 2: O14460;Q9USG7;Q9USZ9;Q9UT64;
URA1, SPAC22G7.06C	5	4.1%	: CONTAINS GLUTAMINE-DEPENDENT CARBAMOYL- PHOSPHATESYNTHASE; CONTAINS ASPARTATE CARBAMOYL TRANSFERASE; SIMILAR TO S. CEREVISIAE URA2: Q09794;
TIF33, SPAC1E11.01C, SPAC4A8.16C, SPAC823.0	2	3.1%	: TRANSLATION INTIATION FACTOR EIF-3 SUBUNIT: O13885;O14164;P78791;Q9P6P4;
MTS4, SPBP19A11.03C	2	3.1%	: 26S PROTEASOME REGULATORY SUBUNIT: P87048;Q9HDV7;
SPCC584.01C	2	2.7%	: PUTATIVE SULFITE REDUCTASE: Q09878;
SPCP31B10.06	2	2.1%	: C2 DOMAIN FAMILY PROTEIN; SIMILAR TO S. CEREVISIAE YML072C: Q9USG8;
LSD1, SPAC4A8.11C, FAS2	2	1.7%	: FATTY ACID SYNTHASE, SUBUNIT ALPHA:O14163;P78973;Q10289;Q96WT6; Q96WT7;Q96WT8;

Table S4. List of proteins identified by mass spectrometry co-purifying with Dnt1-3HA-TAP from wild-type cells [Yeast strain used: YDM2460 *h+ dnt1-3HA-TAP leu1-32 ura4-D18 ade6-210*].

Protein Name/Locus	**#Unique peptides**	Sequence Coverage	**Descriptive Name**
SPCC1739.13	57	57.3%	|ssa2||heat shock protein 70 family| Schizosaccharomyces pombe|chr3|
SPBC25D12.02c	54	51.3%	|||(dnt1) hypothetical protein| Schizosaccharomyces pombe|chr 2||| Manual
SPBC1709.05	18	48.9%	|sks2|hsc1|heat shock protein 70 family (PMID 8973306)|Schizosaccharomyces pombe|chr 2|
SPAC23C11.11	17	47.0%	|cka1|orb5|serine/threonine protein kinase|Schizosaccharomyces pombe|chr1 |
SPAC1851.03	7	46.3%	|ckb1||protein kinase CK2 complex (beta subunit) (regulatory subunit) (PMID 8264625)|Schizosaccharomyces pombe| chr1|
SPBC106.03	13	46.2%	|||hypothetical protein| Schizosaccharomyces pombe|chr 2|
SPAC664.11	30	45.0%	|ssc1|ssp1|heat shock protein 70 family (PMID 2123810)|Schizosaccharomyces pombe|chr 1|
SPCC576.08c	7	44.3%	|rps2||40S ribosomal protein S2| Schizosaccharomyces pombe|chr 3|
SPAC13G7.02c	40	41.9%	|ssa1||heat shock protein 70 family| Schizosaccharomyces pombe|chr 1|
SPAC17G8.10c	7	37.1%	|dma1||zinc finger protein| Schizosaccharomyces pombe|chr 1|
SPBC16H5.02	27	36.7%	|pfk1||6-phosphofructokinase (predicted)|Schizosaccharomyces pombe|chr 2|
SPAC22A12.15c	24	36.2%	|bip1|bip|BiP (PMID 1373379)| Schizosaccharomyces pombe|chr 1|
SPAC23A1.10	21	35.9%	|ef1a-b||translation elongation factor (alpha 2 subunit) (PMID 9099890)| Schizosaccharomyces pombe|chr 1|
SPCC794.09c	21	35.9%	|ef1a-a||translation elongation factor 1 (alpha 1 subunit) (PMID 9099890)| Schizosaccharomyces pombe|chr 3|
SPBC839.15c	21	35.9%	|ef1a-c||translation elongation factor (alpha 1 subunit) (PMID 9099890)| Schizosaccharomyces pombe|chr 2|
SPBC32F12.11	7	35.7%	|gpd1|tdh1|glyceraldehyde 3-phosphate dehydrogenase|Schizosaccharomyces pombe|chr 2|
SPBC11C11.06c	3	35.4%	|||hypothetical protein| Schizosaccharomyces pombe|chr 2|
SPAC4A8.11c	42	33.6%	|lsd1|fas2|fatty acid synthase (subunit alpha) (PMID 9693066)| Schizosaccharomyces pombe|chr 1|
SPBP22H7.08	5	33.3%	|rps1002|rps10-2, rps10B|40S ribosomal protein S10|Schizosaccharomyces pombe|chr 2|
SPBC32H8.12c	12	32.0%	|act1|cps8|actin (PMID 1524835)| Schizosaccharomyces pombe|chr 2|
SPCC16A11.10c	2	30.2%	|oca8||cytochrome b5 (predicted)| Schizosaccharomyces pombe|chr 3|
SPCC5E4.05c	6	28.8%	|||abhydrolase family| Schizosaccharomyces

			pombe|chr 3|
SPAC926.09c	40	27.9%	|fas1||fatty acid synthase (subunit beta) (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC1815.01	6	26.7%	|eno101|eno1|enolase|Schizosaccharomyces pombe|chr 2|
SPCC1906.01	5	26.4%	|||mannose-1-phosphate guanyltransferase|Schizosaccharomyces pombe|chr 3|
SPBC609.05	7	25.6%	|||FACT complex component| Schizosaccharomyces pombe|chr 2|
SPBC365.03c	4	25.6%	|rpl2101|rpl21, rpl21-1|60S ribosomal protein L21|Schizosaccharomyces pombe|chr 2|
SPBC16H5.06	3	25.4%	|rip1||ubiquinol-cytochrome-c reductase complex (sensu Eukarya)| Schizosaccharomyces pombe|chr 2|
SPBC16G5.14c	5	25.3%	|rps3||40S ribosomal protein S3| Schizosaccharomyces pombe|chr 2|
SPAC3A12.14	2	25.3%	|cam1||calmodulin (PMID 3035538)| Schizosaccharomyces pombe|chr 1|
SPAC17C9.09c	2	25.3%	|tim13||protein translocase subunit| Schizosaccharomyces pombe|chr 1|
SPAC1F8.06	6	25.2%	|||glycoprotein (predicted)| Schizosaccharomyces pombe|chr 1|
SPBC3E7.02c	2	25.2%	|hsp16||heat shock protein| Schizosaccharomyces pombe|chr 2|
SPAC26F1.06	4	25.1%	|gpm1||phosphoglycerate mutase (PMID 8110200)|Schizosaccharomyces pombe|chr 1|
SPAC3H5.12c	6	24.8%	|rpl501|rpl5-1, rpl5|60S ribosomal protein L5|Schizosaccharomyces pombe| chr 1|
SPBC11C11.09c	6	24.8%	|rpl502|rpl5-2, rpl5b|60S ribosomal protein L5|Schizosaccharomyces pombe| chr 2|
SPAC17A2.13c	5	24.8%	|rad25||14-3-3 protein| Schizosaccharomyces pombe|chr 1|
SPAC17H9.12c	4	24.8%	|||NADH-cytochrome reductase (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC530.10c	5	24.5%	|anc1||adenine nucleotide carrier (PMID 8675018)|Schizosaccharomyces pombe| chr 2|
SPAC4H3.10c	9	24.4%	|pyk1||pyruvate kinase (predicted)| Schizosaccharomyces pombe|chr1|
SPBC27.08c	7	24.1%	|met3|SPBC28F2.01c|sulfate adenylyltransferase (predicted)| Schizosaccharomyces pombe|chr 2|
SPBC19F8.08	5	24.0%	|rps401|rps4-1, rps4, SPBC25H2.17c|40S ribosomal protein S4A/S4.1| Schizosaccharomyces pombe|chr 2|
SPBC21B10.10	5	24.0%	|rps402|rps4-2|40S ribosomal protein S4|Schizosaccharomyces pombe|chr 2|
SPAC22H12.04c	5	23.8%	|rps102|rps1-2, rps3a-2|40S ribosomal protein S3a|Schizosaccharomyces pombe|chr 1|
SPAC13G6.02c	5	23.8%	|rps101|rps1-1, rps3a-1|40S ribosomal protein S3a|Schizosaccharomyces pombe|chr 1|
SPCC18.14c	4	23.7%	|rpp0||60S acidic ribosomal protein (predicted)|Schizosaccharomyces pombe|chr 3|
SPBC18E5.04	5	23.5%	|rpl1001|rpl10-1|60S ribosomal protein L10|Schizosaccharomyces pombe|chr2 |
SPAP7G5.05	5	23.5%	|rpl1002|rpl10-2|60S ribosomal protein L10|Schizosaccharomyces pombe|chr 1 |

SPCC364.03	7	23.0%	|rpl1702|rpl17-2, rpl17|60S ribosomal protein L17|Schizosaccharomyces pombe|chr 3|
SPCC4G3.13c	2	22.3%	|||CUE domain protein| Schizosaccharomyces pombe|chr 3|
SPBC29A3.04	8	22.0%	|rpl701|rpl7a|60S ribosomal protein L7a (L8)|Schizosaccharomyces pombe|chr2 |
SPBC1703.13c	4	21.9%	|||mitochondrial carrier| Schizosaccharomyces pombe|chr 2|
SPBC4C3.07	4	21.9%	|||COP9/signalosome complex (subunit 6) (predicted)|Schizosaccharomyces pombe|chr 2|
SPCC584.01c	16	21.8%	|||sulfite reductase NADPH flavoprotein subunit (predicted)|Schizosaccharomyces pombe|chr 3|
SPBP8B7.06	2	21.8%	|rpp201|rpp2, rpp2-1|60S acidic ribosomal protein (P2A subunit)| Schizosaccharomyces pombe|chr 2|
SPCC576.10c	5	21.6%	|rpt3||19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 3|
SPBC2F12.04	5	21.4%	|rpl1701|rpl17, rpl17-1|60S ribosomal protein L17|Schizosaccharomyces pombe|chr 2|
SPAC29A4.04c	7	21.3%	|||TruB family|Schizosaccharomyces pombe|chr 1|
SPAC30C2.04	7	21.3%	|||cofactor for methionyl-and glutamyl-tRNA synthetases (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC2D10.08c	4	21.1%	|||mitochondrial ribosomal protein L4| Schizosaccharomyces pombe|chr 2|
SPBC28E12.01c	2	20.7%	|apc13|SPBC9B6.12c|anaphase-promoting complex (APC) (PMID 12477395)| Schizosaccharomyces pombe|chr 2|
SPBC354.12	4	20.6%	|gpd3||glyceraldehyde 3-phosphate dehydrogenase|Schizosaccharomyces pombe|chr 2|
SPCC285.17	8	20.6%	|spp27|uaf30|transcription factor| Schizosaccharomyces pombe|chr 3|
SPBC20F10.01	3	20.6%	|gar1|SPBC25H2.01c|ribonucleoprotein (RNP) complex (PMID 8502556)| Schizosaccharomyces pombe|chr 2|
SPBC16G5.11c	2	20.5%	|bag101|bag1-a, bag1|BAG-family| Schizosaccharomyces pombe|chr 2|
SPAC1F7.04	2	20.3%	|rho1||small GTPase| Schizosaccharomyces pombe|chr 1|
SPAC24C9.12c	6	19.9%	|||serine hydroxymethyltransferase (predicted)|Schizosaccharomyces pombe|chr 1|
SPAC6B12.12	7	19.7%	|tom70||mitochondrial outer membrane translocase complex (predicted)| Schizosaccharomyces pombe|chr 1|
SPAC694.02	24	19.6%	|||DEAD/DEAH box helicase| Schizosaccharomyces pombe|chr 1|
SPCC306.08c	3	19.6%	|||malate dehydrogenase (predicted)| Schizosaccharomyces pombe|chr3 |
SPAC30C2.02	3	19.5%	|mmd1||HEAT repeat| Schizosaccharomyces pombe|chr 1|
SPBC2D10.10c	3	19.3%	|fib1|fib|fibrillarin|Schizosaccharomyces pombe|chr 2|
SPBC336.10c	2	19.1%	|tif512||translation initiation factor| Schizosaccharomyces pombe|chr 2|

SPBC1734.11	5	18.9%	|||chaperone regulator activity (predicted)|Schizosaccharomyces pombe|chr 2|
SPBP19A11.03c	10	18.7%	|mts4|rpn1|19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 2|
SPCC13B11.01	5	18.6%	|adh1|adh|alcohol dehydrogenase| Schizosaccharomyces pombe|chr3|
SPAC19G12.08	4	18.4%	|||fatty acid hydroxylase (predicted)| Schizosaccharomyces pombe|chr 1|
SPCC5E4.07	2	18.2%	|rpl2802|rpl28-2|60S ribosomal protein L27a.2/L28A|Schizosaccharomyces pombe|chr 3|
SPAC8E11.02c	4	18.1%	|rad24||involved in DNA repair| Schizosaccharomyces pombe|chr 1|
SPAC17A5.15c	8	17.9%	|||glutamate-tRNA ligase (predicted)| Schizosaccharomyces pombe|chr 1|
SPBC29A3.18	3	17.9%	|cyt1||cytochrome c1 (predicted)| Schizosaccharomyces pombe|chr 2|
SPBC2G5.06c	5	17.6%	|hmt2|cad1|sulfide-quinone oxidoreductase|Schizosaccharomyces pombe|chr 2|
SPAC19G12.06c	2	17.6%	|hta2||histone H2A (beta)| Schizosaccharomyces pombe|chr1|
SPCC622.08c	2	17.4%	|hta1||histone H2A (alpha) (PMID 3018512)|Schizosaccharomyces pombe|chr 3|
SPAC18G6.12c	3	17.5%	|B22918-1||B22918 domain|Schizosaccharomyces pombe|chr 1|
SPBC14F5.03c	11	17.4%	|kap123||karyopherin|Schizosaccharomyces pombe|chr 2|
SPBC1718.04	7	17.3%	|||phosphate acyltransferase (SMART)| Schizosaccharomyces pombe|chr2|
SPCC1281.06c	4	16.9%	|||acyl-coA desaturase (predicted)| Schizosaccharomyces pombe|chr3|
SPAC3A11.10c	5	16.9%	|||microsomal dipeptidase (predicted)| Schizosaccharomyces pombe|chr1|
SPAC9.07c	4	16.9%	|||GTP binding|Schizosaccharomyces pombe|chr 1|
SPBC36B7.07	2	16.9%	|tlg1||SNARE|Schizosaccharomyces pombe|chr 2|
SPBC36B7.07	2	16.9%	|tlg1||SNARE|Schizosaccharomyces pombe|chr 2|
SPCC16C4.05	2	16.9%	|||RNase P and RNase MRP subunit (predicted)|Schizosaccharomyces pombe|chr 3|
SPBC26H8.06	2	16.8%	|grx5||arsenate reductase (glutaredoxin) activity (predicted)|Schizosaccharomyces pombe|chr 2|
SPAC11E3.03	2	16.7%	|pcs1||monopolin complex component (predicted)|Schizosaccharomyces pombe|chr 1|
SPCC970.03	2	16.6%	|||cytochrome b5 reductase (predicted)| Schizosaccharomyces pombe|chr3|
SPAC227.02c	3	16.6%	|||conserved eukaryotic protein| Schizosaccharomyces pombe|chr1|
SPAC13A11.02c	4	16.4%	|cyp51||cytochrome p45051 (predicted)| Schizosaccharomyces pombe|chr1|
SPAC57A10.12c	6	16.3%	|ura3||dihydroorotate dehydrogenase| Schizosaccharomyces pombe|chr1|
SPAC3A11.07	9	16.2%	|||NADH dehydrogenase (predicted)| Schizosaccharomyces pombe|chr1|

<table>
<tr><td>SPBC8D2.17</td><td>3</td><td>16.0%</td><td>|||galactosyltransferase|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC23C11.17</td><td>4</td><td>15.9%</td><td>|||conserved eukaryotic protein| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAPB1A11.02</td><td>2</td><td>15.9%</td><td>|||esterase/lipase (predicted)| Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAC1071.10c</td><td>9</td><td>15.5%</td><td>|pma1||P-type proton ATPase (PMID 12707717)|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC26H8.08c</td><td>4</td><td>15.3%</td><td>|||GTPase activity (predicted)| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC31F10.06c</td><td>2</td><td>15.3%</td><td>|sar1||GTP binding|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC1B1.02c</td><td>5</td><td>15.1%</td><td>|||NAD kinase (predicted)| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAC26F1.07</td><td>2</td><td>15.0%</td><td>|||aldo/keto reductase| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAC1399.04c</td><td>2</td><td>15.0%</td><td>|||uracil phosphoribosyltransferase (predicted)|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC56F2.09c</td><td>3</td><td>14.9%</td><td>|arg5||carbamoyl-phosphate synthase (predicted)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC644.15</td><td>2</td><td>14.7%</td><td>|rpp101|rpp1-1|60S acidic ribosomal protein|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC3B9.13c</td><td>2</td><td>14.5%</td><td>|rpp102|rpp1-2|60S acidic ribosomal protein|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPBC16H5.08c</td><td>4</td><td>14.6%</td><td>|||ATPase|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPBC1773.10c</td><td>5</td><td>14.6%</td><td>|||asparagine-tRNA ligase (predicted)| Schizosaccharomyces pombe|chr2 |</td></tr>
<tr><td>SPAC4F10.14c</td><td>2</td><td>14.6%</td><td>|btf3||nascent polypeptide-associated complex (predicted) (PMID 8809106)| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPBP4H10.04</td><td>4</td><td>14.4%</td><td>|ppb1||serine/threonine protein phosphatase (catalytic subunit)| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPAC22G7.06c</td><td>20</td><td>14.3%</td><td>|ura1||ATP binding|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAC222.12c</td><td>6</td><td>14.3%</td><td>|atp2||F1-ATPase (beta subunit) (PMID 6228552)|Schizosaccharomyces pombe| chr 1|</td></tr>
<tr><td>SPBC2G5.02c</td><td>4</td><td>14.2%</td><td>|||protein kinase CK2 complex (regulatory subunit) (predicted)| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC14F5.05c</td><td>3</td><td>14.1%</td><td>|sam1||S-adenosylmethionine synthetase (PMID 10620770)| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC83.08</td><td>5</td><td>14.0%</td><td>|||AAA family ATPase| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC776.15c</td><td>4</td><td>13.7%</td><td>|||dihydrolipoamide S-succinyltransferase (e2 component of oxoglutarate dehydrogenase complex) (predicted)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC821.11</td><td>4</td><td>13.7%</td><td>|pro1||gamma-glutamyl phosphate reductase (predicted)| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPBC13G1.01c</td><td>3</td><td>13.5%</td><td>|||mitochondrial ribosomal protein S4|Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC24C6.05</td><td>2</td><td>13.5%</td><td>|sec28||coatomer (epsilon subunit) (predicted)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC23G3.06</td><td>4</td><td>13.4%</td><td>|||ribonucleoprotein (RNP) complex (predicted) (PMID 12068309)| Schizosaccharomyces</td></tr>
</table>

			pombe|chr1|
SPAC29B12.04	2	13.2%	|snz1||involved in pyridoxine metabolism (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC19G7.10c	6	13.0%	|||topoisomerase associated protein (predicted)|Schizosaccharomyces pombe|chr 2|
SPAC323.02c	2	13.0%	|||20S proteasome component (alpha 5) |Schizosaccharomyces pombe|chr1|
SPAC19G12.12	2	12.9%	|dlp1|coq1|decaprenyl diphosphate synthase (subunit 2) (PMID 14519123)| Schizosaccharomyces pombe|chr1|
SPAC4F10.10c	3	12.8%	|||mannosyltransferase complex (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC17D1.06	4	12.5%	|||DEAD/DEAH box helicase| Schizosaccharomyces pombe|chr2|
SPAC1B2.03c	2	12.3%	|||GNS1/SUR4 family protein| Schizosaccharomyces pombe|chr1|
SPBC16E9.14c	2	12.2%	|||cation efflux family| Schizosaccharomyces pombe|chr2|
SPBC1A4.05	8	12.1%	|||hypothetical protein| Schizosaccharomyces pombe|chr2|
SPBP4H10.18c	2	12.1%	|||hypothetical protein| Schizosaccharomyces pombe|chr2|
SPBC27B12.09c	2	11.9%	|||transporter|Schizosaccharomyces pombe|chr 2|
SPBC1539.09c	4	11.7%	|trp1||anthranilate synthase (component II)|Schizosaccharomyces pombe|chr2|
SPCC794.12c	4	11.7%	|mae2||malic enzyme| Schizosaccharomyces pombe|chr3|
SPBC106.06	2	11.6%	|cct4||chaperonin-containing T-complex| Schizosaccharomyces pombe|chr2|
SPAC13G6.11c	4	11.6%	|||mevalonate kinase activity (predicted)|Schizosaccharomyces pombe|chr 1|
SPAC25G10.05c	4	11.6%	|his1||ATP phosphoribosyltransferase (PMID 7732725)|Schizosaccharomyces pombe|chr 1|
SPBC19C7.12c	3	11.5%	|||mannosyltransferase (predicted)| Schizosaccharomyces pombe|chr2|
SPAC2F3.02	2	11.5%	|||TPR repeat protein| Schizosaccharomyces pombe|chr1|
SPBC18H10.17c	2	11.4%	|||sequence orphan| Schizosaccharomyces pombe|chr2|
SPBC26H8.07c	2	11.2%	|nda3|ben1, alp12|tubulin (beta) (PMID 6094012)|Schizosaccharomyces pombe|chr 2|
SPAC22F3.09c	3	11.1%	|mcs1|res2, pct1|transcription factor| Schizosaccharomyces pombe|chr1|
SPAC10F6.01c	10	11.0%	||SPAC4C5.05c|sulfite reductase (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC1105.02c	3	11.0%	|lys4||homocitrate synthase (predicted)| Schizosaccharomyces pombe|chr2|
SPAC4H3.01	4	11.0%	|||DNAJ domain protein| Schizosaccharomyces pombe|chr1|
SPAC17G6.13	3	10.9%	|slt1||involved in response to drug| Schizosaccharomyces pombe|chr1|
SPAC1783.08c	2	10.9%	|rpl1502|rpl15-2|60S ribosomal protein L15b|Schizosaccharomyces pombe|chr1 |
SPCC576.11	2	10.9%	|rpl15||60S ribosomal protein L15|

<table>
<tr><td></td><td></td><td></td><td>Schizosaccharomyces pombe|chr3|</td></tr>
<tr><td>SPAC959.02</td><td>2</td><td>10.7%</td><td>|sec17||alpha SNAP| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAC637.10c</td><td>2</td><td>10.7%</td><td>|pus1|rpn10|19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC146.14c</td><td>5</td><td>10.6%</td><td>|sec26|SPBC337.01c|adaptin|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC513.01c</td><td>5</td><td>10.5%</td><td>|eft201|eft2-1, etf2, SPAPYUK71.04c| translation elongation factor 2 (PMID 9099890)|Schizosaccharomyces pombe| chr1|</td></tr>
<tr><td>SPCP31B10.07</td><td>5</td><td>10.5%</td><td>|eft202||translation elongation factor 2 (PMID 9099890)|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPAC16E8.10c</td><td>2</td><td>10.4%</td><td>|||mitochondrial ribosomal protein S7| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPBC18H10.03</td><td>2</td><td>10.3%</td><td>|tif35||translation initiation factor| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC3E7.15c</td><td>2</td><td>10.2%</td><td>||SPBC4F6.02c|LAG1 domain| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPAC26A3.16</td><td>2</td><td>10.2%</td><td>|dph1||ubiquitin family protein| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPBC14F5.02</td><td>2</td><td>10.1%</td><td>|||sequence orphan| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPBC31A8.01c</td><td>2</td><td>10.1%</td><td>|cwl1|rtn1, SPBC651.13c|reticulon-like protein|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPCC569.06</td><td>2</td><td>10.0%</td><td>|||similar to S. pombe SPCC61.05 and SPAC26H5.07C|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPAC12G12.07c</td><td>2</td><td>10.0%</td><td>|||hypothetical protein| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPBP35G2.07</td><td>5</td><td>9.9%</td><td>|ilv1||acetolactate synthase subunit (PMID 8299177)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPBC17G9.09</td><td>3</td><td>9.9%</td><td>|tif213||translation initiation factor 2 (gamma subunit)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPCC1795.03</td><td>2</td><td>9.9%</td><td>|gms1||UDP-galactose transporter| Schizosaccharomyces pombe|chr3|</td></tr>
<tr><td>SPBC17A3.04c</td><td>5</td><td>9.8%</td><td>|||methionine-tRNA ligase (predicted)| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPAC1834.11c</td><td>5</td><td>9.8%</td><td>|sec18||AAA family ATPase| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPBC11B10.01</td><td>3</td><td>9.8%</td><td>||SPBC32H8.14|glycosyl transferase family 1|Schizosaccharomyces pombe| chr 2|</td></tr>
<tr><td>SPBC13E7.08c</td><td>2</td><td>9.8%</td><td>|||proteasome interacting protein (predicted)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPCPB16A4.05c</td><td>2</td><td>9.8%</td><td>|||urease accessory protein UREG (ISS)|Schizosaccharomyces pombe|chr3 |</td></tr>
<tr><td>SPBC12D12.03</td><td>4</td><td>9.7%</td><td>|cct1||chaperonin-containing T-complex| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPAC3H8.02</td><td>2</td><td>9.7%</td><td>|||sec14 cytosolic factor family| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAC20H4.06c</td><td>2</td><td>9.6%</td><td>|||hypothetical protein| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPCC1840.03</td><td>7</td><td>9.5%</td><td>|sal3|pse1|karyopherin|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPBC215.03c</td><td>2</td><td>9.5%</td><td>|csn1||COP9/signalosome complex (subunit 1)|Schizosaccharomyces pombe| chr 2|</td></tr>
</table>

SPCC757.09c	2	9.5%	|rnc1||RNA-binding protein| Schizosaccharomyces pombe|chr3|
SPBC19C2.07	2	9.5%	|fba1||fructose-bisphosphate aldolase (PMID 8286404)|Schizosaccharomyces pombe|chr 2|
SPBC1289.06c	3	9.4%	|||sequence orphan| Schizosaccharomyces pombe|chr2|
SPBC56F2.12	3	9.4%	|||acetohydroxyacid reductoisomerase (predicted)|Schizosaccharomyces pombe|chr 2|
SPBP4H10.11c	3	9.3%	|||long-chain-fatty-acid-CoA ligase activity (predicted)|Schizosaccharomyces pombe|chr 2|
SPAC21E11.08	3	9.3%	|lcb2|SPAC2C4.02|serine palmitoyltransferase (PMID 8921873) (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC17G9.05	2	9.3%	|cyp6||cyclophilin|Schizosaccharomyces pombe|chr 2|
SPBC19G7.16	3	9.3%	|||transcription elongation factor complex (predicted)| Schizosaccharomyces pombe|chr2|
SPCC16A11.16c	2	9.3%	|||glycoprotein (predicted)| Schizosaccharomyces pombe|chr3|
SPAC1851.02	2	9.3%	|||fatty acyltransferase| Schizosaccharomyces pombe|chr1|
SPBC800.09	2	9.2%	|sum2||involved in G2/M transition checkpoint (required) (PMID 9832516)| Schizosaccharomyces pombe|chr2|
SPBC25B2.03	2	9.0%	|||zinc finger protein| Schizosaccharomyces pombe|chr2|
SPBC18E5.02c	3	9.0%	||SPBC29A3.20c|serine palmitoyltransferase (subunit) (predicted)|Schizosaccharomyces pombe|chr 2|
SPBC354.02c	3	9.0%	|sec61||translocon (alpha subunit) (predicted) (PMID 9427389)| Schizosaccharomyces pombe|chr2|
SPBC32H8.03	2	9.0%	|bem46||suppressor of bem1| Schizosaccharomyces pombe|chr2|
SPAC1F7.05	3	8.9%	|cdc22||ribonucleoside reductase| Schizosaccharomyces pombe|chr1|
SPCC417.08	5	8.7%	|tef3|EF-3|translation elongation factor activity (TAS) (PMID 9099890)| Schizosaccharomyces pombe|chr3|
SPAC3C7.08c	6	8.5%	|elf1||AAA family ATPase| Schizosaccharomyces pombe|chr1|
SPBC17D11.05	4	8.5%	|tif32||translation initiation factor| Schizosaccharomyces pombe|chr2|
SPBC16D10.07c	2	8.5%	|sir2||transcriptional regulator| Schizosaccharomyces pombe|chr2|
SPBC29B5.04c	3	8.4%	|||conserved fungal protein| Schizosaccharomyces pombe|chr2|
SPCC1840.08c	3	8.4%	|||protein disulfide isomerase oxidoreductase family| Schizosaccharomyces pombe|chr3|
SPBC646.11	4	8.4%	|cct6||chaperonin-containing T-complex| Schizosaccharomyces pombe|chr2|
SPAC17H9.05	2	8.4%	|ebp2||P40-like|Schizosaccharomyces pombe|chr 1|
SPAC922.07c	2	8.3%	|||aldehyde dehydrogenase (predicted)| Schizosaccharomyces pombe|chr1|
SPAC926.04c	4	8.2%	|swo1|hsp90|chaperone activity|

			Schizosaccharomyces pombe|chr1|
SPAC3H1.10	2	8.2%	|||phytochelatin synthetase (PMID 10368185) (PMID 10369673)| Schizosaccharomyces pombe|chr1|
SPBC4C3.09	2	8.2%	|||galactosyltransferase family 8| Schizosaccharomyces pombe|chr2|
SPAC926.08c	2	8.2%	|||RNA-binding protein| Schizosaccharomyces pombe|chr1|
SPCC1902.01	3	8.1%	|gaf1|SPCC417.01c|transcription factor (PMID 9714831)|Schizosaccharomyces pombe|chr 3|
SPBC16A3.12c	2	8.1%	|||triglyceride lipase-cholesterol esterase (predicted)|Schizosaccharomyces pombe|chr 2|
SPBC887.10	2	8.0%	|mcs4||mitotic catastrophe suppressor| Schizosaccharomyces pombe|chr2|
SPAC6G9.03c	2	8.0%	|||hypothetical protein| Schizosaccharomyces pombe|chr1|
SPAP8A3.13c	2	7.9%	|||hypothetical protein| Schizosaccharomyces pombe|chr1||| Manual
SPBC23G7.12c	2	7.9%	|rpt6|let1|19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 2|
SPBC19C7.06	3	7.8%	|||proline-tRNA ligase (predicted)| Schizosaccharomyces pombe|chr2|
SPAC3F10.03	3	7.8%	|||glycine tRNA-ligase| Schizosaccharomyces pombe|chr1|
SPBC646.05c	2	7.8%	|erg9||squalene synthase (PMID 8474436)|Schizosaccharomyces pombe| chr 2|
SPBC3B8.03	2	7.8%	|||saccharopine dehydrogenase [NADP+, l-glutamate forming] (predicted)| Schizosaccharomyces pombe|chr2|
SPAC23G3.11	2	7.8%	|rpn6||19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 1|
SPAC26A3.17c	2	7.8%	||SPAC8E11.11|N-methyltransferase (predicted)|Schizosaccharomyces pombe|chr 1|
SPAPB1E7.09	3	7.7%	
SPBC16A3.15c	2	7.7%	|nda2||tubulin (alpha 1)| Schizosaccharomyces pombe|chr2|
SPAC1006.07	2	7.7%	|||translation initiation factor| Schizosaccharomyces pombe|chr1|
SPBC646.09c	2	7.6%	|yin6|int6|translation initiation factor| Schizosaccharomyces pombe|chr2|
SPCC1795.11	2	7.5%	|sum3|ded1, slh3, moc2|DEAD/DEAH box helicase|Schizosaccharomyces pombe|chr 3|
SPAC1786.03	3	7.5%	|cut11|SPAC24C9.01|localization nuclear membrane|Schizosaccharomyces pombe|chr 1|
SPAC23A1.12c	3	7.5%	|||phenylalanine-tRNA ligase (beta subunit) (predicted)| Schizosaccharomyces pombe|chr1|
SPAC3A11.12c	2	7.5%	|rpt5|pam2, tbp1|19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 1|
SPAC186.02c	2	7.5%	|||2-hydroxyacid dehydrogenase (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC19G7.13	2	7.4%	|||Myb family|Schizosaccharomyces pombe|chr 2|
SPCC1259.09c	2	7.2%	|||pyruvate dehydrogenase protein x component (predicted)| Schizosaccharomyces pombe|chr3|

SPAC139.02c	2	7.2%	|||MC oxaloacetate transporter (putative)|Schizosaccharomyces pombe|chr 1|
SPAC18G6.05c	13	7.1%	|||HEAT repeat|Schizosaccharomyces pombe|chr 1|
SPBC30B4.05	4	7.1%	|||karyopherin (predicted)| Schizosaccharomyces pombe|chr2|
SPBC19F5.05c	3	7.1%	|ppp1|SPBC25D12.01c|localization nucleolus (predicted)| Schizosaccharomyces pombe|chr2|
SPAC18B11.02c	2	7.1%	|||DRAP deaminase activity (predicted)| Schizosaccharomyces pombe|chr1|
SPCC1827.03c	2	7.0%	|||long-chain fatty acid transporter (predicted)|Schizosaccharomyces pombe|chr 3|
SPAC4D7.05	2	7.0%	|sum1|tif34|translation initiation factor| Schizosaccharomyces pombe|chr1|
SPAC9.09	3	6.9%	|||homocysteine methyltransferase| Schizosaccharomyces pombe|ch1|
SPBC6B1.09c	2	6.9%	|nbs1||FHA domain (phosphopeptide binding)|Schizosaccharomyces pombe|chr 2|
SPAC31A2.12	2	6.9%	|||arrestin family|Schizosaccharomyces pombe|chr 1|
SPAC4A8.06c	2	6.7%	|||esterase (predicted)| Schizosaccharomyces pombe|chr1|
SPAC1F8.07c	3	6.7%	|||pyruvate decarboxylase (predicted)| Schizosaccharomyces pombe|chr1|
SPBC2G5.01	2	6.7%	|||hypothetical protein| Schizosaccharomyces pombe|chr2|
SPAP8A3.09c	2	6.6%	|paa1||protein phosphotase regulatory subunit|Schizosaccharomyces pombe|chr 1|
SPCC553.10	2	6.6%	|||serine-rich protein| Schizosaccharomyces pombe|chr3|
SPAC9E9.12c	4	6.5%	|||transporter activity| Schizosaccharomyces pombe|chr1|
SPAC25G10.08	3	6.5%	|||translation initiation factor| Schizosaccharomyces pombe|chr1|
SPAC8E11.01c	2	6.5%	||SPAC959.01|glycosyl hydrolase family 32|Schizosaccharomyces pombe|chr1|
SPAC1420.03	2	6.5%	|rpn501|rpn5-a|19S proteasome regulatory subunit (PMID 12783882)| Schizosaccharomyces pombe|chr1|
SPAPB8E5.02c	2	6.5%	|rpn502|rpn5-b|19S proteasome regulatory subunit (PMID 12783882)| Schizosaccharomyces pombe|chr1|
SPBC25H2.02	3	6.4%	|ths1||threonine-tRNA ligase (predicted)| Schizosaccharomyces pombe|chr 2|
SPBP19A11.07c	2	6.4%	||SPBP4H10.02c|hypothetical protein|Schizosaccharomyces pombe|chr 2|
SPBC17F3.02	2	6.4%	|nak1||N-terminal protein kinase| Schizosaccharomyces pombe|chr2|
SPBC1773.01	2	6.4%	|||WD repeat protein| Schizosaccharomyces pombe|chr2|
SPBC2D10.18	2	6.4%	|abc1|coq8|ABC1 family| Schizosaccharomyces pombe|chr2|
SPCC364.06	2	6.4%	|||involved in nucleosome assembly (predicted)|Schizosaccharomyces pombe|chr 3|
SPAC16.04	2	6.2%	|||zinc finger protein| Schizosaccharomyces pombe|chr1|

SPBC119.01	2	6.2%	|rpn3|SPBPJ4664.07|19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 2|
SPBC646.10c	2	6.2%	|||ribonucleoprotein (RNP) complex (predicted) (PMID 12068309)| Schizosaccharomyces pombe|chr2|
SPCC1682.16	2	6.2%	|rpt4||19S proteasome regulatory subunit|Schizosaccharomyces pombe|chr 3|
SPBP4H10.15	4	6.1%	|||aconitate hydratase (predicted)| Schizosaccharomyces pombe|chr2|
SPAC7D4.11c	2	6.1%	|||hypothetical protein| Schizosaccharomyces pombe|chr1|
SPCP1E11.11	3	6.1%	|||RNA-binding protein| Schizosaccharomyces pombe|chr3|
SPCC962.03c	2	6.1%	|cut15||karyopherin|Schizosaccharomyces pombe|chr 3|
SPAC14C4.14	2	6.0%	|atp1||F1-ATPase (alpha subunit) (PMID 1824697)|Schizosaccharomyces pombe|chr 1|
SPAC56E4.04c	8	5.9%	|cut6||acetyl-CoA carboxylase| Schizosaccharomyces pombe|chr1|
SPAC1D4.11c	3	5.9%	|lkh1|kic1|dual specificity protein kinase|Schizosaccharomyces pombe|chr 1|
SPAC12B10.16c	2	5.9%	|||hypothetical protein| Schizosaccharomyces pombe|chr1|
SPAC3H1.05	2	5.9%	|||CAAX prenyl protease (predicted)| Schizosaccharomyces pombe|chr1|
SPBC646.14c	2	5.9%	|orc5||origin recognition complex (subunit 5)|Schizosaccharomyces pombe|chr 2|
SPAC1F12.07	2	5.9%	|||phosphoserine aminotransferase (predicted)|Schizosaccharomyces pombe|chr 1|
SPCC4G3.18	3	5.8%	|||hypothetical protein| Schizosaccharomyces pombe|chr3|
SPCC895.07	2	5.8%	|alp14||localization spindle pole body| Schizosaccharomyces pombe|chr3|
SPAC9E9.03	3	5.8%	|leu2||3-isopropylmalate dehydratase (predicted)|Schizosaccharomyces pombe|chr 1|
SPBP8B7.19	5	5.7%	|||FACT complex component| Schizosaccharomyces pombe|chr2|
SPCC1259.02c	3	5.7%	|||6 predicted transmembrane helices| Schizosaccharomyces pombe|chr3|
SPBC428.01c	2	5.7%	|nup107|SPBC582.11c|nucleoporin (PMID 11309419)|Schizosaccharomyces pombe|chr 2|
SPAC167.05	2	5.7%	||SPAC57A7.01|Usp (universal stress protein) domain|Schizosaccharomyces pombe|chr 1|
SPAC1420.01c	2	5.7%	||SPAC56E4.08c|hypothetical protein| Schizosaccharomyces pombe|chr1|
SPAC56F8.03	3	5.6%	|||translation initiation factor if-2 (predicted)|Schizosaccharomyces pombe|chr 1|
SPBC21H7.04	2	5.6%	|||DEAD/DEAH box helicase| Schizosaccharomyces pombe|chr2|
SPBC21C3.15c	2	5.6%	|||aldehyde-dehydrogenase-like|Schizosaccharomyces pombe|chr 2|
SPBP19A11.06	3	5.5%	|lid2|SPBP4H10.01|transcription factor| Schizosaccharomyces pombe|chr2|
SPBC4F6.17c	2	5.5%	|||AAA family ATPase| Schizosaccharomyces pombe|chr2|

SPBC651.01c	2	5.5%	||SPBC725.18c|GTPase activity (predicted)|Schizosaccharomyces pombe|chr 2|
SPAC22F8.08	2	5.4%	|||COPII-coated vesicle component (predicted)|Schizosaccharomyces pombe|chr 1|
SPAC29A4.02c	2	5.4%	|||translation elongation factor 1 (gamma subunit) (PMID 9099890)| Schizosaccharomyces pombe|chr1|
SPAC26A3.05	6	5.3%	|chc1||clathrin heavy chain (predicted)| Schizosaccharomyces pombe|chr1|
SPBC83.16c	3	5.3%	|||conserved protein| Schizosaccharomyces pombe|chr2|
SPAC1D4.12	2	5.2%	|rad15|rhp3|transcription factor TFIIH complex|Schizosaccharomyces pombe|chr 1|
SPBC21.01	2	5.2%	||SPBC776.19|hypothetical protein| Schizosaccharomyces pombe|chr2|
SPBPJ4664.06	4	5.1%	|gpt1||glycosyl transferase family 8| Schizosaccharomyces pombe|chr2|
SPBC17G9.11c	3	5.1%	|pyr1||pyruvate carboxylase| Schizosaccharomyces pombe|chr2|
SPBC29A3.14c	2	5.1%	|trt1||telomerase catalytic subunit (PMID 9774280)|Schizosaccharomyces pombe|chr 2|
SPBC660.08	2	5.1%	|||sequence orphan| Schizosaccharomyces pombe|chr2|
SPAC1805.17	3	5.0%	|crm1|caf2, SPAC1B2.01|chromosome region maintenance protein 1| Schizosaccharomyces pombe|chr1|
SPBC3D6.13c	2	5.0%	|||protein disulfide isomerase oxidoreductase family| Schizosaccharomyces pombe|chr2|
SPBC1A4.09	2	5.0%	|||conserved protein| Schizosaccharomyces pombe|chr2|
SPAC22H10.07	2	5.0%	|scd2|ral3|involved in conjugation (regulation)|Schizosaccharomyces pombe|chr 1|
SPBC1105.01	3	4.9%	||SPBPB7E8.03|HEAT repeat (ISS) (PMID 14729571)|Schizosaccharomyces pombe|chr 2|
SPBC17D1.07c	2	4.9%	|||calcium binding protein| Schizosaccharomyces pombe|chr2|
SPCP1E11.06	2	4.9%	|apl4||adaptin (predicted)| Schizosaccharomyces pombe|chr3|
SPCC757.04	2	4.8%	|||transcriptional regulator (predicted)| Schizosaccharomyces pombe|chr3|
SPCC1494.03	2	4.7%	|||hypothetical protein| Schizosaccharomyces pombe|chr3|
SPAC328.01c	2	4.6%	||SPAC3A11.01|importin-beta family| Schizosaccharomyces pombe|chr1|
SPAC1B3.13	2	4.6%	|||WD repeat protein| Schizosaccharomyces pombe|chr1|
SPAPB8E5.07c	3	4.5%	|||HEAT repeat|Schizosaccharomyces pombe|chr 1|
SPCC4G3.12c	2	4.5%	|||zinc finger protein| Schizosaccharomyces pombe|chr3|
SPCC1020.01c	3	4.4%	|pma2|SPCC1393.01|P-type proton ATPase (PMID 12707717)| Schizosaccharomyces pombe|chr3|
SPAC24H6.01c	2	4.4%	||SPAPB21F2.01|O-acyl transferase (predicted)|Schizosaccharomyces pombe|chr 1|
SPAC23A1.07	1	4.4%	|||zinc finger protein| Schizosaccharomyces pombe|chr1|

SPAC9G1.10c	2	4.3%	|||inositol polyphosphate phosphatase (predicted)|Schizosaccharomyces pombe|chr 1|
SPAPB2C8.01	4	4.3%	|||glycoprotein (predicted)| Schizosaccharomyces pombe|chr1|
SPBC3B8.11	2	4.3%	|||hypothetical protein| Schizosaccharomyces pombe|chr2|
SPBC19C7.11	2	4.3%	|||ClC chloride channel (predicted)| Schizosaccharomyces pombe|chr2|
SPBP8B7.20c	2	4.3%	|||methyltransferase (predicted)| Schizosaccharomyces pombe|chr2|
SPAC20G8.09c	2	4.2%	|||conserved protein| Schizosaccharomyces pombe|chr1|
SPCC31H12.07	2	4.2%	|sec231|sec23a, SPCC5E4.01|GTPase activating protein (ISS)| Schizosaccharomyces pombe|chr3|
SPBC4F6.13c	2	4.2%	|||WD repeat protein| Schizosaccharomyces pombe|chr2|
SPBC337.08c	1	4.2%	|ubi4||ubiquitin family protein| Schizosaccharomyces pombe|chr2|
SPAC6F6.06c	3	4.1%	|||involved in cell polarity (predicted)| Schizosaccharomyces pombe|chr1|
SPCC550.11	2	4.1%	|||RanBP7/importin-beta/Cse1p family| Schizosaccharomyces pombe|chr3|
SPBC20F10.05	2	4.1%	|||sequence orphan| Schizosaccharomyces pombe|chr2|
SPAC29B12.07	3	4.0%	|sec16||involved in ER to Golgi transport|Schizosaccharomyces pombe|chr 1|
SPBC17G9.04c	2	4.0%	|nup85||nuclear pore complex| Schizosaccharomyces pombe|chr2|
SPBC691.05c	2	4.0%	|pi030|SPBP22H7.01c|ion channel (predicted)|Schizosaccharomyces pombe|chr 2|
SPBC13A2.04c	2	4.0%	|ptr2||PTR family peptide transporter| Schizosaccharomyces pombe|chr2|
SPAC19A8.08	2	3.9%	|upf2||involved in mRNA catabolism, nonsense-mediated (required) (PMID 11073994)|Schizosaccharomyces pombe|chr 1|
SPBC25H2.11c	2	3.9%	|||bromodomain protein| Schizosaccharomyces pombe|chr2|
SPBC25H2.13c	3	3.8%	|cdc20|pol2|DNA polymerase epsilon (catalytic subunit a) (PMID 9356477)| Schizosaccharomyces pombe|chr2|
SPBC1105.08	2	3.8%	|||EMP70 family|Schizosaccharomyces pombe|chr 2|
SPAC19B12.07c	2	3.8%	|||zinc finger protein| Schizosaccharomyces pombe|chr1|
SPCC962.01	3	3.7%	||SPCP31B10.09|C2 domain| Schizosaccharomyces pombe|chr3|
SPBC4.03c	2	3.7%	|||COPII-coated vesicle component (putative)|Schizosaccharomyces pombe|chr 2|
SPBC21D10.09c	2	3.6%	|||zinc finger protein| Schizosaccharomyces pombe|chr2|
SPAC2F3.06c	2	3.6%	|kap104||karyopherin|Schizosaccharomyces pombe|chr 1|
SPAC4F10.09c	2	3.6%	|||involved in ribosome biogenesis and assembly (predicted)| Schizosaccharomyces pombe|chr1|
SPCC1223.07c	2	3.6%	|||aspartate-tRNA ligase (predicted)| Schizosaccharomyces pombe|chr3|

SPAC17A5.14	2	3.5%	|exo2||exonuclease II (PMID 8781170)|Schizosaccharomyces pombe|chr1|
SPAC29E6.10c	2	3.5%	||SPAC30.14c|conserved protein|Schizosaccharomyces pombe|chr1|
SPAC110.04c	2	3.5%	|pss1|ssp1, SPAP14E8.01c|heat shock protein 70 family|Schizosaccharomyces pombe|chr 1|
SPCC63.04	3	3.4%	|mok14||a-1,3-glucan synthase|Schizosaccharomyces pombe|chr3|
SPAC57A7.10c	2	3.4%	|sec21||adaptin|Schizosaccharomyces pombe|chr 1|
SPBC20F10.07	2	3.4%	|||hypothetical protein| Schizosaccharomyces pombe|chr2|
SPBC947.15c	2	3.3%	|||NADH dehydrogenase (predicted)|Schizosaccharomyces pombe|chr2|
SPAC4F8.13c	3	3.2%	|rng2||IQGAP|Schizosaccharomyces pombe|chr 1|
SPAC3G6.01	2	3.2%	|hrp3||CHD family|Schizosaccharomyces pombe|chr 1|
SPAC1565.08	2	3.2%	|cdc48|SPAC6F12.01|AAA family ATPase|Schizosaccharomyces pombe|chr1|
SPCC736.14	2	3.1%	|dis1||microtubule-associated protein (PMID 7628693)|Schizosaccharomyces pombe|chr 3|
SPAC20G8.06	3	3.0%	|||CCR4-Not complex (predicted)|Schizosaccharomyces pombe|chr1|
SPAC26F1.13c	2	3.0%	|||leucine-tRNA ligase (predicted)|Schizosaccharomyces pombe|chr1|
SPAC1834.02	3	2.9%	|aro1||pentafunctional aromatic polypeptide|Schizosaccharomyces pombe|chr 1|
SPCC18B5.01c	3	2.9%	|bfr1|hba2, SPCPJ732.04c|ABC transporter family|Schizosaccharomyces pombe|chr 3|
SPAPYUK71.03c	2	2.9%	|||C2 domain|Schizosaccharomyces pombe|chr 1|
SPAPB15E9.01c	2	2.9%	||SPAPB18E9.06c|hypothetical protein|Schizosaccharomyces pombe|chr1|
SPAC2F7.16c	3	2.8%	|||phospholipase D (predicted)|Schizosaccharomyces pombe|chr1|
SPAC2G11.02	2	2.8%	|||hypothetical protein| Schizosaccharomyces pombe|chr1|
SPBC36.07	2	2.7%	|||RNA polymerase II (elongator subunit) (predicted)|Schizosaccharomyces pombe|chr 2|
SPAC13G6.01c	2	2.7%	|rad8|SPAC5H10.14c|zinc finger protein|Schizosaccharomyces pombe|chr 1|
SPCC417.07c	3	2.6%	|mbo1||involved in microtubule cytoskeleton organization and biogenesis (pers. comm. Sally McFall)| Schizosaccharomyces pombe|chr3|
SPBC11C11.04c	2	2.6%	|alp1||tubulin specific chaperone (cofactor D)|Schizosaccharomyces pombe|chr 2|
SPBC211.03c	2	2.5%	|||Sec7 domain|Schizosaccharomyces pombe|chr 2|
SPAC15A10.16	3	2.5%	|fat1|SPAC15E1.01|actin-binding protein (predicted)|Schizosaccharomyces pombe|chr 1|
SPAC1071.02	2	2.4%	|||involved in DNA repair (predicted)|Schizosaccharomyces pombe|chr1|
SPBC28F2.12	2	2.3%	|rpb1||DNA-directed RNA polymerase (II subunit) (large subunit) (PMID 2011520)|Schizosaccharomyces pombe|chr2|

<table>
<tr><td>SPAC688.10</td><td>2</td><td>2.3%</td><td>|rev3||DNA polymerase zeta (catalytic subunit)|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAC23C4.19</td><td>2</td><td>2.3%</td><td>|spt5||involved in transcriptional regulation|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC16D10.08c</td><td>2</td><td>2.3%</td><td>|||AAA family ATPase| Schizosaccharomyces pombe|chr2|</td></tr>
<tr><td>SPCC1919.10c</td><td>2</td><td>2.2%</td><td>|myo52||myosin (type V)| Schizosaccharomyces pombe|chr3|</td></tr>
<tr><td>SPCC1672.11c</td><td>2</td><td>2.2%</td><td>|||P-type ATPase (predicted) (PMID 12707717)|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPBC17D11.07c</td><td>2</td><td>2.2%</td><td>|rpn2||19S proteasome regulatory subunit| Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC1F8.03c</td><td>2</td><td>2.2%</td><td>|str3||membrane transporter| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAC1F5.04c</td><td>2</td><td>2.1%</td><td>|cdc12||formin|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAC6G9.10c</td><td>2</td><td>2.1%</td><td>|sen1||DNA2/NAM7 family| Schizosaccharomyces pombe|chr1|</td></tr>
<tr><td>SPAC1782.01</td><td>2</td><td>2.1%</td><td>||SPAPYUG7.07|conserved eukaryotic protein| Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPCC1620.14c</td><td>2</td><td>2.1%</td><td>||SPCC830.01c|SNF2 family| Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPCC290.03c</td><td>2</td><td>2.1%</td><td>|||nucleoporin|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPAC31A2.05c</td><td>2</td><td>2.1%</td><td>|mis4||adherin|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAC23D3.06c</td><td>2</td><td>2.1%</td><td>|||nucleoporin|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC19C7.02</td><td>2</td><td>2.0%</td><td>|ubr1|SPBC32F12.14|ubiquitin-protein ligase (E3)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAP27G11.10c</td><td>2</td><td>2.0%</td><td>|nup184||nucleoporin|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBPJ4664.02</td><td>3</td><td>1.9%</td><td>|||hypothetical protein| Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC19B12.03</td><td>2</td><td>1.9%</td><td>|bgs3||1,3-beta-glucan synthase (subunit) (PMID 12582133)| Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAPB24D3.09c</td><td>2</td><td>1.9%</td><td>|||ABC transporter family| Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAC1093.06c</td><td>5</td><td>1.8%</td><td>|dhc1|SPAC30C2.01c|dynein heavy chain (PMID 10855500)|Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPAPB1E7.07</td><td>2</td><td>1.8%</td><td>|||glutamate synthase (predicted)| Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPBC216.05</td><td>2</td><td>1.6%</td><td>|rad3||ATR (ATM) checkpoint kinase| Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPAC3G9.14</td><td>1</td><td>1.6%</td><td>|sak1||RFX domain| Schizosaccharomyces pombe|chr 1|</td></tr>
<tr><td>SPCC1281.01</td><td>2</td><td>1.5%</td><td>|ags1|mok1, SPCC17A7.01, SPCC338.01c|a-1,3-glucan synthase|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPBC16C6.02c</td><td>3</td><td>1.4%</td><td>|vps1302|vps13b|involved in intracellular protein transport (predicted)|Schizosaccharomyces pombe|chr 2|</td></tr>
<tr><td>SPCC23B6.03c</td><td>3</td><td>1.4%</td><td>|tel1||phosphotidylinositol kinase|Schizosaccharomyces pombe|chr 3|</td></tr>
<tr><td>SPAC23G3.02c</td><td>4</td><td>1.2%</td><td>|||peptide synthetase (predicted)|Schizosaccharomyces pombe|chr 1|</td></tr>
</table>

SPBP19A11.04c	2	1.1%	|mor2|cps12|involved in cellular morphogenesis (required) (PMID 12234926)|Schizosaccharomyces pombe|chr 2|
SPCC737.08	2	0.7%	|||midasin (predicted)|Schizosaccharomyces pombe|chr 3|