## Web Table F: Middle genes.

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|---|---|---|
| **Cell cycle regulators** | | |
| *cdc13* | SPBC582.03 | G2/mitotic-specific cyclin |
| *cdc25* | SPAC24H6.05 | M-phase inducer phosphatase; G2/M transition |
| *rem1* | SPBC16E9.17C | meiotic cyclin |
| *slp1* | SPAC821.08C | *CDC20/fizzy* family of APC activators; spindle assembly checkpoint protein |
| | SPAC13G6.08 | *CDC20/fizzy* family of APC activators |
| *mfr1 fzr1* | SPBC1198.12 | *CDC20/fizzy* family of APC activators, required for sporulation |
| *clp1 flp1* | SPAC1782.09C | dual specificity protein-tyrosine phosphatase; similar to *S. cerevisiae CDC14* |
| **Meiotic regulators** | | |
| *mde3* | SPBC8D2.19 | protein kinase; similar to *S. cerevisiae IME2* |
| *mes1* | SPAC5D6.08C | meiosis-II protein |
| *spo4* | SPBC21C3.18 | protein kinase involved in meiotic spindle formation |
| *spo6* | SPBC1778.04 | required for meiosis II and sporulation |
| **Condensin (some less than 4x induction)** | | |
| *cnd2* | SPCC306.03C | condensin subunit |
| *cnd1* | SPBC776.13 | condensin subunit |
| *cut3* | SPBC146.03C | condensin subunit; similar to *S. cerevisiae SMC4* |
| *cnd3* | SPCC188.03 | condensin subunit |
| *cut14* | SPBP4H10.06C | condensin subunit; similar to *S. cerevisiae SMC2* |
| **Mitosis/chromosome seggregation/spindle pole body components** | | |
| *pcp1* | SPAC6G9.06C | spindle pole body component; binds calmodulin; similar to *S. cerevisiae NUF1* |
| *ncd10* | SPBC11C11.03 | centromere associted spindle component; possibly involved in chromosome segregation; similar to *S. cerevisiae NCD80* |
| *dis1* | SPCC736.14 | microtubule and spindle pole body associated protein |
| *cut17* | SPCC962.02C | required for mitotic chromosome segregation |
| *sad1* | SPBC12D12.01 | spindle pole body associated protein |
| *alp4* | SPBC365.15 | putative gamma tubulin interacting spindle pole body associated protein |
| *cut12* | SPBC649.05 | spindle pole body component |
| *ark1* | SPCC320.13C | kinase; aurora homolog; required for spindle formation and chromosome segregation |
| *plo1* | SPAC23C11.16 | kinase; polo family ; involved in spindle formation and cytokinesis |
| *fin1* | SPAC19E9.02 | kinase; promoter of chromatin condensation |
| *mis6* | SPAC1687.20C | inner centromere protein |
| *cut2* | SPBC14C8.01C | securin; similar to *S. cerevisiae PDS1* |
| *ubc11* | SPCC1259.15C | ubiquitin conjugating enzyme |
| *klp5* | SPBC2F12.13 | kinesin-like protein; KIP3 subfamily |
| *klp6* | SPBC1685.15C | kinesin-like protein; KIP3 subfamily |
| **Anaphase-promoting complex (APC)** | | |
| *cut23* | SPAC6F12.14 | APC component; similar to *S. cerevisiae CDC23* |
| *cut4* | SPBC106.09 | APC component |
| *cut9* | SPAC6F12.15C | APC component |
| *nuc2* | SPAC17C9.01C | putative APC component |
| *apc1* | SPBC1A4.01 | APC component |
| *cut20 lid1* | SPAC19G12.01C | APC component; similar to *S. cerevisiae APC4* |
| *apc5* | SPAC959.09C | putative component of anaphase-promoting Complex (APC) |
| | SPAC343.03 | putative APC component; similar to *S. cerevisiae APC11* |
| | SPBP23A10.04 | putative APC component |
| *hcn1* | SPAC23C11.12 | APC component; similar to *S. cerevisiae CDC26* |
| **Ubiquitin/proteasome related** | | |
| | SPCC1682.12C | ubiquitin carboxyl-terminal hydrolase |
| | SPAC3A12.03C | zinc finger, C3HC4 type (possible E2) |
| *ubc6* | SPAC10F6.05C | putative ubiquitin-conjugating enzyme (EC 6.3.2.19) |

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|---|---|---|
| | SPAC12B10.01C | putative ubiquitin fusion degradation protein |
| *ufd2* | SPAC20H4.10 | ubiquitin fusion degradation protein-2 |
| *ubi4* | SPBC337.08C | ubiquitin family protein |
| *ubc16* | SPBC1198.09 | putative ubiquitin conjugating enzyme, E2 |
| *shp1 phs1* | SPBC409.05 | required for degradation of cig2p; putative *S. cerevisiae SKP1* homolog |
| *pof3* | SPCC338.16 | F-box protein |
| *pof2 sud1* | SPAC4D7.03 | F-box/WD-repeat protein |
| *pof11* | SPAC29E6.01 | F-box/WD repeat protein |
| *pof12* | SPBC56F2.01 | F-box protein |
| *tbp1* | SPAC3A11.12C | 19s proteasome regulatory subunit |
| | SPAC6F6.12 | putative nexin sorting protein; possibly involved in proteasome function by similarity to *S. cerevisiae SNX4* |
| **S phase** | | |
| *cdc23* | SPBC1347.10 | required for initiation of DNA replication; similar to *S. cerevisiae DNA43/MCM10* |
| *hsk1* | SPBC776.12C | kinase component of the Hsk1-Him1p/Dfp1p complex; S phase initiation; similar to *S. cerevisiae CDC7* |
| **DNA repair** | | |
| *hhp1* | SPBC3H7.15 | casein kinase i; required for DNA repair; similar to *S. cerevisiae HRR25* |
| *hhp2* | SPAC23C4.12 | casein kinase i homolog |
| *exo1* | SPBC29A10.05 | exonuclease i; Mismatch repair; 5'-3' exonuclease; similar *to S. cerevisiae EXO1* |
| *exo2* | SPAC17A5.14 | exonuclease ii |
| *msh6* | SPCC285.16C | *mutS* family DNA mismatch repair protein |
| *rhp23* | SPBC2D10.12 | nucleotide excision repair protein *S. cerevisiae RAD23*/ human HHR23A homolog |
| | SPAC22A12.01C | DNA repair protein for interstrand crosslinks; by similarity to S.cerevisiae *POS2* |
| **Morphogenesis** | | |
| *cdc42* | SPAC110.03 | *ras*-like GTPase; involved in mating; involved in cell morphology |
| *cka1 orb5* | SPAC23C11.11 | casein kinase ii, alpha chain; involved in cell growth regulation |
| *for3* | SPCC895.05 | formin-homology family; cell polarity and actin reorganization |
| *kin1* | SPBC4F6.06 | protein kinase; role in regulation of cell morphology |
| *ras1* | SPAC17H9.09C | *ras*-like protein; involved in pheromone response and cell morphogenesis |
| *ssp1* | SPCC297.03 | serine/threonine protein kinase; mediates a rapid osmotic stress response |
| *pob1* | SPBC1289.04C | required for cell polarity and elongation; similar to *S. cerevisiae BOI1* and *BOI2* |
| **Rho/rho regulators** | | |
| | SPAC1006.06 | putative *rho1* GDP-GTP exchange protein |
| | SPAC1565.02C | putative rho GTPase activating protein |
| | SPAC16A10.04 | *rho1*-like protein. |
| | SPAC20H4.11C | *rho1* protein paralogue; ras family |
| **Septins** | | |
| *spn2* | SPAC821.06 | septin |
| *spn5 mde9* | SPAC24C9.15C | septin |
| *spn6* | SPCC188.12 | septin |
| *spn7* | SPBC21.08C | septin |
| **Cytokinesis** | | |
| *cdc7* | SPBC21.06C | protein kinase; required for septum formation and cytokinesis |
| *cdc11* | SPCC1739.11C | involved in cytokinesis and septation; putative spindle pole body protein; similar to *S. cerevisiae NUD1* |
| *myo51* | SPBC2D10.14C | class V myosin; component of the cytokinetic actin ring |
| | SPBC17D1.07C | possible protein involved in cytokinesis by similarity to *S. cerevisiae IQG1* |
| **Other cytoskeleton** | | |
| | SPBC56F2.03 | actin related protein; *S. cerevisiae ARP10* homolog |
| | SPAC688.06C | very putative actin-related protein, regulator of microtubule stability by similarity to yeast *AME1* |
| | SPBC119.12 | myosin heavy chain-like coiled-coil protein |
| **Secretion/membrane traffic** | | |

| | | |
|---|---|---|
| *bet1* | SPAC23C4.13 | putative ER-Golgi v-SNARE |
| *bos1* | SPAP14E8.03 | ER to Golgi v-SNARE |
| *ykt6* | SPBC13G1.11 | synaptobrevin-like v-SNARE |
| *snc1* | SPAC6G9.11 | synaptobrevin homolog1 |
| *sso1* | SPCC825.03C | putative syntaxin plasma membrane (t-SNARE) |
| *ufe1* | SPCC895.04C | putative ER syntaxin (t-SNARE) |
| *sec9* | SPBC26H8.02C | component of t-SNARE complex |
| *ypt3* | SPAC18G6.03 | Golgi *rab11* protein |
| *hos1 ryh1* | SPAC4C5.02C | Golgi rab protein |
| | SPCC306.02C | putative rab-interacting protein by similarity |
| | SPAC4G8.04 | TBC domain protein; putative GTPase activating protein of rab-like GTPase |
| | SPBC530.01 | TBC domain protein; putative GTPase activating protein of rab-like GTPase |
| *gdi1 sec19* | SPAC22H10.12C | putative rab recycling protein |
| | SPBC4C3.04C | putative guanine nucleotide exchange factor |
| *pep7* | SPAC17G6.08 | putative *YPT5* effector with FYVE zinc finger; PI3P-binding |
| | SPCC285.14 | putative component of the TRAPP (Transport Protein Particle) complex involved in vesicular transport between the ER and the Golgi |
| *srp102* | SPAC23H4.07C | putative signal recognition particle receptor beta subunit |
| | SPBC36B7.03 | putative component of ER protein-translocation subcomplex; DNA J protein |
| *hut1* | SPBC839.11C | protein which maintains folding environment in secretory pathway |
| | SPCC4B3.02C | putative Membrane protein required for ER to Golgi transport; by similarity to *S. cerevisiae GOT1* |
| *sec16* | SPAC29B12.07 | putative protein required for vesicle formation in ER to Golgi transport |
| | SPAC1565.08 | *S. cerevisiae CDC48* homologue; transitional endoplasmic reticulum atpase |
| *emp24* | SPCC24B10.17 | putative component of COPII-coated vesicles |
| | SPBC691.02C | hypothetical protein; similar to *S. cerevisiae TIP20* required for protein transport from the ER to the Golgi |
| | SPBP8B7.24C | putative autophagy protein; by similarity to *S. cerevisiae AUT7* -mediates attachment of autophagosomes to microtubules; involved in sporulation |
| *sec23b* | SPBC776.04 | putative protein transport protein |
| *sly1* | SPCC74.01 | stxbp-*unc-18-SEC1* family vesicle trafficking protein |
| | SPAC4F8.01 | putative Class E vacuolar protein-sorting factor; similar to *S. cerevisiae DID4* |
| *vac8* | SPBC354.14C | putative vacuolar protein; beta-catenin family; similar to *S. cerevisiae VAC8* |
| *vps1* | SPAC767.01C | vacuolar sorting protein; dynamin family |
| *vps13a* | SPBC21C3.01C | putative vacuolar sorting protein |
| *vps24* | SPAC9E9.14 | putative endosomal vps protein complex subunit |
| *vps29* | SPAC15E1.06 | putative vacuolar sorting protein |
| *vps32 snf7* | SPAC1142.07C | putative vacuolar sorting protein |
| *vps9b* | SPBC29A10.11C | vacuolar sorting protein |
| **Complex lipid metabolism** | | |
| | SPAC22E12.16C | putative phosphatidylinositol 4-kinase |
| | SPCC1442.12 | CDP-diacylglycerol-serine O-phosphatidyltransferase |
| | SPBC16E9.18 | phosphatidylserine decarboxylase proenzyme |
| | SPAC589.09 | putative phosphatidylinositol metablolism |
| | SPCC4F11.04C | putative transferase; possibly involved in the production of sphingolipids |
| | SPBC21B10.11 | putative dolichol phosphate mannose regulatory protein |
| **GPI-anchor-synthesis** | | |
| | SPBC3D6.07 | N-acetylglucosaminyl-phosphatidylinositol |
| *gpi1* | SPBC30D10.11 | N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein gpi1. |
| | SPBC27B12.06 | putative Protein involved in glycosylphosphatidylinositol biosynthesis; by similrity to *S. cerevisiae GPI13* |
| | SPBC839.08C | putative protein required for glycosylphosphatidylinositol (GPI) anchor synthesis |
| | SPCC1450.15 | putative short-chain dehydrogenase; possibly involved in GPI biosynthesis, by similarity to human PIG-F and *S. cerevisiae GPI11* |

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| **Glycoprotein metabolism** | | |
| | SPBC56F2.10C | dolichyl-phosphate beta-glucosyltransferase |
| | SPAC23C4.14 | putative beta-mannosyltransferase |
| *och1* | SPAC1006.05C | 1,6-mannosyltransferase; involved in the outer chain elongation of N-linked oligosaccharides |
| **Cell wall** | | |
| | SPBC342.03 | putative *GAS1* family protein; glucanosyltransferase, glycophospholipid-anchored surface glycoprotein; cell wall associated |
| *scc1* | SPBC32F12.01C | sphingomyelinase family similarity, required for cell wall formation |
| *mok11* | SPAC1527.01 | alpha-glucan synthase |
| *mok13* | SPBC16D10.05 | alpha-glucan synthase |
| *mok14* | SPCC63.04 | alpha-glucan synthase |
| *bgs2 meu21* | SPAC24C9.07C | 1,3-beta-glucan synthase subunit; required for spore formation |
| *chs1* | SPAC13G6.12C | chitin synthase 1; essential for normal spore formation |
| *chs2* | SPBC1709.01 | chitin synthase 2 |
| *pck1* | SPAC17G8.14C | protein kinase C |
| | SPAC1B2.03C | *GNS1/SUR4* family protein; putative fatty acid elongation protein |
| | SPAC1639.01C | *SUR4* family protein; putative fatty acid elongation protein |
| *exg2* | SPAC12B10.11 | putative exo-1,3-beta-d-glucanohydrolase |
| **Transcriptional regulation** | | |
| | SPBC19G7.04 | conserved protein; possible transcriptional regulator; may contain HMG box |
| | SPBP8B7.30C | binuclear cluster DNA-binding domain |
| | SPAPB1A11.04C | binuclear cluster DNA-binding domain |
| | SPAC959.06C | similarity to viral late transcription factor |
| *atf21* | SPBC2F12.09C | atf creb-family transcription factor |
| *atf31* | SPAC22F3.02 | atf creb-family transcription factor |
| *mei4* | SPBC32H8.11 | fork head protein type transcription factor |
| | SPBC16G5.15C | fork head protein type transcription factor |
| | SPAC1142.08 | fork head protein type transcription factor |
| *rsv1* | SPBP4H10.09 | stationary phase viability protein (zinc finger) |
| | SPBC14C8.17C | putative transcriptional. activator; putative SAGA complex; similar to *S. cerevisiae SPT8* |
| | SPBC1861.07 | putative regulator of transcription elongation, elongin c homolog |
| | SPCC18.03 | shuttle craft like transcriptional regulator with 8 zf-NF-X1 zinc fingers and R3H domain |
| | SPBC1826.01C | transcriptional Accessory Protein (TAF) involved in RNA polymerase II transcriptional, member of the Snf2p family of DNA helicases |
| *crk1 mop1 mcs5* | SPBC19F8.07 | cdk-activating kinase; putative transcription initiation factor TFIIH subunit; cyclin-dependent kinase activating kinase (CAK); similar to *S. cerevisiae KIN28* |
| | SPAC12G12.05C | putative transcription initiation factor TFIID subunit; component of TAF(II) complex (TBP-associated protein complex); putative component of the SAGA complex |
| | SPAC343.11C | putative transcriptional regulatory protein; PHD finger; similarity to retinoblastoma binding proteins |
| | SPCC584.02 | putative metal-binding regulatory protein |
| *ccr4* | SPCC31H12.08C | putative *CCR4*-Not complex; similar to *S. cerevisiae* carbon catabolite repressor protein 4 |
| *clr4* | SPBC428.08C | histone H3 methyltransferase; mating-type locus protein; centromeric silencing protein; SET domain; chromodomain |
| *png1* | SPAC3G9.08 | conserved protein; PHD finger domain; putative histone acetyltransferase complex; similar to *S. cerevisiae YNG2* |
| | SPAC13G7.10 | hypothetical Myb-like DNA-binding protein |
| **Checkpoint** | | |
| *mik1* | SPBC660.14 | mitosis inhibitor protein kinase; DNA replication checkpoint control; similar to *S. cerevisiae SWE1* |
| *chk1 rad27* | SPCC1259.13 | protein kinase; DNA damage checkpoint; similar to *S. cerevisiae CHK1* |
| *brc1* | SPBC582.05C | BRCT domain protein; (cell-cycle checkpoint superfamily) |
| *dma1* | SPAC17G8.10C | component of the spindle assembly checkpoint; required to prevent septum formation and |

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|---|---|---|
| | | premature exit from mitosis if spindle function is compromised |
| **Splicing** | | |
| | SPAC4F10.13C | possibly involved in splicing-by similarity with *S. cerevisiae* homologue *SMY2* |
| | SPAC145.03 | putative pre-mrna splicing factor; ATP-dependent RNA helicase |
| | SPBC3E7.13C | putative pre-MRNA splicing factor; similar to *S. cerevisiae SYF2* |
| *dsk1* | SPBC530.14C | serine/threonine protein kinase; pre-mRNA splicing factor specific kinase |
| **Stress/heat shock** | | |
| *hsp16* | SPBC3E7.02C | heat shock protein 16-complex expression profile!! |
| | SPAC13G7.02C | heat shock protein 70 |
| *pyp2* | SPAC19D5.01 | protein-tyrosine phosphatase 2 |
| *uvi15* | SPBC649.04 | protien required for the maintenance of viability of cells in stationary phase and in starvation condition; induced by UV, alkylating agents and heat shock |
| | SPBC713.11C | UPF0057 family protein; possible stress response protein |
| **Trehalose synthesis –probably related to stress resistance** | | |
| *tpp1* | SPAC19G12.15C | trehalose-6P phosphatase |
| *tps1* | SPAC328.03 | alpha,alpha-trehalose-phosphate synthase [UDP-forming] |
| | SPAC22F8.05 | putative alpha,alpha-trehalose-phosphate synthase |
| | SPCC1322.04 | putative UTP-glucose-1-phosphate uridylyltransferase |
| | SPBC32F12.10 | putative phosphoglucomutase |
| **Transporters** | | |
| | SPAC2E1P3.02C | ammonium transporter |
| *meu22* | SPBC19F8.06C | APC amino acid transporter; meiotic expression upregulated |
| | SPCC4B3.13 | conserved protein; UPF0013 protein family; putative membrane transporter |
| | SPCC794.04C | MFS drug efflux transporter of unknown specificity |
| *ght5* | SPCC1235.14 | MFS glucose transporter. |
| *ght6 meu12* | SPCC1235.13 | MFS glucose transporter; meiotic expression upregulated |
| | SPCC61.01C | MFS multidrug efflux transporter |
| | SPBC947.06C | MFS multidrug efflux transporter |
| | SPAC1002.16C | MFS transporter of unknown specificity |
| | SPCC548.06C | putative glucose transporter protein; highly similar to *ght5* |
| | SPAC4F10.16C | P-type calcium ATPase |
| | SPAC6C3.06C | P-type calcium ATPase |
| | SPBC887.12 | P-type calcium ATPase |
| | SPAPB2B4.04C | putative P-type calcium ATPase |
| | SPAC3A12.06C | CaCA sodium/calcium exchanger |
| | SPCC1840.12 | major facilitator superfamily member |
| **Metabolic** | | |
| | SPBC3H7.03C | 2-oxoglutarate dehydrogenase E1 component |
| | SPBC725.14 | acetylglutamate synthase |
| | SPAC13G7.05 | acyl-CoA:sterol acyltransferase |
| *dps* | SPBPJ4664.01 | decaprenyl diphosphate synthase |
| *idh1 glu3* | SPAC11G7.03 | isocitrate dehydrogenase (NAD+) subunit 1 ; mitochondrial |
| | SPAC11D3.10 | nifS homolog, putative aminotransferase |
| *ndk1* | SPAC806.07 | nucleoside diphosphate kinase |
| | SPBC83.11 | phosphate-phosphoenolpyruvate translocator precursor |
| | SPAC1952.09C | probable acetyl-CoA hydrolase |
| | SPAC513.05 | probable alpha-mannosidase |
| | SPBC1773.08C | probable mannosyltransferase |
| | SPBP8B7.29 | probable para-aminobenzoate synthase |
| *coq3* | SPCC162.05 | putative 3-demethylubiquinone-9 3-methyltransferase; 4th step of the coenzyme q (ubiquinone) biosynthesis pathway |
| | SPBC2D10.09 | putative 3-hydroxyisobutyryl-coenzyme a hydrolase; Enoyl-CoA isomerase family |
| | SPBC17G9.06C | putative acetyltransferase;Pfam-B_12207; Pfam-B_5757; simlar to bacterial siderophore |

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|---|---|---|
| | | bioynthesis protein |
| | SPBC8E4.05C | putative adenylosuccinate lyase |
| | SPCC965.08C | putative alanine racemase |
| | SPCC569.07 | putative aromatic aminotransferase |
| | SPAC9.05 | putative ATP-dependent RNA helicase |
| | SPBC30D10.07C | putative biotin-protein ligase |
| | SPCC417.12 | putative carboxylesterase-lipase family member |
| | SPCC1827.02C | putative cholinephosphate cytidylyltransferase |
| | SPAC23A1.14C | putative cystathionine gamma-synthase |
| | SPAC959.05C | putative disulphide isomerase; thioredoxin domain |
| | SPAC1039.11C | putative family 31 glucosidase |
| | SPBPB2B2.12C | putative gal10 bifunctional protein; includes UDP-glucose 4-epimerase |
| | SPBPB2B2.13 | putative galactokinase |
| | SPAC4G9.12 | putative glucokinase |
| | SPAC24B11.05 | putative haloacid dehalogenase-like hydrolase |
| | SPBC30D10.14 | putative hydrolase |
| | SPBC947.15C | putative mitochondrial NADH dehydrogenase that catalyzes cytosolic NADH oxidation; by similarity to *S. cerevisiae YMR145C* |
| | SPCC1020.13C | putative phospholipase |
| | SPAC144.12 | putative ribose 5-phosphate isomerase |
| | SPCPJ732.02C | putative xylulose kinase |
| | SPCC1682.11C | similarity to NADH dehydrogenase (ubiquinone) subunit 1; by multiple alignment |
| | SPAC23C4.16C | very putative phospholipase |
| | SPBC1778.03C | putative NADH pyrophosphatase I of the Nudix family of hydrolases; by similarity to *S. cerevisiae* NYP1 |
| | SPBC1683.07 | alpha-glucosidase |
| | SPBC646.03 | putative glutamyl-tRNA amidotransferase subunit |
| | SPAC3F10.06C | putative initiator tRNA phosphoribosyl transferase |
| | SPAC9G1.10C | putative inositol polyphosphate phosphatase |
| | SPAC11G7.05C | putative malonyl coa-acyl carrier protein transacylase (EC 2.3.1.39) |
| | SPAC6G10.06 | hypothetical protein; possible reductase |
| | SPAC13C5.05C | N-acetylglucosamine-phosphate mutase |
| | SPCC1840.05C | putative phosphomannomutase |
| **Transposons** | | |
| *wtf1* | SPCC1906.03 | hypothetical wtf protein |
| *wtf10* | SPCC1620.02 | hypothetical wtf protein |
| *wtf11 meu24* | SPCC1281.08 | hypothetical wtf protein |
| *wtf12* | SPCC162.04 | hypothetical wtf protein |
| *wtf13* | SPCC548.03C | hypothetical wtf protein |
| *wtf2* | SPCC970.11C | hypothetical wtf protein |
| *wtf3* | SPCC1739.15 | hypothetical wtf protein |
| *wtf4* | SPCC794.02 | hypothetical wtf protein |
| *wtf5* | SPCC285.07C | hypothetical wtf protein |
| *wtf6* | SPCC1906.04 | hypothetical wtf protein |
| *wtf7* | SPCC1183.10 | hypothetical wtf protein |
| *wtf8* | SPCC1450.08C | hypothetical wtf protein |
| *wtf9* | SPCC1919.06c | hypothetical wtf protein |
| | SPAC2E12.05 | hypothetical wtf protein, pseudogene |
| **Non-coding RNAs** | | |
| *meu11* | AB054531 (EMBL) | antisense RNA |
| *meu16* | SPAC15A10 | putative non-coding RNA; possibly antisense SPAC15A10.10 |
| *meu19* | AB0545303 | putative non-coding RNA |
| | cosmid SPAC27E2 | putative non-coding RNA; misc_RNA_1.1.28 |

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|---|---|---|
| | cosmid SPAC1B2 | putative non-coding RNA; misc_RNA_1.1.46.RC |
| **Sequence orphans** | | |
| | SPAC1006.04C | hypothetical protein; sequence orphan; predicted coiled-coil |
| | SPAC10F6.07C | hypothetical protein; sequence orphan |
| | SPAC11H11.02C | hypothetical protein; sequence orphan; 8 predicted transmembrane helices |
| | SPAC1250.02 | hypothetical protein; sequence orphan |
| | SPBC1271.06C | hypothetical protein; sequence orphan |
| | SPBC146.11C | hypothetical protein; sequence orphan; 2 predicted transmembrane helices |
| | SPBC14C8.11C | hypothetical protein; sequence orphan |
| | SPBC1539.02 | hypothetical protein; sequence orphan |
| | SPBC15D4.12C | hypothetical protein; sequence orphan |
| | SPAC1610.04 | hypothetical protein; sequence orphan |
| | SPCC1620.03 | hypothetical protein; sequence orphan |
| | SPAC1687.10 | hypothetical protein; sequence orphan; predicted coiled-coil |
| | SPBC16E9.07 | hypothetical protein; sequence orphan |
| | SPBC16E9.08 | hypothetical protein; sequence orphan; predicted coiled-coil |
| | SPAC1782.04 | hypothetical protein; sequence orphan |
| | SPAC17G8.12 | hypothetical protein; sequence orphan |
| | SPAC17H9.03C | hypothetical protein; sequence orphan |
| | SPAC212.02 | hypothetical protein; sequence orphan; telomeric region |
| | SPBC21D10.08C | hypothetical protein; sequence orphan |
| | SPAC22A12.02C | hypothetical protein; sequence orphan |
| | SPCC24B10.14C | hypothetical protein; sequence orphan |
| | SPAC24H6.08 | hypothetical protein; sequence orphan |
| | SPBC25B2.07C | hypothetical proline-serine rich protein; sequence orphan |
| | SPAC25H1.04 | hypothetical protein; sequence orphan |
| | SPAC26F1.05 | hypothetical protein; sequence orphan |
| | SPBC26H8.13C | hypothetical protein; sequence orphan |
| | SPAC27D7.05C | hypothetical protein; sequence orphan |
| | SPAC27D7.12C | hypothetical protein; sequence orphan |
| | SPAC27E2.11C | hypothetical protein; sequence orphan; putative glycoprotein |
| | SPAC29A4.12C | hypothetical protein; sequence orphan |
| | SPAC29A4.14C | hypothetical protein; sequence orphan |
| | SPAC2E1P5.02C | hypothetical protein; sequence orphan; 3 predicted transmembrane helices |
| | SPBC2G2.10C | hypothetical protein.; sequence orphan |
| | SPBC31F10.17C | hypothetical protein; sequence orphan |
| | SPCC31H12.06 | hypothetical protein; sequence orphan; 12 predicted transmembrane helices; predicted N-term signal sequence |
| | SPBC32F12.08C | hypothetical protein; sequence orphan |
| | SPCC338.02 | hypothetical protein; sequence orphan |
| | SPAC3F10.05C | hypothetical protein; sequence orphan |
| | SPCC4F11.03C | hypothetical protein; sequence orphan |
| | SPAC4F8.08 | hypothetical protein; sequence orphan |
| | SPAC56F8.14C | hypothetical protein; sequence orphan |
| | SPAC5D6.02C | hypothetical protein; sequence orphan |
| | SPAC5D6.10C | hypothetical protein; sequence orphan |
| | SPAC607.10 | hypothetical protein; sequence orphan; predicted N-term signal sequence |
| | SPCC645.11C | hypothetical protein; sequence orphan |
| | SPBC651.06 | hypothetical protein; sequence orphan |
| | SPBC651.07 | hypothetical protein; sequence orphan |
| | SPBC660.08 | hypothetical protein; sequence orphan; predicted coiled-coil region |
| | SPBC660.09 | hypothetical protein; sequence orphan |
| | SPCC663.15C | hypothetical protein; sequence orphan |

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|---|---|---|
| | SPBC336.15 | hypothetical serine-rich protein; sequence orphan |
| | SPAC6F6.16C | hypothetical protein; sequence orphan |
| | SPAC6F6.18C | hypothetical protein; sequence orphan |
| | SPBC725.12 | hypothetical protein; sequence orphan |
| | SPAC7D4.11C | hypothetical protein; sequence orphan |
| | SPBC83.04 | hypothetical protein; sequence orphan |
| | SPBC28E12.01C | hypothetical protein; sequence orphan |
| | SPACUNK4.15 | hypothetical protein; sequence orphan |
| | SPCP1E11.03 | hypothetical protein; sequence orphan |
| | SPBP35G2.03C | hypothetical protein; sequence orphan |
| | SPAPB17E12.09 | hypothetical protein; sequence orphan |
| *pdh1* | SPCC1235.08C | hypothetical protein; sequence orphan; predicted N-terminal signal sequence; 7 predicted transmembrane helices |
| | SPBC32H8.02C | hypothetical protein; sequence orphan |
| | SPBP22H7.04 | hypothetical protein; sequence orphan |
| | SPAC13C5.06C | hypothetical protein; sequence orphan |
| | SPBC13E7.06 | hypothetical protein; sequence orphan; predicted coiled-coil region |
| | SPCC1620.07C | hypothetical protein; sequence orphan; predicted N-terminal signal sequence; 2 predicted transmembrane helicies |
| | SPCC1682.03C | hypothetical protein; sequence orphan |
| | SPCC1682.15 | hypothetical protein; sequence orphan; PXA domain and PX domain; implicated in intracellular signalling |
| | SPCC16C4.17 | hypothetical serine rich protein; sequence orphan |
| | SPCC1795.08C | hypothetical protein; sequence orphan |
| | SPCC188.07 | hypothetical protein; sequence orphan; putative coiled-coil region |
| | SPBC19C2.06C | hypothetical protein; sequence orphan |
| | SPAC1A6.08C | hypothetical protein; sequence orphan |
| | SPAC1B3.20 | hypothetical protein with confirmed intron; sequence orphan |
| | SPAC23C4.07 | hypothetical protein; sequence orphan |
| | SPAC24H6.06 | hypothetical protein; sequence orphan; putative coiled-coil region |
| | SPBC3H7.14 | hypothetical protein; sequence orphan |
| | SPAC4F10.08 | hypothetical protein; sequence orphan; 4 predicted transmembrane helices |
| | SPAC4H3.11C | hypothetical protein; sequence orphan; predicted coiled-coil region |
| | SPAC630.15 | hypothetical protein; sequence orphan |
| | SPCC830.04C | hypothetical protein; sequence orphan |
| | SPAC8C9.09C | hypothetical protein; sequence orphan |
| | SPBC21C3.17C | hypothetical protein; sequence orphan |
| | SPBC2G2.07C | hypothetical protein; Pfam-B_20797; possibly *S. pombe* specific; similar to *S. pombe* SPAC23A1.17c |
| | SPAC1348.07 | hypothetical protein; duplicated at *S. pombe* telomeres; possibly *S. pombe* specific; 3 predicted transmembrane helices; highly similar to *S. pombe* SPAC212.01c; highly similar to *S. pombe* SPAC1348.01 |
| | SPAC212.04C | hypothetical protein; duplicated in *S. pombe* telomeric region; possibly *S. pombe* specific; highly similar to SPAC212.01c etc |
| | SPAC212.01C | hypothetical protein; duplicated region in *S. pombe* telomeric region; possible fortuitous reading frame; possibly *S. pombe* specific |
| | SPBPB2B2.07C | hypothetical protein; duplicated telomeric reading frame; or miscellaneous cellular RNA; possibly *S. pombe* specific |
| | SPAC1348.01 | hypothetical protein; duplicated telomeric region; has 4 predicted transmembrane helix; possibly *S. pombe* specific; has late log phase cDNA; highly similar to *S. pombe* SPAC212.01c; highly similar to *S. pombe* SPAC1348.07 |
| | SPCC622.03C | hypothetical protein; possibly *S. pombe* specific |
| | SPAC750.06C | hypothetical protein; possibly *S. pombe* specific; highly similar to *S. pombe* SPAC212.01; highly similar to SPBPB2B2.20c |
| | SPAC977.06 | hypothetical protein; possibly *S. pombe* specific; similar to *S. pombe* SPAC1348.07, |

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|---|---|---|
| | | SPAC1348.01, SPAC750.06, and SPAC212.01 |
| | SPAC8F11.05C | hypothetical protein; similar to *S. pombe* mde1p; possibly *S. pombe* specific; likely to play a role in meiosis or sporulation- by similarity |
| *mde1* | SPAC16E8.05C | requires mei4p for transcriptional activation; similar to *S. pombe* SPAC8F11.05c; possibly *S. pombe* specific |
| *meu23* | SPCC613.11C | protein with Pfam-B_13958 domain; *S. pombe* specific |
| | SPBC1861.06C | protein with Pfam-B_8647 domain; *S. pombe* specific |
| | SPAC11G7.06C | protein with Pfam-B_8647 domain; *S. pombe* specific |
| | SPAC4G9.07 | protein with Pfam-B_8647 domain; *S. pombe* specific |
| | SPAC10F6.15 | protein with Pfam-B_8647 domain; *S. pombe* specific |
| | SPBC106.08C | hypothetical repeat containing protein; possibly *S. pombe* specific |
| | SPCC330.04C | biased repeat-containing protein; possibly *S. pombe* specific |
| | SPBC4C3.08 | hypothetical protein; possibly *S. pombe* specific |
| *meu27* | SPCC1259.14C | protein with Pfam-B_8647 domain; *S. pombe* specific |
| **Others** | | |
| | SPAP27G11.03 | hypothetical protein; similar to *S. cerevisiae CDC123* |
| | SPAC26H5.11 | hypothetical protein; similar to *S. cerevisiae SPO1* which is involved in spore wall formation; PH (pleckstrin homology) domain |
| | SPAC5D6.04 | hypothetical protein; similar to *S. cerevisiae* YBR287W; 6 predicted transmembrane helices |
| | SPAC694.03 | hypothetical protein; similar to *S. cerevisiae* YCL047C |
| | SPAC589.12 | hypothetical protein; similar to *S. cerevisiae* YCR017C- integral membrane protein involved in drug sensitivity; 20 predicted TM helices |
| | SPCC4G3.11 | hypothetical protein; similar to *S. cerevisiae* YDL089W (low); 4 predicted transmembrane helices |
| | SPAC57A7.05 | hypothetical protein; similar to *S. cerevisiae* YDL231C at the C-term; 11 predicted transmembrane helices |
| | SPBC146.10 | hypothetical protein; similar to *S. cerevisiae* YDR262W (low) |
| | SPBC36B7.02 | hypothetical protein; similar to *S. cerevisiae* YDR346C and paralogs; low similarity to NIFD/NIFK/NIFE/NIFN family |
| | SPAC20H4.01 | hypothetical protein; similar to *S. cerevisiae* YDR398W which is null lethal |
| | SPAC24H6.01C | hypothetical protein; similar to *S. cerevisiae* YGL084C |
| | SPBC19C2.11C | hypothetical protein; similar to *S. cerevisiae* YGL219C; possibly fungal specific |
| | SPAC105.02C | hypothetical protein; similar to *S. cerevisiae* YGL242C; similarity to ankyrin |
| | SPAC1F3.09 | hypothetical protein; similar to *S. cerevisiae* YGR093W |
| | SPAC6G10.03C | hypothetical protein; similar to *S. cerevisiae* YGR110W- which is induced during aerobic growth; containd Pfam abhydrolase motif, alpha/beta hydroalse fold |
| | SPAC630.09C | hypothetical protein; similar to *S. cerevisiae* YGR205W |
| | SPAC823.16C | hypothetical protein; similar to *S. cerevisiae* YGR223C |
| | SPBPB2B2.02 | hypothetical protein; similar to *S. cerevisiae* YGR263C; low similarity to esterases |
| | SPAC8F11.06 | hypothetical protein; similar to *S. cerevisiae* YHR036W |
| | SPAC144.10C | hypothetical protein; similar to *S. cerevisiae* YJL091C; 13 predicted transmembrane helices |
| | SPBC119.16C | hypothetical protein; similar to *S. cerevisiae* YKL047W |
| | SPBC27.02C | hypothetical protein; similar to *S. cerevisiae* YKL052 C |
| | SPAC9B6.13 | hypothetical protein; similar to *S. cerevisiae* YLL032C (low) |
| | SPAC14C4.05C | hypothetical protein; similar to *S. cerevisiae* YML034W a protein with cell cycle regulated expression; ATP/GTP-binding site motif; subcellular localization of GFP fusion- Nuclear rim |
| | SPBC32F12.12C | hypothetical protein; similar to *S. cerevisiae* YMR071C |
| | SPBC215.14C | hypothetical protein; similar to *S. cerevisiae* YMR077C; predicted coiled-coil |
| | SPAC15A10.05C | hypothetical protein; similar to *S. cerevisiae* YNL200C |
| | SPAC6G9.03C | hypothetical protein; similar to *S. cerevisiae* YNL206C; similarity to SSRP proteins |
| | SPBC146.05C | hypothetical protein; similar to *S. cerevisiae* YNL245C which is null lethal; predicted coiled coil |

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|---|---|---|
| | SPAC6B12.09 | hypothetical protein; similar to *S. cerevisiae* YOL093W |
| | SPAC22F3.04 | hypothetical protein; similar to *S. cerevisiae* YOR093C |
| | SPAC8C9.16C | hypothetical protein; similar to *S. cerevisiae* YPL196W |
| | SPAC30C2.08 | hypothetical protein; similar to *S. cerevisiae* YPl260W; putative surface protein adhesion molecule |
| | SPBC30D10.09C | hypothetical protein; similar to *S. cerevisiae* YPR027w; putative integral membrane protein |
| | SPAC56F8.05C | hypothetical protein; similar to *S. cerevisiae* YPR148C and YIL041W; possibly fungal specific |
| | SPAC1296.04 | hypothetical protein; this *may* be the ortholog of *S. cerevisiae SPO73*; similarity is *very low* but they are reciprocal best hits |
| | SPAC25H1.03 | hypothetical protein with low similarity to *Drosophila* CG7053; human cDNA FLJ11773 |
| | SPAPYUG7.06 | hypothetical protein; conserved domain in *Arabidopsis*; *C. elegans*, *Drosophila* and human, motif Y.G..YHL{IM}.{KR}NCNHF |
| | SPAC6C3.07 | hypothetical protein; ankiryin repeats (5) |
| | SPAC14C4.10C | hypothetical protein; Mut-T like domain- family of NUDIX hydrolases; hydrolysis of nucleoside diphosphate derivatives |
| | SPCC584.14 | hypothetical protein; Pfam-B_13174 |
| | SPAC12B10.16C | hypothetical protein; Pfam-B47901; N-terminal signal peptide |
| | SPBC13E7.05 | hypothetical protein; has transmembrane domain Pfam-B_29230; similar to *C. elegans* b0491.1 protein; *Drosophila* CG9865 protein; and *S. cerevisiae* YJR013W, but has large N terminal extension |
| | SPAC3A12.13C | hypothetical protein; low similarity to *Drosophila* CG12131 |
| | SPAC56E4.05 | hypothetical protein; similar to *A. thaliana* T29E15.14 and T4G30500 (low, by multiple alignment) |
| | SPBC32H8.04C | conserved hypothetical protein; similar to *S. cerevisiae* YDR339C |
| | SPBC12C2.04 | conserved hypothetical protein |
| | SPAC3G6.03C | conserved hypothetical protein |
| | SPAC3H1.03 | conserved hypothetical protein |
| | SPAC458.06 | conserved hypothetical protein |
| | SPAC24C9.05C | conserved hypothetical protein; 4 CBS domains; Octicosapeptide repeat |
| | SPBC577.12 | conserved hypothetical protein; *DUF10* |
| | SPAC1952.13 | conserved hypothetical protein; may be involved in respiration by similarity to *SMP2* |
| | SPCC1902.02 | conserved hypothetical protein; similar to *S. cerevisiae PAM1* |
| | SPCC31H12.02C | conserved hypothetical protein; similar to *S. cerevisiae* YBR054W ; similarity to heat shock protein |
| | SPBC1346.03 | hypothetical protein |
| | SPAC16A10.08C | hypothetical protein |
| | SPCC16C4.01 | hypothetical 51.9 kd protein |
| | SPCC1183.09C | hypothetical protein; Uncharacterized protein family UPF0057; predicted N terminal signal sequence |
| | SPAC4A8.02C | hypothetical protein; UPF0047 family |
| *meu15* | SPCPJ732.03 | meiotic expression upregulated |
| *meu29* | SPAC25H1.05 | meiotic expression upregulated |
| *meu31* | SPAC1A6.06C | meiotic expression upregulated |
| *meu1 meu2* | SPAC1556.06 | meiotic expression upregulated; leucine zipper; NLS; coiled-coil |
| *meu6* | SPBC428.07 | hypothetical lysine rich; putative coiled-coil region; putative NLS |
| *isp3 meu4* | SPAC1F8.05 | sexual differentiation process protein isp3; meiotic expression upregulated |
| *mde4* | SPBC6B1.04 | mei4p dependent expression |
| *mde2* | SPBC31F10.08 | mei4p dependent expression |
| *mde6* | SPAC15A10.10 | mei4p-dependent expression; Muskelin homolog; Kelch repeat family |
| *meu25* | SPBC27.03 | protein with low similarity to a region of *S. cerevisiae* YJL020C |
| | SPCC1223.04C | putative methyl-transferase |
| *ufd2* | SPAC145.04 | putative ubiquitin fusion degradation protein |
| | SPBC4.03 | unknown function |

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|---|---|---|
| | SPAC6B12.06C | unknown function |
| *cyp6* | SPBC17G9.05 | cyclophilin-RNAinteracting protein |
| *alp41* | SPAC22F3.05C | adp-ribosylation factor-like protein |
| | SPBC4B4.10C | apoptosis specific protein homolog; *S. cerevisiae* homolog *APG5* is involved in autophagy |
| | SPAC4F10.07C | appears to localize to the nucleolar region; possible involvement in autophagy by similarity to *S. cerevisiae APG13* |
| *cid2* | SPCC338.04 | caffeine-induced death protein Cid2p |
| *cam1* | SPAC3A12.14 | calmodulin |
| | SPAC29A4.05 | calmodulin |
| *cki2* | SPBP35G2.05C | casein kinase I homolog |
| *crm1 caf2* | SPAC1805.17 | chromosome region maintenance protein 1 |
| *cid11* | SPBC1685.06 | cid1-related putative nucleotidyl transferase; putative DNA polymerase kappa |
| | SPAC6G9.04 | pleckstrin homology domain |
| | SPBC1D7.03 | cyclin-like protein |
| | SPBC13G1.10C | DEAD box helicase; similar to *S. cerevisiae SLH1*; mRNA turnover/processing |
| *mip1* | SPCC24B10.22 | DNA polymerase gamma; mitochondrial |
| | SPCC364.02C | ES2 nuclear protein (deleted in Di George syndrome) homologue; Pfam-B_38208 |
| *etd1* | SPAC1006.08 | |
| | SPAC589.11 | eukaryotic conserved hypothetical protein; similar to human ds-1 protein which shows modulated expression during colon carcinoma cell differentiation |
| | SPAC2G11.04 | G-patch domain protein |
| *git5* | SPBC32H8.07 | G-protein beta subunit |
| | SPAC222.14C | GTP-binding protein; similar to S. cerevisiae YOR165W- similarity in the C-terminal region to human *GBP1*, an interferon-induced GTP-binding protein |
| | SPBC3E7.15C | homology to longevity assurance protein. |
| | SPAC22A12.13 | human downs syndrome critical region-like |
| | SPBC1773.09C | hypothetical DNA-J protein |
| | SPCC4B3.04C | hypothetical UPF0028 family protein; cyclic nucleic acid binding family protein |
| | SPBC30D10.08 | mitochondrial genome maintenance protein precursor. |
| | SPBC11G11.01 | possibly involved in mitochondrial division by similarity to *S. cerevisiae FIS1* |
| | SPAC589.06C | probable membrane protein involved in the regulation of inorganic phosphate transport; *S. cerevisiae PHO88* homologue |
| *abc1* | SPAC9E9.12C | involved in assembly of cytochrome bc1 complex |
| | SPBC3B9.17 | HesB-like domain; required for iron metabolism by similarity to *S. cerevisiae ISA1* |
| | SPCC645.03C | HesB-like domain; required for iron metabolism by similarity to *S. cerevisiae ISA1* |
| *kms2* | SPBC947.12 | protein with possible coiled coil; similar to *S. pombe kms1* a protein required for the formation of meiotic prophase-specific nuclear architecture |
| | SPCC16A11.04 | protein with PX and PXA domain-associated with intracellular signalling pathways; RGS domain- regulator of G protein signalling; similar domain arrangement to human SNX13- sorting nexin; similar to *S. cerevisiae MDM1* Intermediate filament protein involved in organelle inheritance and in the regulation of mitochondrial morphology |
| | SPBC3E7.04C | pseudo; gag acceptor, and out of frame |
| | SPAC212.05C | pseudogene; fragment similar to hypothetical protein-duplicated in telomeric region |
| | SPAC23C11.04C | putative DNA 3' phosphatase; similar to *S. cerevisiae TPP1*; Pfam-B_11748 domain |
| | SPAC6B12.08 | putative DNA-J-like protein |
| | SPAC1782.08C | putative exonuclease |
| | SPAC1002.11 | putative glycosylphosphatidylinositol anchor attachment protein |
| | SPAC5D6.09C | putative GPR/FUN34 family protein |
| | SPAC20H4.02 | putative guanine nucleotide binding protein similar to YOR223w. |
| | SPAC25B8.01 | putative MAPR family steroid-binding protein; similarity to steroid membrane receptors |
| | SPCC1322.06 | Putative member of the RanBP7-importin-beta-Cse1p superfamily |
| | SPCC16A11.16C | putative membrane glycoprotein Pfam-b_16447 |
| | SPAC22F8.07C | putative myb-like dna-binding protein |

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|---|---|---|
|  | SPBC1711.11 | putative nexin sorting protein with PX domain |
|  | SPAC29E6.04 | putative nuclear envelope protein by similarity to *S. cerevisiae NNF1* |
|  | SPBC19F8.04C | putative nuclease |
|  | SPCC1620.11 | putative nucleoporin complex subunit |
|  | SPCC11E10.05C | putative nucleotide phosphatase |
|  | SPBC1778.10C | putative phosphoinositide-dependent protein kinase 1 |
|  | SPCC1322.01 | putative ribonuclease II (RNB) family member |
|  | SPBC83.05 | putative role in early maturation of pre-rRNA and mitochondrial maintenance |
|  | SPBC14F5.11C | putative sorting nexin; by similarity |
|  | SPBC1706.03 | putative transmembrane GTPase required for mitochondrial fusion by similarity to *S. cerevisiae FZO1* |
|  | SPAC31F12.01 | related to yeast zds family proteins |
| *stm1* | SPAC17C9.10 | seven transmembrane protein |
| *csh3* | SPBC119.05C | SH3 domain containing protein |
|  | SPCC1259.12C | similar to human ranbpm |
|  | SPBC1773.11C | similar to *S. cerevisiae CDC50* |
|  | SPBC947.11C | similar to *S. cerevisiae EFD* (required for stability of direct DNA repeats) |
| *tcg1* | SPBC660.11 | single-stranded TG1-3 telomeric binding protein |
| *scp3* | SPAC3A11.02 | spindle poison sensitivity related protein. |
|  | SPAC30.03C | translin-like protein |
|  | SPAC3F10.07C | very hypothetical protein- overlaps N term of SPAC3F10.06c; expression pattern on microarray is identical to c3F10.06c |
|  | SPAC16C9.01C | *S. cerevisiae* MAK32-like protein which is required for structural stability of dsRNA-containing particles |
|  | SPAC31G5.02 | *S. cerevisiae ROT1* homolog; possible cell-cycle control |
|  | SPAC1610.02C | mitochondrial ribosomal protein L1 |
|  | SPAC31A2.03 | mitochondrial ribosomal protein L10 |
|  | SPAC4F8.06 | mitochondrial ribosomal protein S12 |
|  | SPAC23H3.07C | mitochondrial ribosomal protein S14 |
| *psk1* | SPCC4G3.08 | serine/threonine protein kinase |
|  | SPAC890.03 | putative serine/threonine protein kinase |
|  | SPBC8D2.01 | putative serine/threonine protein kinase |
|  | SPBC16E9.13 | putative serine/threonine protein kinase; similar to *S. cerevisiae KSP1* |
|  | SPAC16C9.07 | serine/threonine protein kinase |
|  | SPCC417.06C | putative serine-threonine-protein kinase |
|  | SPBC32H8.06 | similar to serine/threonine protein phosphatase; no PFAM domain |
| *ptc1* | SPCC4F11.02 | protein phosphatase 2C homolog 1 |
|  | SPAC227.15 | similar to *S. cerevisiae HEX2*; putative regulatory subunit for protein phosphatase |
| *meu5* | SPAC1610.03C | putative rna-binding protein; possible polyadenylate; meiotic expression upregulated |
|  | SPAC4G9.05 | RNA binding protein, pumilio-family |
|  | SPCC1682.08C | RNA binding protein, pumilio-family |
|  | SPCC74.09 | RNA-binding protein |
| *mde7* | SPCC320.07C | RNA-binding protein |
|  | SPAC343.07 | RNA-binding protein |
|  | SPCC1919.11 | SH3 domain protein |
|  | SPAC1006.01 | RNA-binding protein |
|  | SPACUNK4.12C | protease, possible pheromone response |
|  | SPBC119.17 | putative zinc metalloprotease |
| *ape1* | SPBC1921.05 | aminopeptidase I |
|  | SPAC17A5.04C | probable zinc metallopeptidase, disintegrin; localization of GFP fusion- Spore rim |
|  | SPAC23H3.05C | WD repeat protein |
|  | SPBC27B12.05 | WD repeat protein |
|  | SPAC3H5.08C | WD repeat protein |

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|  | SPBC32H8.09 | WD domain protein; by similarity |
|  | SPAC19A8.10 | hypothetical zinc finger protein |
|  | SPAC24C9.14 | hypothetical zinc finger protein |
|  | SPBC15D4.02 | hypothetical zinc-finger protein |
|  | SPAC328.02 | protein of unknown function, has a TRIAD composite zinc finger domain |
|  | SPCC126.07C | putative PHD-type zinc finger |
|  | SPBC15C4.06C | putative serine-rich zinc-finger protein |
|  | SPBC31F10.10C | putative zinc finger protein which may be involved in regulation cell polarity by similarity to *S. cerevisiae MUB1* |
| *meu14* | SPBC1347.03 | RING zinc finger; putative coiled-coil region; meiotic expression upregulated |
|  | SPCC4G3.12C | serine-rich, C3HC4 type (RING finger) protein; possibly LIM domain interacting by similarity to mouse *RNF12* |
|  | SPBC3H7.09 | conserved hypothetical protein; zinc finger-DHHC |
|  | SPBC2F12.15C | zinc finger-DHHC protein |
|  | SPAC23D3.14C | alpha-amylase |
| *mde5 meu30* | SPAC25H1.09 | alpha-amylase a precursor |
|  | SPCC11E10.09C | putative alpha-amylase precursor |
|  | SPAC27E2.01 | putative alpha-amylase precursor |
| *meu7* | SPBC16A3.13 | similar to alpha-amylase precursor but with large repeat insertion |
| *eng2* | SPAC23D3.10C | endo-1,3-beta-glucanase |
|  | SPBC646.06C | putative Glucanase; by similarity to *Penicillium purpurogenum* mutanase |
|  | SPAC14C4.09 | putative Glucanase; by similarity to *Penicillium purpurogenum* mutanase |
|  | SPCC306.05C | possible growth response protein; Pfam-B_35059 |