# Web Table A: Previously known genes expressed in meiosis and/or with a meiotic function.

In 61 out of 63 cases our results are very similar to published expression data. In the remaining two cases (*meu8* and *meu26*) we failed to detect a significant signal above background.

| Biological name Systematic name Expression patte |               | <b>Expression</b> pattern             | Reference  |
|--|---------------|---------------------------------------|------------|
|  | •             | (microarray)                          | (Northern) |
| Recombination:                                   |               | · · · · · · · · · · · · · · · · · · · | · · · ·    |
| rec7   | SPCC1753.03C  | early                                 | 1          |
| rec8   | SPBC29A10.14  | early                                 | 1          |
| rec10  | SPAC25G10.04C | early                                 | 1          |
| rec11  | SPCC4E9.01C   | early                                 | 1          |
| rec12  | SPAC17A5.11   | early                                 | 2          |
| rec14  | SPBC32F12.02  | early                                 | 1          |
| rec15  | SPBC1711.14   | early                                 | 1          |
| dmc1   | SPAC8E11.03C  | early                                 | 3          |
| meu13  | SPAC222.15    | early                                 | 4          |
| rep1/rec16                                       | SPBC2D10.06   | early                                 | 1          |
| S phase:   | L             |                                       |            |
| cdc22  | SPAC1F7.05    | early                                 | 5          |
| cdc18  | SPBC14C8.07C  | early                                 | 6          |
| Cell cycle genes:                                |               |                                       | -          |
| cdc2   | SPBC11B10.09  | early                                 | 7          |
| cdc13  | SPBC582.03    | middle                                | 7          |
| cdc25  | SPAC24H6.05   | middle                                | 7          |
| mei4n targets:                                   |               |                                       |            |
| mei4   | SPBC32H8.11   | middle                                | 8          |
| mes1   | SPAC5D6.08C   | middle                                | 8          |
| mde1   | SPAC16E8.05C  | middle                                | 8          |
| mde2   | SPBC31F10.08  | middle                                | 8          |
| mde3   | SPBC8D2.19    | middle                                | 8          |
| mde4   | SPBC6B1.04    | middle                                | 8          |
| mde5/meu30                                       | SPAC25H1.09   | middle                                | 8          |
| mde6   | SPAC15A10.10  | middle                                | 8          |
| mde7   | SPCC320.07C   | middle                                | 8          |
| mde8/spn7  | SPBC21.08C    | middle                                | 8          |
| mde9/spn5  | SPAC24C9.15C  | middle                                | 8          |
| meu1/meu2  | SPCC1259.14C  | middle                                | 9          |
| meu4/isp3  | SPAC1F8.05    | middle                                | 9          |
| meu5   | SPAC1610.03C  | middle                                | 9          |
| теиб   | SPBC428.07    | middle                                | 9          |
| meu7   | SPBC16A3.13   | middle                                | 9          |
| meu11  | SPBC18H10.04C | middle                                | 9          |
| meu12/ght6                                       | SPCC1235.13   | middle                                | 9          |
| meul4  | SPBC1347.03   | middle                                | 9          |
| meu15  | SPCPJ732.03   | middle                                | 9          |
| meu16  | SPAC15A10     | middle                                | 9          |
| meu17  | SPBC14C8.05C  | middle                                | 9          |
| meu18  | SPBC409.11    | middle                                | 9          |
| meu21/bgs2                                       | SPAC24C9.07C  | middle                                | 9          |
| meu25  | SPBC27.03     | middle                                | 9          |
| meu26  | SPAC6B12.16   | not detected                          | 9          |
| meu27  | SPCC1259.14C  | middle                                | 9          |
| meu29  | SPAC25H1.05   | middle                                | 9          |
| meu31  | SPAC1A6.06C   | middle                                | 9          |

| spo3         | SPAC607.10         | middle       | 10    |
|--------------|--------------------|--------------|-------|
| spo4         | SPBC21C3.18        | middle       | 11    |
| spo6         | SPBC1778.04        | middle       | 8     |
| Other genes: |                    |              |       |
| cam1         | SPAC3A12.14        | middle       | 7     |
| chs1         | SPAC13G6.12C       | middle       | 12    |
| exo1         | SPBC29A10.05       | middle       | 13    |
| meu3         | SPCC1884(AB020594) | early        | 9     |
| meu8         | SPCC550.10         | not detected | 9     |
| meu10        | SPCC1223.12C       | early        | 9     |
| meu19        | SPCC569(AB054303)  | middle       | 9     |
| meu20        | SPCC4F11(AB054304) | early        | 9     |
| meu22        | SPBC19F8.06C       | middle       | 9     |
| meu23        | SPCC613.11C        | middle       | 9     |
| meu24        | SPCC1281.08        | middle       | 9     |
| mfr1/fzr1    | SPBC1198.12        | middle       | 14,15 |
| psy1         | SPCC825.03C        | middle       | 10    |
| spo15        | SPAC1F3.06C        | constitutive | 16    |
| spo20        | SPAC3H8.10         | constitutive | 17    |
| ssm4         | SPAC27D7.13C       | early        | 18    |

## Web Table B: Genes induced in response to starvation/pheromone (transient).

| Metab   | olic response            |  |
|---------|--------------------------|--|
| Allanto | oin metabolism           |  |
|         | SPAC1F7.09C              | putative allantoicase (EC 3.5.3.4)   |
|         | SPAC19G12.04             | putative ureidoglycolate hydrolase   |
|         | SPCC1223.09              | uricase  |
| Salvag  | e pathway                |  |
| 8       | SPCC1672.03C             | putative guanine deaminase   |
|         | SPBC1683.03C             | MFS transporter  |
| pcd1    | SPAC1556.04C             | putative cytidine deaminase  |
|         | SPAC1805.16C             | putative purine nucleoside phosphorylase   |
|         | SPAC1002.17C             | probable uracil phosphoribosyltransferase  |
|         | SPAC1399.04C             | putative uracil phosphoribosyltransferase  |
|         | SPBC16G5.02C             | ribokinase; pfkB family carbohydrate kinase                                      |
|         | SPBC1683.06C             | putative inosine-uridine preferring nucleoside hydrolase                         |
|         | SPCC162.11C              | putative uridine kinase  |
|         | SPBC800.11               | putative inosine-uridine prefering nucleoside hydrolase                          |
|         | SPBC3D6.06C              | putative ribose-phosphate pyrophosphokinase                                      |
|         | SPBPB2B2.05              | putative GMP synthase  |
| Degrad  | lation of other nitroger | 1 sources  |
|         | SPAPB24D3.03             | putative agmatinase precursor  |
|         | SPBC8E4.03               | putative agmatinase precursor  |
|         | SPAC11D3.09              | arginase family protein; putative agmatinase precursor                           |
|         | SPAC186.03               | L-asparaginase precursor   |
|         | SPAC869.01               | putative aminotransferase  |
|         | SPAC27F1.05C             | probable aminotransferase  |
|         | SPBC1773.03C             | aminotransferase class III   |
|         | SPAC19D5.07              | 4-aminobutyrate aminotransferase (GABA transaminase)                             |
|         | SPCC1450.07C             | putative d-amino acid oxidase  |
|         | SPAC922.07C              | probable aldehyde dehydrogenase  |
|         | SPAC1002.12C             | probable succinate-semialdehyde dehydrogenase                                    |
|         | SPAC869.04               | formamidase-like protein   |
|         | SPCC550.07               | acetamidase  |
|         | SPAC922.03               | probable 1-aminocyclopropane-1-carboxylate deaminase                             |
| Others  | -metabolic               |  |
| isp7    | SPAC25B8.13C             | putative iron/ascorbate oxidoreductase   |
|         | SPCC1494.01              | putative iron/ascorbate oxidoreductase   |
|         | SPAC1F7.12               | oxidoreductase similar to pyridoxal reductase                                    |
|         | SPAC922.06               | probable oxidoreductase, short chain dehydrogenase/reductase family              |
|         | SPAC30D11.01C            | putative family 31 glucosidase   |
|         | SPAC3A11.10C             | putative microsomal dipeptidase precursor  |
|         | SPAC521.03               | putative short chain dehydrogenase   |
|         | SPAC19G12.03             | possible polysaccharide deacetylase  |
|         | SPBC1861.05              | pfkB family carbohydrate kinase; with Pfam-B_2675 2                              |
|         | SPAC806.06C              | putative Nicotinamide mononucleotide (NMN) adenylyltransferase; by similarity to |
|         |                          | S. cerecisiae YLR328W  |
|         | SPAC1039.03              | putative esterase/lipase   |
|         | SPCC576.02               | putative hydantoin racemase  |

Transient genes are induced within 1 h of nitrogen removal, and their levels decrease during the following 2-3 h.

|        | SPAC1399.05C  | putative involvement in maltose fermentation  |
|--------|---------------|---|
|        | SPBPB2B2.06C  | putative 5' nucleotidase family protein; possibly involved in the degradation of          |
|        |               | external UDP-glucose  |
|        | SPAC1039.06   | putative metal activated pyridoxal enzyme   |
|        | SPAC14C4.09   | putative Glucanase; by similarity to Penicillium purpurogenum mutanase                    |
|        | SPAC14C4.09   | putative Glucanase; by similarity to Penicillium purpurogenum mutanase                    |
|        | SPBC1683.11C  | isocitrate lyase (EC 4.1.3.1)   |
|        | SPAC1039.02   | membrane protein; similar to S. cerevisiae YHR202W; putative esterase; contains           |
|        |               | Pfam-B_34335; contains Pfam-B_34336; which co-occur in 5' nucleotidase                    |
|        | SPAC2E1P3.04  | peroxisomal copper amine oxidase  |
|        | SPCC11E10.01  | cystathionine beta-lyase  |
|        | SPAC1039.07C  | aminotransferase class-III pyridoxal-phosphate; putative 2,2-dialkylglycine decarboxylase |
|        | SPAC1039.08   | serine acetyltransferase  |
|        | SPAC1F7.10    | putative hydantoin racemase   |
| Trans  | porters       |   |
|        | SPCC285.04    | putative transthyretin precursor  |
|        | SPBC1683.05   | NCS1 allantoate transporter   |
|        | SPCC417.10    | putative MFS allantoate transporter   |
|        | SPAC1039.04   | MFS transporter of unknown specificity  |
|        | SPBC1683.12   | MFS transporter of unknown specificity  |
|        | SPAC3H1.06C   | MFS transporter of unknown specificity  |
|        | SPAC1399.02   | MFS transporter of unknown specificity  |
|        | SPBC1271.09   | MFS transporter of unknown specificity  |
| fnx1   | SPBC12C2.13C  | MFS multidrug efflux transporter  |
|        | SPAC17C9.16C  | MFS multidrug efflux transporter  |
|        | SPCC965.13    | MFS amilorlide efflux transporter; car1 homologue   |
|        | SPAC29B12.14C | NCS1 uracil transporter   |
|        | SPCC285.05    | purine transporter  |
|        | SPAC1399.01C  | purine permease   |
| fur4   | SPAC1399.03   | uracil permease   |
|        | SPBC887.17    | uracil permease   |
|        | SPAP7G5.06    | amino acid permease   |
|        | SPCPB1C11.02  | putative amino acid permease  |
|        | SPBPB2B2.01   | putative amino acid permease  |
|        | SPAC11D3.08C  | APC amino acid transporter  |
|        | SPAC1039.01   | APC amino acid transporter  |
|        | SPAC869.03C   | SSS urea transporter  |
|        | SPAC323.07C   | conserved protein; UPF0013; putative membrane transporter                                 |
| Seque  | nce orphans   | 1   |
|        | SPAC11D3.16C  | hypothetical protein; sequence orphan   |
|        | SPBC800.14C   | hypothetical protein; sequence orphan; contains 4 predicted transmembrane helices         |
|        | SPAC630.07C   | hypothetical protein; sequence orphan   |
|        | SPCC191.05C   | hypothetical protein; sequence orphan   |
|        | SPCC191.06    | hypothetical protein; sequence orphan   |
|        | SPBC1347.11   | hypothetical protein; sequence orphan   |
|        | SPBC651.04    | hypothetical protein; sequence orphan   |
|        | SPCC1322.10   | hypothetical protein; sequence orphan; S-T protein; similar to cell-surface proteins;     |
|        |               | similar to proteoglycans  |
|        | SPBC1289.15   | low similarity to seripauperin (PAU) family of possible cell wall mannoproteins           |
| Stress | response      |   |
| hos3   | SPCC417.02    | protein necessary for growth under high osmotic stress                                    |

| Trans   | criptional regulatio | n   |
|---------|----------------------|---|
|         | SPAC1039.05C         | C2H2 zinc finger protein  |
|         | SPAC11D3.17          | putative transcription factor btd   |
|         | SPBC1773.12          | putative transcriptional regulator, zinc-finger, binuclear cluster domain                                     |
| Cell cy | ycle regulators      |   |
| puc1    | SPBC19F5.01C         | cyclin  |
| Other   | s                    |   |
|         | SPAC20G4.03C         | serine/threonine protein kinase; probably regulates initiation of translation by phosphorylation of eIF2alpha |
|         | SPAC977.13C          | putative hydrolase pseudogene   |
|         | SPAC1002.18          | hypothetical protein, conserved in other yeasts   |
|         | SPBC3E7.12C          | very putative chitin synthase regulatory factor   |
|         | SPAC2F3.05C          | aldo/keto reductase family oxidoreductase   |
|         | SPBC215.11C          | putative oxidoreductase; aldo-keto family   |
|         | SPBC9B6.03           | hypothetical zinc finger protein  |
|         | SPCC576.04           | putative receptor-associated protein  |
|         | SPAC11D3.03C         | conserved hypothetical protein  |
|         | SPBC839.02           | hypothetical protein; possibly fungal specific  |
|         | SPCC18.01C           | hypothetical protein; SUN family; serine-rich; contains predicted N-terminal signal sequence                  |
|         | SPBP35G2.11C         | protein containing 3 ZZ domain zinc finger domains  |
|         | SPCC965.06           | putative potassium channel subunit  |
|         | SPCC63.08C           | putative serine/threonine protein kinase; <i>S. cerevisiae</i> homologue <i>APG1</i> is involved in autophagy |
|         | SPBC800.11           | putative inosine-uridine preferring nucleoside hydrolase  |

## Web Table C: Genes induced in response to starvation/pheromone (continuous).

Continuous genes are induced immediately upon nitrogen starvation and remain activated throughout the experiment.

| Metaboli   | c response    |  |
|------------|---------------|--|
|            | SPBC1289.16C  | putative amine oxidase   |
|            | SPBPB2B2.10C  | putative galactose-1-phosphate uridylyltransferase   |
|            | SPCC417.11C   | putative glutamate-1-semialdehyde aminotransfera se  |
|            | SPAC3G9.11C   | pyruvate decarboxylase   |
|            | SPAC1F8.04C   | putative chlorohydrolase/deaminase   |
|            | SPCC306.08C   | malate dehydrogenase, mitochondrial precursor  |
|            | SPAC18B11.09C | putative acetyltransferase   |
|            | SPAC3C7.13C   | glucose-6-phosphate 1-dehydrogenase  |
|            | SPAC4D7.02C   | putative glycerophosphoryl diester phosphodiesterase   |
| Transpor   | ters          |  |
|            | SPAC2G11.13   | MFS transporter of unknown specificity   |
| Mating     |               |  |
| isp6       | SPAC4A8.04    | sexual differentiation process protein; putative subtilase-type proteinase                                     |
| gpa1       | SPBC24C6.06   | guanine nucleotide-binding protein alpha-1 subunit; required for mating and sporulation                        |
| ste7       | SPAC23E2.03C  | required for mating and meiosis  |
| Sequence   | orphans       |  |
|            | SPCC576.01C   | hypothetical protein; sequence orphan  |
|            | SPAC6B12.03C  | hypothetical protein; sequence orphan  |
|            | SPCC338.18    | hypothetical protein; sequence orphan  |
|            | SPBC428.10    | hypothetical protein; sequence orphan  |
|            | SPBC56F2.06   | hypothetical protein; sequence orphan  |
|            | SPCC70.04C    | hypothetical protein; sequence orphan; 4 predicted transmembrane helices                                       |
|            | SPBC8E4.02C   | hypothetical protein; sequence orphan  |
|            | SPAC4D7.11    | hypothetical protein; sequence orphan  |
|            | SPAC25B8.18   | hypothetical protein; sequence orphan  |
|            | SPAC29B12.13  | hypothetical protein; sequence orphan  |
|            | SPAC637.03    | hypothetical protein; sequence orphan; 8 predicted transmembrane segments;<br>predicted N-term signal sequence |
|            | SPCC63.14     | hypothetical protein; sequence orphan; coiled-coil region  |
|            | SPBC11C11.06C | hypothetical protein; sequence orphan  |
| Stress res | sponse        |  |
| hsp9       | SPAP8A3.04C   | heat shock protein   |
| gpx1       | SPBC32F12.03C | glutathione peroxidase   |
| 01         | SPCC63.13     | hypothetical DNAJ domain protein   |
|            | SPBC106.13    | conserved hypothetical protein; similar to <i>S. cerevisiae</i> YIL097W, involved in stress response           |
| ntp1       | SPBC660.07    | neutral trehalase  |
| Others     |               |  |
|            | SPBC18H10.05  | WD repeat protein  |
|            | SPAC589.07C   | WD domain protein: highly similar to S. cerevisiae YFR021W   |
|            | SPCC1322.08   | putative serine/threenine protein kinase   |
| nim1 ntr?  | SPBC557.03C   | nim1 GTPase protein  |
| p p 2      | SPCC338 12    | putative proteinase precursor  |
|            | ST CC330.12   | putative proteinase procursor  |
| 1          | SFAF14E0.04   | putative zine inetanopepituase   |

|       | SPAPJ691.02  | hypothetical zinc binding protein yipee-like   |
|-------|--------------|--|
| isp4  | SPBC29B5.02C | sexual differentiation process protein   |
|       | SPBC1271.05C | zinc finger zf-AN1 protein   |
|       | SPAC1039.10  | putative translation initiation inhibitor  |
|       | SPBC1652.01  | may bind Pst1 histone deacytylase B; by similarity to <i>S. cerevisiae</i> SIN complex protein (transcriptional regulator of RNA polymerase II)        |
|       | SPAPB8E5.04C | putative phosphatidylglycerol/phosphatidylinositol transfer  |
|       | SPCC1739.08C | short chain dehydrogenase; putative sorbitol utilization   |
|       | SPCC736.13   | short chain dehydrogenase  |
|       | SPAC19G12.09 | putative aldose reductase  |
|       | SPBC16A3.02C | putative quinone oxidoreductase; zinc binding oxidoreductase   |
|       | SPBC725.10   | similar to peripheral-type benzodiazepine receptor   |
|       | SPAC26F1.14C | putative flavoprotein; similar to human Mitochondrial apoptosis-inducing factor;<br>flavoprotein inducing chromatin condensation and DNA fragmentation |
|       | SPAC630.05   | TBC domain protein; putative GTPase activating protein of Rab-like GTPase  |
|       | SPCP31B10.06 | C2-domain protein; synaptotagmin family  |
| vps27 | SPAC19A8.05C | putative vacuolar sorting protein  |
|       | SPAC19B12.08 | putative Protein that mediates attachment of autophagosomes to microtubules, by similarity to <i>S. cerevisiae AUT2</i>                                |
|       | SPAC4H3.04C  | hypothetical protein; similar to S. cerevisiae YJR008W; UPF0103 FAMILY   |
|       | SPBC365.12C  | hypothetical protein; similar to S. cerevisiae YML128C (low)   |
|       | SPAC10F6.11C | hypothetical protein; similar to <i>S. cerevisiae APG17</i> ; contains Pfam-B_36869; putative coiled-coil  |
|       | SPAC31G5.18C | conserved hypothetical protein   |
|       | SPAC12B10.13 | conserved hypothetical protein; contains Pfam-B_8841   |
|       | SPAC688.03C  | conserved hypothetical protein   |
|       | SPCC622.11   | hypothetical protein; contains Pfam-B_37204  |
|       | SPCC285.11   | hypothetical protein with UBX, Domain present in ubiquitin-regulatory proteins   |
|       | SPCC1020.05  | hypothetical protein; Pfam-B_7731 domain   |
|       | SPAC3C7.05C  | hypothetical protein; contains Pfam-B_11461 domain   |
|       | SPBC660.05   | hypothetica protein; pombe specific domain Pfam-B_15930  |
|       | SPAC20G4.05C | hypothetical protein; UPF0061 family   |
|       | SPAC167.06C  | hypothetical protein   |
|       | SPBC16E9.16C | pseudogene   |
|       | SPCC1450.01C | putative pseudogene  |
|       | SPAC186.04C  | putative pseudogene, has similarity to transmembrane channels  |

## Web Table D: Genes induced in response to nitrogen starvation (delayed).

| Pheromo    | ne/entry into meio | sis  |
|------------|--------------------|--|
| mam1       | SPBC25B2.02C       | ABC efflux transporter; putative mating factor                                 |
| mam2       | SPAC11H11.04       | pheromone P-factor receptor  |
| mam4       | SPAC10F6.12C       | protein-S isoprenylcysteine O-methyltransferase (EC 2.1.1.100)                 |
| mfm1       | SPAPB8E5.05        | M-factor precursor 1; mating pheromone produced by M-type cells                |
| mfm2       | SPAC513.03         | M-factor precursor 2   |
| mfm3       | SPBPJ4664.03       | M-factor precursor 3   |
| sxa2       | SPAC1296.03C       | putative serine carboxypeptidase; involved in mating response                  |
| map1       | SPAC11E3.06        | pheromone receptor transcription activator                                     |
| map2       | SPCC1795.06        | P-factor; mating pheromone produced by P-type cells                            |
| map3       | SPAC3F10.10C       | pheromone M-factor receptor  |
| ste4       | SPAC1565.04C       | sexual differentiation protein; involved in mating and meiosis; leucine zipper |
| rgsl       | SPAC22F3.12C       | regulator of G-protein signaling   |
| ste6       | SPCC1442.01        | guanine-nucleotide releasing factor; involved in conjugation                   |
| spk1       | SPAC31G5.09C       | MAP kinase (MAPK); pheromone signaling; similar to S. cerevisiae FUS3          |
| matPc      | P10841 (SwissProt) | mating-type P-specific polypeptide Pc  |
| matMc      | SPBC1711.02        | mating-type M-specific polypeptide Mc  |
| matPi      | P10842 (SwissProt) | mating-type P-specific polypeptide Pi  |
| matMi      | SPBC23G7.17C       | mating-type M-specific polypeptide Mi  |
| mei2       | SPAC27D7.03C       | regulator of entry into meiosis  |
| mei3       | SPBC119.04         | inhibitor of pat1p   |
| ran1 pat1  | SPBC19C2.05        | protein kinase; negative regulator of sexual conjugation and meiosis           |
| fus1       | SPAC20G4.02C       | cell fusion protein  |
| meiRNA     | D31852 (GenBank)   | mei2p binding RNA  |
| Sequence   | orphans            |  |
|            | SPBC4.01           | hypothetical protein; sequence orphan; N-term signal peptide                   |
|            | SPCC1753.05        | hypothetical protein; sequence orphan  |
|            | SPBC146.02         | hypothetical protein; sequence orphan  |
|            | SPAC1565.03        | hypothetical protein; sequence orphan  |
|            | SPBC21D10.06C      | hypothetical protein; S/T rich; sequence orphan                                |
| Transcrij  | ptional regulation |  |
|            | SPAC2H10.01        | hypothetical fungal binuclear cluster domain protein                           |
| stell affl | SPBC32C12.02       | transcription factor; HMG box; regulates genes required for mating             |
| Metaboli   | c/transporter      |  |
|            | SPAPB1A10.02       | Sequence orphan  |
| dak2       | SPAC977.16C        | dihydroxyacetone kinase  |
|            | SPAC27D7.04        | pterin-4-alpha-carbinolamine dehydratase                                       |
| gut2       | SPCC1223.03C       | glycerol-3-phosphate dehydrogenase, mitochondrial precursor                    |
| yam8       | SPAC1F5.08C        | MID1 calcium channel   |
| Others     | •                  |  |
|            | SPAPB15E9.02C      | very hypothetical protein  |
|            | SPCC162.10         | putative serine/threonine protein kinase                                       |
| shk2 pak2  | SPAC1F5.09C        | p21 activated MAP kinase   |
|            | SPAC31G5.07        | possible involvement in mating response; similar to <i>S. cerevisiae FIG1</i>  |
|            | SPAP11E2.02c       | hypothetical protein; glycoamylase/agglutinin-like                             |
|            | SPBC1604.01        | conserved hypothetical protein   |
|            |                    |  |

Delayed genes start to increase only after 1 h of starvation.

# Web Table E: Early genes.

| Metabolic: |                     |  |
|------------|---------------------|--|
| Glucose t  | ransport            |  |
| gti l      | SPAC1751.01C        | required for gluconate-H+ symport  |
| ght1       | SPCC548.07C         | putative glucose transporter protein.  |
| ght3       | SPAC1F8.01          | MFS glucose transporter  |
| ght4       | SPBC1683.08         | putative glucose transporter protein   |
| Gluconeo   | ogenesis            |  |
| fbp1       | SPBC660.04C         | fructose-1,6-bisphosphatase  |
| Entry int  | o pentose phosphate | cycle  |
|            | SPCC794.01C         | glucose-6-phosphate 1-dehydrogenase  |
| gnd        | SPBC660.16          | 6-phosphogluconate dehydrogenase, decarboxylating 1                                |
| S phase    |                     |  |
| cdc20      | SPBC25H2.13C        | dna polymerase epsilon, similar to S. cerevisiae POL2                              |
| rti l      | SPBC119.14          | double-strand break repair component; essential for S phase completion             |
| pht1       | SPBC11B10.10C       | histone H2a variant  |
| dfp1 him1  | SPCC550.13          | regulatory subunit of Dfp1p kinase;G1/S transition; similar to S. cerevisiae DBF4  |
| cdc18      | SPBC14C8.07C        | replication initiation factor; similar to S. cerevisiae CDC6                       |
| Recomb     | ination             |  |
| mus81      | SPCC4G3.05C         | required for recombination   |
| meu13      | SPAC222.15          | pairing of homologue chromosomes in meiosis, similar to S. cerevisiae HOP2         |
| rec10      | SPAC25G10.04C       | meiotic recombination protein; involved in sister chromatid cohesion               |
| rec11      | SPCC550.16C         | meiotic recombination protein; involved in sister chromatid cohesion               |
| rec12      | SPAC17A5.11         | meiotic recombination protein; similar to S. cerevisiae SPO11                      |
| rec15      | SPBC1711.14         | meiotic recombination protein  |
| rec6       | SPBC21B10.12        | meiotic recombination protein  |
| rec7       | SPCC1753.03C        | meiotic recombination protein  |
| rec8       | SPBC29A10.14        | meiotic cohesin; similar to S. cerevisiae REC8                                     |
| dmc1       | SPAC8E11.03C        | meiotic recombination protein; strand exchange; similar to S. cerevisiae DMC1      |
| rhp51      | SPAC644.14C         | DNA repair; meiotic recombination protein; similar to S. cerevisiae RAD51          |
| Cell cyc   | le regulators       |  |
| cig2       | SPAPB2B4.03         | S phase-specific cyclin  |
| cdt2       | SPAC17H9.19C        | target of cdc10p transcription factor: coupling START with cytokinesis; WD domain  |
| spd1       | SPAC29B12.03        | S-phase delaying protein 1   |
|            | SPCC1620.04C        | CDC20/Fizzy family, APC regulator  |
| Chromo     | some segregation    |  |
| cnp1       | SPBC1105.17         | centromere-specific histone; chromosome segregation; similar to S. cerevisiae CSE4 |
| smc1       | SPBC29A10.04        | cohesin subunit; similar to S. cerevisiae SMC1                                     |
| smc3       | SPAC10F6.09C        | cohesin subunit; similar to S. cerevisiae SMC3                                     |
| Nuclear    | movement            |  |
|            | SPBC646.17C         | putative cytoplasmic dynein intermediate chain; WD repeat                          |
| dhc1       | SPAC1093.06C        | dynein heavy chain; required for nuclear movement in meiotic prophase              |
|            | SPBC216.02          | putative coiled coil; similar to C-term of nuclear migration protein               |
| ssm4       | SPAC637.01C         | microtubule-associated protein; involved in meiosis                                |
| Nuclear    | fusion              |  |
| tht1       | SPAC13C5.03         | nuclear fusion protein   |
| DNA re     | pair                |  |
|            | SPAC22F3.03C        | hypothetical helicase; putative DNA repair   |
|            | SPCC553.07C         | putative translesion DNA repair polymerase   |
| Transcr    | iptional regulators | :  |
| rep1 rec1  | 6 SPBC2D10.06       | regulator of pre-meiotic dna synthesis   |

| res2 pct1  | SPAC22F3.09C         |  |
|------------|----------------------|--|
|            | SPAC1002.05C         | similarity to retinoblastoma binding proteins                                  |
|            | SPCC290.04           | putative transcriptional regulator; GATA zinc finger                           |
|            | SPCC4G3.07C          | similarity to retinoblastoma binding protein 2                                 |
|            | SPBC1718.02          | hypothetical protein with PHD zinc finger, possibly chromatin regulation       |
| cdc10      | SPBC336.12C          | MluI-box binding factor (MBF) transcriptional activation complex               |
|            | SPAC31G5.10          | myb DNA-binding domainprotein  |
|            | SPBC21B10.13C        | homeodomain protain  |
| Putative o | cell wall biosynthes | is   |
|            | SPCC417.05C          | SEL1/TPR repeat protein  |
| meu10      | SPCC1223.12C         | required for spore cell wall formation   |
| Non-codi   | ng RNAs:             |  |
| meu20      | AB054304 (EMBL)      | putative non-coding RNA  |
| теи3       | AB020594 (EMBL)      | meiotic expression upregulated mRNA  |
| Sequence   | orphans:             |  |
|            | SPAC458.04C          | hypothetical protein; sequence orphan  |
|            | SPAC1002.02          | hypothetical protein; sequence orphan  |
|            | SPAC6C3.05           | hypothetical protein; sequence orphan  |
|            | SPBP8B7.04           | hypothetical protein; sequence orphan  |
|            | SPAC32A11.01         | hypothetical protein; sequence orphan  |
|            | SPBC31F10.05         | hypothetical protein; sequence orphan  |
|            | SPBC1921.06C         | hypothetical protein; sequence orphan; predicted N-terminal signal sequence    |
|            | SPBC582.06C          | hypothetical protein; sequence orphan; predicted coiled-coil                   |
|            | SPCC1393.07C         | hypothetical protein; sequence orphan  |
|            | SPAC22F8.02C         | hypothetical protein; sequence orphan; predicted N-terminal signal sequence    |
|            | SPAC1834.09          | hypothetical protein; sequence orphan  |
|            | SPAC1002.06C         | hypothetical protein; sequence orphan  |
|            | SPAC14C4.08          | hypothetical protein; sequence orphan  |
|            | SPAC57A10.04         | hypothetical protein; sequence orphan  |
|            | SPAC57A10.06         | hypothetical protein; sequence orphan;   |
|            | SPAPB1A10.14         | hypothetical protein; sequence orphan  |
|            | SPAC17H9.18C         | hypothetical protein; sequence orphan  |
|            | SPAC22H12.01C        | hypothetical protein; sequence orphan  |
|            | SPAC17A5.18C         | hypothetical protein; sequence orphan; predicted coiled-coil                   |
|            | SPBC36B7.06C         | hypothetical protein; sequence orphan  |
|            | SPAC1952.15C         | hypothetical protein; sequence orphan  |
|            | SPAC27E2.07          | hypothetical protein; sequence orphan  |
|            | SPCC338.08           | hypothetical protein; sequence orphan  |
|            | SPBC409.03           | encodes 85aa predicted protein with no homology                                |
|            | SPBC2G2.09C          | hypothetical protein; sequence orphan  |
|            | SPAP27G11.08C        | hypothetical protein; sequence orphan  |
|            | SPBC577.05C          | hypothetical protein; sequence orphan  |
|            | SPCC584.12           | hypothetical protein; sequence orphan  |
|            | SPBC800.02           | hypothetical serine-rich protein; sequence orphan                              |
| Others     | ·                    |  |
|            | cosmid SPCC4F11      | possible cellular RNA, misc RNA 1.1.41.RC                                      |
|            | SPAC19G12.16C        | S/T rich protein; unknown function   |
|            | SPBC359.06           | putative class II aldolase and adducin N terminal domain                       |
|            | SPCC1739.10          | putative signal transduction component protein                                 |
| zym l      | SPAC22H10.13         | putative metallothionein   |
| yps1       | SPCC1795.09          | aspartic protease  |
|            | SPBC28F2.07          | hypothetical protein; low similarity to the C terminal region of S. pombe swi2 |

| SPAC6G9.13C  | hypothetical protein   |
|--------------|--|
| SPCC11E10.03 | putative protein with short coiled-coil region                                   |
| SPBC36B7.05C | putative phosphatidylinositol(3)-phosphate binding protein; FYVE zinc finger     |
| SPBC25H2.14  | hypothetical protein; similar to S. cerevisiae YKR030W                           |
| SPBC409.08   | putative membrane transport protein  |
| SPBC6B1.05C  | putative protein involved in autophagy; similar to S. cerevisiae APG7            |
| SPBC660.18C  | hypothetical protein; similar to S. cerevisiae SPO72                             |
| SPBC19C7.04C | hypothetical protein; similar to S. cerevisiae YMR295; possibly fungal specific  |
| SPCC70.09C   | hypothetical protein; similar to S. cerevisiae YMR295C; possibly fungal specific |
| SPAC13A11.03 | hypothetical protein; similar to S. cerevisiae YGL183; predicted coiled-coil     |
| SPBC365.18   | RNA-binding protein  |
| SPBC800.02   | serine rich, hypothetical protein; sequence orphan                               |
| SPCC1739.08C | short chain dehydrogenase; putative sorbitol utilization                         |
| SPAC343.09   | UBX domain   |
| SPCC306.05C  | possible growth response protein; contains Pfam-B_35059                          |

# Web Table F: Middle genes.

| 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 regu          | lators               |  |
| mde3                  | SPBC8D2.19           | protein kinase; similar to S. cerevisiae IME2  |
| mesl                  | SPAC5D6.08C          | meiosis-II protein   |
| spo4                  | SPBC21C3.18          | protein kinase involved in meiotic spindle formation                                 |
| spoб                  | SPBC1778.04          | required for meiosis II and sporulation  |
| Condensin (s          | ome less than 4x ind | luction)   |
| 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/chron         | mosome seggregation  | n/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   |
| dis 1                 | 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                  |
| finl                  | 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-pr           | omoting complex (A   | 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/pr          | oteasome 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)                                  |

|             | 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 <i>S. cerevisiae SNX4</i> |
| 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 <i>S. cerevisiae CDC7</i>          |
| 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                                   |
| Morphogen   | esis            |   |
| 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 reg | gulators        |   |
|             | SPAC1006.06     | putative <i>rho1</i> GDP-GTP exchange protein   |
|             | SPAC1565.02C    | putative rho GTPase activating protein  |
|             | SPAC16A10.04    | <i>rho1</i> -like protein.  |
| ~           | SPAC20H4.11C    | <i>rho1</i> protein paralogue; ras family   |
| Septins     |                 |   |
| spn2        | SPAC821.06      | septin  |
| spn5 mde9   | SPAC24C9.15C    | septin  |
| spn6        | SPCC188.12      | septin  |
| spn/        | SPBC21.08C      | septin  |
|             |                 |   |
| cdc/        | SPBC21.06C      | protein kinase; required for septum formation and cytokinesis   |
| cac11       | SPCC1739.11C    | involved in cytokinesis and septation; putative spindle pole body protein; similar to S.                            |
| mvo51       | SPBC2D10 14C    | class V myosin: component of the cytokinetic actin ring   |
| my051       | SPBC17D1.07C    | nossible protein involved in cytokinesis by similarity to <i>S</i> cerevisiae IOG1                                  |
| Other cytos | keleton         | possible protein involved in cytokinesis by similarity to 5. et evisite 1901  |
| Still Cytos | SPBC 56F2 03    | actin related protein: S cerevisige ARP10 homolog   |
|             | SPAC688.06C     | very putative actin-related protein regulator of microtubule stability by similarity to yeast                       |
|             | SPDC110-12      | AME1  |
| Samet /     | SPBC119.12      | myosin neavy chain-like coiled-coil protein   |
| secretion/m | condrane trainc |   |

| 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   |
| ssol               | SPCC825.03C    | putative syntaxin plasma membrane (t-SNARE)  |
| ufe1               | SPCC895.04C    | putative ER syntaxin (t-SNARE)   |
| sec9               | SPBC26H8.02C   | component of t-SNARE complex   |
| vpt3               | SPAC18G6.03    | Golgi <i>rab11</i> 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   |
| 0                  | 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 <i>S. cerevisiae GOT1</i>   |
| 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 <i>S. cerevisiae TIP20</i> required for protein transport from the ER to the Golgi                                    |
|                    | SPBP8B7.24C    | putative autophagy protein; by similarity to <i>S. cerevisiae AUT7</i> -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   |
| <b>Complex</b> lip | oid 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         | r-svnthesis    |  |
|                    | SPBC3D6.07     | N-acetylglucosaminyl-phosphatidylinositol  |
| gpil               | SPBC30D10 11   | N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein gni1  |
| or                 | 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-E and <i>S. cerevisiae GPI11</i>                 |
|                    | 1              | w numur 110 1 und 5. cereriside 01 111   |

| Glycoprotei  | n 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    | ſ               |  |
|              | SPBC342.03      | putative <i>GAS1</i> 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   |
| Transcriptio | onal 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    | SPBC19F8.07     | cdk-activating kinase; putative transcription initiation factor TFIIH subunit; cyclin-   |
| mcs5         |                 | dependent kinase activating kinase (CAK); similar to S. cerevisiae KIN28   |
|              | SPAC12G12.05C   | putative transcription initiation factor TFIID subunit; component of TAF(II) complex<br>(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   |
| pngl         | SPAC3G9.08      | conserved protein; PHD finger domain; putative histone acetyltransferase complex; similar to <i>S. cerevisiae YNG2</i>   |
|              | SPAC13G7.10     | hypothetical Myb-like DNA-binding protein  |
| Checkpoint   |                 |  |
| mik1         | SPBC660.14      | mitosis inhibitor protein kinase; DNA replication checkpoint control; similar to <i>S. cerevisiae SWE1</i>   |
| chk] rad27   | SPCC1259.13     | protein kinase: DNA damage checkpoint: similar to S. cerevisiae CHK1   |
| brcl         | SPBC582.05C     | BRCT domain protein; (cell-cycle checkpoint superfamily)   |
| dma1         | SPAC17G8.10C    | component of the spindle assembly checkpoint; required to prevent septum formation and   |
|              |                 |  |

|               |                      | 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 s | hock                 |   |
| 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 sy  | nthesis –probably re | elated 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   |
| Transporter   | <u>s</u>             |   |
|               | 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 |

|              |                 | 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    | nutative analysis and somethies, unoredown domain                                     |
|              | SPRPB2B2 12C    | nutative sal10 hitunctional protein: includes UDP-solucose 4-enimerase                |
|              | SPBPB2B213      | nutative galactokinase  |
|              | SPAC4G9.12      | nutative ducokinase   |
|              | SPAC24B11.05    | putative glucokinase  |
|              | SPRC30D10.14    | putative haloacid denalogenase-like hydrolase   |
|              | SPDC047 15C     | putative hydroidse  |
|              | SFBC947.15C     | 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    | nutative NADH nyronhosphatase L of the Nudix family of hydrolases: by similarity to S |
|              | 51 501770.050   | 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 l | RNAs            |   |
| meul1        | 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  |

|              | cosmid SPAC1B2 | putative non-coding RNA; misc_RNA_1.1.46.RC  |
|--------------|----------------|--|
| Sequence orp | hans           |  |
|              | 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  |
|              | SPBC16E9.07    | hypothetical protein; sequence orphan: predicted coiled-coil                           |
|              | SPAC1782.04    | hypothetical protein: sequence orphan  |
|              | SPAC1762.04    | 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  |
|              | SPCC24B1014C   | hypothetical protein; sequence orphan  |
|              | SPAC24B10.14C  | hypothetical protein; sequence orphan  |
|              | SIRC24110.08   | hypothetical protein, sequence orphan  |
|              | SFBC25B2.0/C   | hypothetical protein: sequence orphan  |
|              | SPAC25H1.04    | hypothetical protein; sequence orphan  |
|              | SDDC26U9 12C   | hypothetical protein; sequence orphan  |
|              | SPAC27D7 05C   | hypothetical protein; sequence orphan  |
|              | SPAC27D7.03C   | hypothetical protein; sequence orphan  |
|              | SPAC27E2 11C   | hypothetical protein; sequence orphan  |
|              | SPAC29A4 12C   | hypothetical protein; sequence orphan  |
|              | SPAC20A4.14C   | hypothetical protein; sequence orphan  |
|              | SPAC25A4.14C   | hypothetical protein; sequence orphan; 3 predicted transmembrane belieses              |
|              | SPRC2G2 10C    | hypothetical protein ; sequence orphan   |
|              | SPPC21E10.17C  | hypothetical protein:, sequence orphan   |
|              | SPDC31H12.06   | hypothetical protein; sequence orphan: 12 prediated transmombrane balicae: prediated N |
|              | 51 CC511112.00 | 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  |
| 1            |                | I Jr   |

|      | 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 belices                                    |
|      | 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  |
|      | 51 0 0 1 0 2 0 0 7 0 | 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 <i>S. pombe</i> specific; similar to <i>S. pombe</i>   |
|      | SPAC1248.07          | SFAC2SA1.1/C  |
|      | SI AC 1546.07        | predicted transmembrane helices: highly similar to S nombe SPAC212 01c; highly  |
|      |                      | similar to <i>S. pombe</i> SPAC1348.01  |
|      | SPAC212.04C          | hypothetical protein; duplicated in <i>S. pombe</i> telomeric region; possibly <i>S. pombe</i>  |
|      |                      | specific; highly similar to SPAC212.01c etc   |
|      | SPAC212.01C          | hypothetical protein; duplicated region in <i>S. pombe</i> telomeric region; possible fortuitous reading frame; possibly <i>S. pombe</i> specific |
|      | SPBPB2B2.07C         | hypothetical protein; duplicated telomeric reading frame; or miscellaneous cellular RNA; possibly <i>S. pombe</i> 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,  |

|        |               | 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   |
| mdel   | SPAC16E8.05C  | requires mei4p for transcriptional activation; similar to <i>S. pombe</i> SPAC8F11.05c;                                  |
| may 22 | SPCC612 11C   | possibily <i>S. pomoe</i> specific   |
| meu25  | SPCC015.11C   | protein with Pfam P. 9647 domain: S. nowbe specific  |
|        | SPAC11G7.06C  | protein with Pfam B 2647 domain; S. pombe specific   |
|        | SPAC4C0.07    | protein with Pfam P_9647 domain; S. pombe specific   |
|        | SPAC409.07    | protein with Pfam P_9647 domain; S. pombe specific   |
|        | SPDC106.09C   | burgethetical repeat containing protain: possibly S now be enabled   |
|        | SPBC106.08C   | highed repeat containing protein, possibly S. pombe specific   |
|        | SPCC350.04C   | blased repeat-containing protein, possibly <i>S. pombe</i> specific  |
|        | SPDC4C3.08    | nypotnetical protein, possibly <i>S. pombe</i> specific  |
| meu27  | SPCC1259.14C  | protein with Plam-B_8647 domain, <i>S. pombe</i> specific  |
| Others | SDA D27C11 02 | hymothesical pratains similar to S. convision CDC122   |
|        | SPAP2/011.05  | hypothetical protein, similar to S. <i>cereviside</i> CDC125   |
|        | SPAC20H5.11   | formation; PH (pleckstrin homology) domain   |
|        | SPAC5D6.04    | hypothetical protein; similar to <i>S. cerevisiae</i> YBR287W; 6 predicted transmembrane belies                          |
|        | SPAC694 03    | hypothetical protein: similar to S <i>cerevisige</i> YCL047C   |
|        | SPAC589.12    | hypothetical protein: similar to <i>S. cerevisiae</i> YCR017C- integral membrane protein                                 |
|        | 51110009112   | involved in drug sensitivity; 20 predicted TM helices  |
|        | SPCC4G3.11    | hypothetical protein; similar to <i>S. cerevisiae</i> YDL089W (low); 4 predicted transmembrane helices                   |
|        | SPAC57A7.05   | hypothetical protein; similar to <i>S. cerevisiae</i> 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 <i>S. cerevisiae</i> YDR346C and paralogs; low similarity to NIED/NIEK/NIEE/NIEN family |
|        | SPAC20H4.01   | hypothetical protein: similar to <i>S. cerevisiae</i> YDR398W which is null lethal                                       |
|        | SPAC24H6.01C  | hypothetical protein: similar to <i>S. cerevisiae</i> YGL084C  |
|        | SPBC19C2.11C  | hypothetical protein: similar to <i>S. cerevisiae</i> YGL219C: possibly fungal specific                                  |
|        | SPAC105.02C   | hypothetical protein: similar to <i>S. cerevisiae</i> YGL242C: similarity to ankyrin                                     |
|        | SPAC1F3.09    | hypothetical protein: similar to <i>S. cerevisiae</i> 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 <i>S. cerevisiae</i> 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 <i>S. cerevisiae</i> YNL245C which is null lethal; predicted coiled coil                |

|           | 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 YPI260W; putative surface protein adhesion  |
|           |               | molecule   |
|           | SPBC30D10.09C | hypothetical protein; similar to <i>S. cerevisiae</i> YPR027w; putative integral membrane protein  |
|           | SPAC56F8.05C  | hypothetical protein; similar to <i>S. cerevisiae</i> YPR148C and YIL041W; possibly fungal specific  |
|           | SPAC1296.04   | hypothetical protein; this *may* be the ortholog of <i>S. cerevisiae SPO73</i> ; similarity is *very low* but they are reciprocal best hits  |
|           | SPAC25H1.03   | hypothetical protein with low similarity to <i>Drosophila</i> CG7053: human cDNA FLJ11773  |
|           | SPAPYUG7.06   | hypothetical protein; conserved domain in <i>Arabidopsis</i> ; <i>C. elegans</i> , <i>Drosophila</i> and   |
|           |               | human, motif Y.GYHL {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 <i>C. elegans</i> b0491.1 protein; <i>Drosophila</i> CG9865 protein; and <i>S. cerevisiae</i> YJR013W, but has large |
|           | SPAC3A1213C   | N terminal extension   |
|           | SPAC56E4.05   | hypothetical protein; similar to <i>A. thaliana</i> T29E15 14 and T4G30500 (low by multiple  |
|           | 51 AC3014.03  | 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; <i>DUF10</i>   |
|           | SPAC1952.13   | conserved hypothetical protein; may be involved in respiration by similarity to <i>SMP2</i>  |
|           | SPCC1902.02   | conserved hypothetical protein; similar to <i>S. cerevisiae PAM1</i>   |
|           | SPCC31H12.02C | conserved hypothetical protein; similar to <i>S. cerevisiae</i> YBR054W; similarity to heat  |
|           | 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   |
|           | 51001105.070  | 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   |
| теиб      | 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 <i>S. cerevisiae</i> YJL020C  |
|           | SPCC1223.04C  | putative methyl-transferase  |
| ufd2      | SPAC145.04    | putative ubiquitin fusion degradation protein  |
|           | SPBC4.03      | unknown function   |

|           | SPAC6B12.06C  | unknown function  |
|-----------|---------------|---|
| сурб      | 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 <i>S. cerevisiae SLH1</i> ; 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           |
|           | SDDC2E7 15C   | homology to longevity assurance protein   |
|           | SPAC22A1212   | human downs sundrome aritical ragion like   |
|           | SPRC22A12.15  | human downs syndrome entrear region-fike  |
|           | SPDC1775.09C  | hypothetical LIRE0028 family protein: avalia pualoia acid hinding family protein              |
|           | SPCC4D3.04C   | mitoshondrial ganama maintananaa protain proguraar  |
|           | SPBC30D10.08  | national and genome maintenance protein precusor.   |
|           | SPAC580.06C   | possibly involved in innochondrial division by similarity to <i>S. cereviside F1S1</i>        |
|           | SI AC 589.00C | S cerevisiae PHO88 homologue  |
| abcl      | SPAC9E9 12C   | involved in assembly of cytochrome bc1 complex  |
|           | SPBC3B9.17    | HesB-like domain: required for iron metabolism by similarity to <i>S. cerevisiae ISA1</i>     |
|           | SPCC645.03C   | HesB-like domain: required for iron metabolism by similarity to <i>S. cerevisiae ISA1</i>     |
| kms2      | SPBC947.12    | protein with possible coiled coil: similar to <i>S. pombe kms1</i> 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 <i>S. cerevisiae TPP1</i> ; 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   |

|        | 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 <i>S</i> .             |
|        | SDA C21E12.01 | cerevisiae F201   |
| atus 1 | SPAC51F12.01  | related to yeast Zds family proteins  |
| stm1   | SPAC1/C9.10   | SU2 downing containing materia  |
| csn3   | SPBC119.05C   | similar to human containing protein   |
|        | SPCC1239.12C  |   |
|        | SPBC1//5.11C  | similar to S. cereviside CDC50  |
| 41     | SPBC947.11C   | similar to S. <i>Cereviside EFD</i> (required for stability of direct DNA repeats)                      |
| icg1   | SPBC000.11    | sningle-stranded 101-5 terometric binding protein   |
| scps   | SPAC3A11.02   | spindle poison sensitivity related protein.   |
|        | SPAC30.03C    | vary hypothetical protein overlans N term of SDAC2E10.06e; expression pattern on                        |
|        | SFACSF10.07C  | 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   |
| ptc l  | SPCC4F11.02   | protein phosphatase 2C homolog 1  |
|        | SPAC227.15    | similar to <i>S. cerevisiae HEX2</i> ; putative regulatory subunit for protein phosphatase              |
| теи5   | 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   |
| 1.7    | SPCC74.09     | RNA-binding protein   |
| mde/   | 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   |
| an c 1 | SPBC119.17    | putative zinc metalloprotease   |
| aper   | SPBC1921.05   | anniopepudase 1<br>probable zine motellopentidage disintegring localization of CED fusion. Source since |
|        | SPAC1/AJ.040  | WD repeat protain   |
|        | SPRC27D12.05  | WD repeat protein   |
|        | SFDC2/D12.03  | WD repeat protein   |
|        | SPAC5H3.08C   | w D repeat protein  |

|            | 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 <i>S. cerevisiae MUB1</i> |
| 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 <i>RNF12</i>        |
|            | 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  |

## Web Table G: Late genes.

| Cell cycle | e regulation |  |
|------------|--------------|--|
| wee1       | SPCC18B5.03  | mitosis inhibitor protein kinase; negatively regulates G2/M transition   |
| srw1 ste9  | SPAC144.13C  | APC regulator, CDC20/fizzy family; required for conjugation  |
|            | SPBP8B7.27   | putative ubiquitin-protein ligase, HECT domain   |
|            | SPBC14F5.10C | RING domain protein, possible E3 ubiquitin ligase  |
| Cell wall  |              |  |
|            | SPAC23H3.11C | putative beta-glucan synthesis-associated protein  |
|            | SPBC11C11.05 | putative cell-wall synthesis protein   |
| mok12      | SPBC32H8.13C | alpha glucan synthase  |
| cAMP pa    | nthway       |  |
| git11      | SPBC215.04   | G gamma subunit of the gpa2/git5/git11 heterotrimeric G protein  |
| cgsl       | SPAC8C9.03   | cAMP-dependent protein kinase regulatory chain; similar to S. cerevisiae BCY1  |
| pkal git6  | SPC110.10    | cAMP-dependent protein kinase catalytic subunit  |
| git3       | SPCC1753.02C | adenylate cyclase activation protein   |
| Transcrip  | ption        |  |
|            | SPBC1105.14  | putative zinc-finger transcriptional activator for genes involved in the multistress response by similarity to <i>S. cervisiae MSN2</i> (also in stress group) |
|            | SPCC1919.14C | putative transcription factor tfiiib component   |
|            | SPBC25B2.03  | putative zinc finger protein   |
| DNA rep    | air          |  |
| rhp16      | SPCC330.01C  | nucleotide excision repair protein; SNF2 type DNA helicase; similar to S. cerevisiae RAD16   |
|            | SPAC2F7.06C  | DNA polymerase X family; involved in repair  |
| rad17      | SPCC330.02   | dna repair protein, nucleotide excision repair, S. cerevisiae RAD7 homolog   |
| uvel       | SPBC19C7.09C | UV-endonuclease.   |
| Stress     |              |  |
| mpr1 spy1  | SPBC725.02   | stress response regulator phosphotransmitter; respone regulator phospotransferase; similar to <i>S. cerevisiae YPD1</i>  |
| ptc4       | SPAC4A8.03C  | protein phosphatase 2C isoform   |
|            | SPAC688.04C  | glutathione S transferase 3  |
| cta l      | SPCC757.07C  | catalase   |
| rds 1      | SPAC343.12   | stress response protein rds1p  |
|            | SPBC1105.14  | putative zinc-finger transcriptional activator for genes involved in the multistress response by similarity to <i>S. cervisiae MSN2</i>                        |
| Mitochon   | idrial genes |  |
|            | P05501       | mitochondrial-cytochrome b   |
|            | P05511       | mitochondrial-hypothetical 91 KDa protein in cob intron  |
|            | P07657       | mitochondrial-cytochrome C oxidase polypeptide I (EC 1.9.3.1).   |
|            | P14575       | mitochondrial- cytochrome C oxidase polypeptide III (EC 1.9.3.1).  |
|            | P21535       | mitochondrial-ATP synthase A chain precursor (EC 3.6.3.14) (protein 6).  |
|            | P21536       | mitochondrial-ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).   |
|            | P21537       | mitochondrial-ATP synthase protein 9, mitochondrial (EC 3.6.3.14) (lipid-binding protein).   |
|            | P21547       | mitochondrial-hypothetical 25.5 KDa protein in ATP6-ATP8 intergenic region (urfA).   |
|            | P22191       | mitochondrial-hypothetical cox1 intron-1 45.6 Kda protein (probable maturase).   |
| Metaboli   | c            |  |
|            | SPAC869.08   | putative protein-l-isoaspartate o-methyltransferase  |
|            | SPAC750.02C  | putative membrane transporter  |
|            | SPAC13A11.06 | putative pyruvate decarboxylase (EC 4.1.1.1)   |
|            | SPCC663.07C  | short chain dehydrogenase pseudogene   |
|            | SPBC1198.01  | putative glutathione-dependent formaldehyde dehydrogenase  |
|            | SPCC1281.07C | protein with Glutathione S transferase domain  |

|       | SPAPB1A11.03  | putative FMN dependent dehydrogenase; similar to lactate dehydrogenase   |
|-------|---------------|--|
|       | SPAC186.02C   | 2-hydroxyacid dehydrogenase homolog  |
|       | SPCC663.13C   | putative acetyltransferase; similar to <i>S. cerevisiae</i> YOR253W  |
|       | SPCC1450.13C  | riboflavin synthase alpha chain  |
|       | SPAP27G11.09C | putative gtp cyclohydrolase; possible riboflavin biosynthesis  |
|       | SPAC1002.19   | putative GTP cyclohydrolase; riboflavin biosynthesis   |
|       | SPCC1281.04   | pyridoxal reductase homolog  |
|       | SPAC869.07C   | putative alpha-galactosidase   |
| gmhl  | SPAC5H10.11   | putative galactosyltransferase; high similarity to Gmh3p, which is an alpha-1,2-<br>galactosyltransferase  |
| gna1  | SPAC16E8.03   | acetyltransferase involved in UDP-N-acetylglucosamine synthesis  |
|       | SPAC513.02    | protein with similarity to phosphoglycerate mutases  |
|       | SPAC4H3.08    | putative short chain dehydrogenase   |
|       | SPAC22A12.17C | short chain dehydrogenase; possible sorbitol utilization   |
|       | SPBC1773.06C  | alcohol dehydrogenase  |
|       | SPAC2E1P3.01  | putative dehydrogenase by similarity   |
|       | SPAC23D3.05C  | alcohol dehvdrogenase pseudogene   |
|       | SPAC139.05    | probable succinate semialdehyde dehydrogenase  |
| tms1  | SPBC1773.05C  | putative sorbitol dehydrogenase  |
|       | SPACUNK4.17   | putative sugar oxidoreductase; possible sorbitol utilisation   |
|       | SPBC24C6.09C  | similarity to transketolase; Pfam-B 53149; Pfam-B 17168  |
| Orpha | ns            |  |
|       | SPCC1235.03   | hypothetical protein; sequence orphan  |
|       | SPAC15F9.01C  | hypothetical protein; sequence orphan  |
|       | SPAC15A10.07  | hypothetical protein; sequence orphan  |
|       | SPCC24B10.16C | hypothetical protein; sequence orphan; has transcript on microarray  |
|       | SPAC32A11.02C | hypothetical protein; sequence orphan; contians predicted coiled-coil region   |
|       | SPAPB8E5.10   | hypothetical protein; sequence orphan; similarity (low) to to Drosophilla CG12569  |
|       | SPAC23H3.04   | hypothetical protein; similar to S. pombe SPAC1952.10C; possible S. pombe specific protein   |
|       | SPBC3H7.08C   | hypothetical protein; sequence orphan  |
|       | SPBC685.03    | hypothetical serine-rich protein; sequence orphan; predicted N-term signal sequence  |
|       | SPAPB1A10.08  | hypothetical protein.; sequence orphan   |
|       | SPBC409.17C   | hypothetical protein; sequence orphan  |
|       | SPBC17D1.01   | hypothetical protein; sequence orphan  |
|       | SPAC4F10.17   | hypothetical protein; sequence orphan; predicted N-terminal signal sequence  |
|       | SPCC1494.03   | hypothetical protein; sequence orphan  |
|       | SPCC1682.06   | hypothetical protein; 2 predicted transmembrane helices; Pfam-B_23431; similar to <i>S. pombe</i> SPBC18H10.18C; possibly <i>S. pombe</i> specific   |
|       | SPAC18G6.09C  | hypothetical serine-rich protein; sequence orphan  |
|       | SPCC16A11.15C | hypothetical protein; sequence orphan  |
|       | SPAC343.20    | hypothetical protein; sequence orphan; has transcript profile on microarray  |
|       | SPBPB2B2.19C  | hypothetical protein; duplicated at telomere; almost identical to SPAC1348.02 and SPAC756.05; 5 predicted transmembrane helices; possibly <i>S. pombe</i> specific   |
|       | SPCC569.03    | hypothetical repeat containing protein; see also SPCC569.01 SPCC613.11C; SPBC106.08C; SPCC330.04C; possibly <i>S. pombe</i> specific   |
|       | SPCC736.05    | hypothetical wtf-like protein; S. pombe-specific   |
|       | SPBP4G3.03    | hypothetical protein; possibly S. pombe specific; similar at the N-term to SPBP7G5.01  |
|       | SPAC1348.02   | hypothetical protein; 5 predicted transmembrane helix; low similarity to membrane transporter; highly similar to SPBPB2B2.19C SPAC750.05C SPAC977.01; possibly <i>S. pombe</i> specific                      |
|       | SPAC977.01    | hypothetical protein; possibly <i>S. pombe</i> specific; telomeric duplication; highly similar to <i>S. pombe</i> SPAC750.05C SPAC1348.02 and SPBPB2B2.19C   |
|       | SPAC750.05C   | hypothetical protein; low similarity to <i>S. cerevisiae</i> YHL017W is probably spurious; highly similar to <i>S. pombe</i> SPAC1348.02; highly similar to <i>S. pombe</i> SPBPB2B2.19c; possibly <i>S.</i> |

|        |                             | pombe specific   |  |  |  |  |
|--------|-----------------------------|--|--|--|--|--|
|        | SPBC18H10.18C               | hypothetical protein; 2 predicted transmembrane helices; very high similarity to   |  |  |  |  |
|        | SPAC15E1 10                 | hypothetical protein: possibly <i>S. pombe</i> specific: similar to SPBP4G3.03   |  |  |  |  |
|        | SPCC737.04                  | hypothetical protein: possibly <i>S. pombe</i> specific  |  |  |  |  |
|        | SPAC14C4 01C                | hypothetical protein: sequence orphan  |  |  |  |  |
|        | SPAC23H3 15C                | hypothetical serine-rich protein: sequence ornhan  |  |  |  |  |
|        | SPCC1393-12                 | hypothetical protein: sequence orphan  |  |  |  |  |
|        | SPAC15E1.02C                | hypothetical protein: sequence orphan: 3 predicted transmembrane belices   |  |  |  |  |
|        | SPCC191.01                  | hypothetical protein: sequence orphan  |  |  |  |  |
| Others | 51 001 71.01                |  |  |  |  |  |
|        | cosmid SPAC1D4              | cDNA, no corresponding ORF could be predicted: misc RNA 2.2.20 RC  |  |  |  |  |
|        | SPAC11D3.13                 | conserved hypothetical protein: ThiJ domain  |  |  |  |  |
|        | SPAP14E8 05C                | conserved hypothetical protein: 3 predicted transmembrane helices  |  |  |  |  |
|        | SPAC1F7.06                  | conserved hypothetical protein   |  |  |  |  |
|        | SPCC663.14C                 | hypothetical protein; similar to <i>S. cerevisiae</i> YPL221W; predicted N-terminal signal sequence;<br>8 predicted transmembrane helices                                    |  |  |  |  |
|        | SPBC1685.14C                | hypothetical protein; similar to S. cerevisiae YNL212W   |  |  |  |  |
|        | SPCC16A11.01                | hypothetical protein; similar to S. cerevisiae YKL051W   |  |  |  |  |
|        | SPCC1322.03                 | hypothetical protein; similar to S. cerevisiae YAL053W; 11 predicted transmembrane helices   |  |  |  |  |
|        | SPCC830.08C                 | hypothetical protein; similar to <i>S. cerevisiae YIP2</i> ; possibly involved in membrane trafficking by similarity   |  |  |  |  |
|        | SPBC947.09                  | hypothetical protein; similar to S. cerevisiae YPL280W; possibly fungal specific   |  |  |  |  |
|        | SPAC23C11.06C               | hypothetical protein; similar to S. cerevisiae YNL115C; 5 predicted transmembrane helices  |  |  |  |  |
|        | SPBC21C3.19                 | hypothetical protein; similar to S. cerevisiae YHR087W   |  |  |  |  |
|        | SPCC4G3.03                  | hypothetical protein similar to <i>S. cerevisiae</i> YLR149C; putative apoptotic protease activating factor, by low similarity to human spaf1 (conserved catalytic residues) |  |  |  |  |
|        | SPBC725.03                  | hypothetical protein; similar to S. cerevisiae YGR017W   |  |  |  |  |
|        | SPBC6B1.03C                 | hypothetical protein; similar to S. cerevisiae YHR097C   |  |  |  |  |
|        | SPAC16E8.02                 | hypothetical protein; similar to S. cerevisiae YGL010W; 4 predicted transmembrane helices  |  |  |  |  |
|        | SPAC3C7.02C                 | hypothetical protein; similar to S. cerevisiae YPL004C   |  |  |  |  |
|        | SPCC970.02                  | hypothetical protein; similar to S. cerevisiae YKL046C   |  |  |  |  |
|        | SPAC5H10.02C                | hypothetical protein; similar to S. cerevisiae YPL280W   |  |  |  |  |
|        | SPCC757.03C                 | conserved hypothetical protein   |  |  |  |  |
|        | SPBC20F10.03                | hypothetical protein; Pfam-B_11425; similarity to mouse and rat interferon-related developmental regulator 1- nerve growth factor; also conserved in C. elegans              |  |  |  |  |
|        | SPCC1742.01                 | hypothetical protein; sequence orpahn; large repeated threonine-rich region; 4 Tryp_mucin,   |  |  |  |  |
|        | SPCC1795.13                 | Mucin-like glycoprotein repeat; predicted N-terminal signal sequence   |  |  |  |  |
|        | SPCC594.04C                 | hypothetical protein; low similarity to a region of <i>S. cerevisiae</i> Farnesyl cysteine:carboxyl methyltransferase; conserved residues G{VL}{FW}.{WY}SRHPN{FY}{FL}{GA}{E} |  |  |  |  |
|        | SPAC869.09                  | hypothetical protein; similar to N. crassa conidiation protein 6   |  |  |  |  |
|        | SPAC22G7.11C<br>SPAC4G8.01C | hypothetical protein; similar to N. crassa conidiation -specific protein 6   |  |  |  |  |
|        | SPAC11D3.01C                | protein with similarity to neurospora conidiation specific protein   |  |  |  |  |
|        | SPCC757.02C                 | hypothetical protein; conserved in A. thaliana; Pfam-B_37808 domain  |  |  |  |  |
|        | SPAC869.06C                 | hypothetical protein; low similarity to S. coelicolor SC9H11.25C   |  |  |  |  |
|        | SPAC3G6.07                  | very hypothetical protein  |  |  |  |  |
|        | SPBC11C11.12                | hypothetical protein   |  |  |  |  |
|        | SPBC3D6.01                  |  |  |  |  |  |
|        | SPBP19A11.02C               | putative membrane glycoprotein; predicted N-term signal sequence   |  |  |  |  |
|        | SPBP4H10.10                 | membrane protein of unknown function, possibly involved in respiration by similarity to YGR101W; rhomboid family   |  |  |  |  |
|        | SPAC328.04                  | AAA family ATPase with similarity to katanin; putative microtubule severing protein by   |  |  |  |  |

|      |   | similarity   |  |  |
|------|---|--|--|--|
| cmk1 | SPACUNK12.02C   | calmodulin kinase i homolog.   |  |  |
|      | SPAC22G7.08   | putative serine/threonine protein kinase   |  |  |
|      | SPBC725.06C   | putative serine/threonine protein kinase   |  |  |
|      | SPBC21.07C  | putative serine/threonine protein kinase   |  |  |
| rga5 | SPBC17F3.01C  | RhoGAP GTPase activating protein   |  |  |
| n150 | similar to S. cerevisiae MAF1; putative nuclear-cytoplasmic transport |  |  |  |
|      | SPAC3H8.09C   | putative RNA-binding protein   |  |  |
|      | SPBC2G2.17C   | sun family protein; S. cerevisiae homolog involved in aging process and cell cycle regulation  |  |  |
|      | SPBC1711.12   | putative dipeptidyl peptidase; possibly secreted   |  |  |
|      | SPAC227.01C   | potential Protein required for retention of luminal ER proteins; similar to S. cerevisiae ERD1 |  |  |
|      | SPBC609.01  | hypothetical protein; ribonuclease II (RNB) family   |  |  |
|      | SPBC1685.05   | putative serine protease   |  |  |
|      | SPAC4H3.03C   | putative family 15 glycosyl hydrolase  |  |  |
| agl  | SPAPB24D3.10C   | alpha-glucosidase; family 31 glycosyl hydrolase  |  |  |
| cmd1 | SPBC12D12.02C   | DNA polymerase delta subunit   |  |  |
| sco1 | SPBC119.06  | putative cytochrome C oxidase assembly protein   |  |  |

#### Web Table H: Potential regulatory motifs.

The upstream sequences of all ORFs (500 bp) were scanned for the presence of short oligomers overrepresented in a cluster with respect to the whole genome. The identified sequences were similar to previously known binding sites (related motif column). The frequencies of motif occurrence both within the clusters and in random genomic sequences are indicated. The p values indicate the probabilities that the observed results are due to chance. The last column shows the percentage of genes containing more than one copy of the motif in their upstream sequences.

| Cluster                  | Sequence                  | Related Motif<br>(Reference) | Orientation | Frequency<br>(cluster) | Frequency<br>(genome) | p value | >1 copy |
|--------------------------|---------------------------|------------------------------|-------------|------------------------|-----------------------|---------|---------|
| Starvation/<br>pheromone | TCTTTGT                   | TR box<br>(19)               | forward     | 40%<br>(16/40)         | 9.5%                  | 0.036   | 52%     |
| (delayed)                |                           |                              | reverse     | 45%<br>(18/40)         | 4.8%                  | 1.0e-8  |         |
| Early                    | ACGCGT                    | MluI box<br>(20)             | palindrome  | 32%<br>(30/94)         | 4.1%                  | 0.013   | 25%     |
| Middle                   | GTAAACA                   | FLEX<br>(8)                  | forward     | 22.6%<br>(122/540)     | 9.12%                 | 9.6e-16 | 30%     |
|                          |                           |                              | reverse     | 35.0%<br>(189/540)     | 12.3%                 | 4.2e-37 |         |
| Late                     | TGACGGT<br>(0/1 mismatch) | ARE<br>(21)                  | forward     | 44%<br>(58/129)        | 21.06%                | 2.8e-4  | 22%     |

# Web Table I: Known and potential transcriptional regulators induced during meiosis and sporulation.

| <b>Biological name</b> | Systematic name    | Meiotic role <sup>Ref</sup> | Description  |
|------------------------|--------------------|-----------------------------|--|
| Starvation/pheron      | none response      | •                           | -  |
| stel l                 | SPBC32C12.02       | yes <sup>19</sup>           | HMG box transcription factor                         |
| matPi                  | P10842 (SwissProt) | yes <sup>22</sup>           | homeodomain protein                                  |
| matMc                  | SPBC1711.02        | yes <sup>22</sup>           | HMG box transcription factor                         |
|                        | SPAC1039.05C       | unknown                     | zinc finger C2H2                                     |
|                        | SPAC11D3.17        | unknown                     | zinc finger C2H2                                     |
|                        | SPBC1773.12        | unknown                     | binuclear cluster DNA-binding domain                 |
| Early                  |                    |                             |  |
| cdc10                  | SPBC336.12C        | yes <sup>23</sup>           | MluI-box binding factor (MBF) complex                |
| res1/pct1              | SPAC22F3.09C       | yes <sup>24,25</sup>        | MluI-box binding factor (MBF) complex                |
| rep1/rec16             | SPBC2D10.06        | yes <sup>1,5</sup>          | regulator of pre-meiotic DNA synthesis               |
|                        | SPAC1002.05C       | unknown                     | similar to retinoblastoma binding proteins           |
|                        | SPCC4G3.07C        | unknown                     | similar to retinoblastoma binding protein            |
|                        | SPC21B10.13C       | unknown                     | homeodomain protein                                  |
|                        | SPCC290.04         | unknown                     | GATA Zinc finger                                     |
|                        | SPBC1718.02        | unknown                     | PhD zinc finger                                      |
|                        | SPAC31G5.10        | unknown                     | myb DNA-binding-domain protein                       |
| Middle                 |                    |                             |  |
| mei4                   | SPBC32H8.11        | yes <sup>8</sup>            | fork head protein type transcription factor          |
|                        | SPBC16G5.15C       | unknown                     | fork head protein type transcription factor          |
|                        | SPAC1142.08        | unknown                     | fork head protein type transcription factor          |
| atf21                  | SPBC2F12.09C       | yes (this work)             | atf creb-family transcription factor                 |
| atf31                  | SPAC22F3.02        | yes (this work)             | atf creb-family transcription factor                 |
| rsvl                   | SPBP4H10.09        | unknown                     | stationary phase viability (Zinc finger C2H2)        |
|                        | SPCC18.03          | unknown                     | 8 Zinc finger NFX domains                            |
|                        | SPBC19G7.04        | unknown                     | HMG box transcription factor                         |
|                        | SPBP8B7.30C        | unknown                     | binuclear cluster DNA-binding domain                 |
|                        | SPAPB1A11.04C      | unknown                     | binuclear cluster DNA-binding domain                 |
|                        | SPAC959.06C        | unknown                     | similarity to viral late transcription factor        |
|                        | SPCC584.02         | unknown                     | copper-fist transcription factor                     |
|                        | SPCC31H12.08C      | unknown                     | similar to carbon catabolite repressor proteins      |
|                        | SPAC12G12.05C      | unknown                     | TFIID or SAGA complex (histone acetyl transferase)   |
|                        | SPBC14C8.17C       | unknown                     | SAGA complex (histone acetyl transferase)            |
| pngl                   | SPAC3G9.08         | unknown                     | PHD finger; poss. histone acetyl transferase complex |
| clr4                   | SPBC428.08C        | unknown                     | histone H3 methyltransferase; involved in silencing  |
|                        | SPAC343.11C        | unknown                     | similarity to retinoblastoma binding proteins        |
|                        | SPBC1861.07        | unknown                     | elongin c homologue                                  |
|                        | SPBC1826.01C       | unknown                     | SNF2 family helicase, possibly transcrip. repression |
| Late                   |                    |                             |  |
|                        | SPBC1105.14        | unknown                     | zinc finger C2H2                                     |
|                        | SPAC32A11.03C      | unknown                     | homeodomain protein                                  |
|                        | SPCC1919.14C       | unknown                     | putative transcription factor TFIIIb component       |

#### Web Table J: Core meiotic transcriptome conserved in fission and budding yeasts.

Note that  $\sim 50$  genes would be expected to be part of the core meiotic transcriptome by chance (Fig. 4). Fission yeast early genes correspond approximately to budding yeast cluster 4, middle genes to clusters 5-6 and late genes to cluster 7<sup>26</sup>. Cell cycle genes, APC components and recombination genes tend to belong to the corresponding clusters in both species.

| S.cerevisiae |               |           | S. pombe         | Cluster (S.c./S.p)    | Function                      |  |
|--------------|---------------|-----------|------------------|-----------------------|-------------------------------|--|
| Anapha       | se-promotin   | g comple  | x                |                       | ·                             |  |
| CDC27        | YBL084C       | nuc2      | SPAC1851.01      | 5/middle              | APC component                 |  |
| APC4         | YDR118W       | cut20     | SPAC19G12.01C    | 5/middle              | APC component                 |  |
| CDC16        | YKL022C       | cut9      | SPAC6F12.15C     | 6/middle              | APC component                 |  |
| APC1         | YNL172W       | cut4      | SPBC106.09       | 7/middle              | APC component                 |  |
| APC5         | YOR249C       | apc5      | SPAC959.09C      | 5/middle              | APC component                 |  |
| CDC23        | YHR166C       | cut23     | SPAC6F12.14      | 6/middle              | APC component                 |  |
| CDC26        | YFR036W       | hcn1      | SPAC23C11.12     | 6/middle              | APC component                 |  |
| HCT1         | YGL003C       | ste9      | SPAC144 13c      | 5/early(SPCC1620.04C) | APC regulator $(CDC20/fizzv)$ |  |
| CDC20        | YGL116W       | mfr1/fzr1 | SPBC660.02       | middle(SPAC13G6.08C.  |                               |  |
| AMA1         | YGR225W       | slp1s     | SPAC821.08C      | slp1,mfr1)/late(ste9) |                               |  |
|              |               |           | SPAC13G6.08      |                       |                               |  |
|              |               |           | SPCC1620.04C     |                       |                               |  |
| Septins      |               |           | 1                | I                     | 1                             |  |
| CDC10        | YCR002C       | spn2      | SPAC821.06       | 5/middle              | septins                       |  |
| CDC3         | YLR314C       | spn5      | SPAC24C9.15C     |                       |                               |  |
| SPR3         | YGR059W       | spn6<br>7 | SPCC188.12       |                       |                               |  |
| SPR28        | YDR218C       | spn/      | SPBC21.08C       |                       |                               |  |
|              | le regulators | <b>s</b>  | GD 4 G1 700 00 G | c/ :111               |                               |  |
| CDC14        | YFR028C       | clp1/flp1 | SPAC1/82.09C     | 5/middle              | protein phosphatase           |  |
| CDC5         | YMR001C       | ploI      | SPAC23C11.16     | 5/middle              | polo kinase                   |  |
| CLB1         | YGR108W       | cig2      | SPAPB2B4.03      | 5-6/middle            | B-tpe cyclin                  |  |
| CLB3         | YDL155W       | cdc13     | SPBC582.03       |                       |                               |  |
| CLB4<br>CLB5 | YLK210W       |           |                  |                       |                               |  |
| CLBS<br>CLBS | VGR100C       |           |                  |                       |                               |  |
| Recomb       | pination/chro | omosome   | cohesion         |                       |                               |  |
| REC114       | YMR133W       | rec7      | SPCC1753_03C     | 4/early               | recombination protein         |  |
|              | VFR179W       | dmc1      | SPAC8F11.03C     | 4/early               | recombination protein         |  |
| MND1         | VGL 183C      | ume i     | SPAC13A11.03     | 1/early               | recombination protein         |  |
| HOP          | VGL 033W      | may 13    | SPAC222 15       | 4/early               | recombination protein         |  |
| SMC2         | VIL 074C      | meurs     | SPAC222.13       | 4/carly               |                               |  |
| SMC5         | YJL0/4C       | smc3      | SPAC 10F6.09C    | 4/early               |                               |  |
| REC8         | YPR00/C       | recð      | SPC29A10.14      | 4/early               | cohesin                       |  |
| Chromo       | osome segreg  | gation    | I                | 1                     |                               |  |
| STU1         | YLR045C       | dis l     | SPCC736.14       | 5/middle              | spindle pole body component   |  |
| TID3         | YIL144W       | ncd10     | SPBC11C11.03     | 6/middle              | chromosome segregation        |  |
| UBC11        | YOR339C       | ubc11     | SPCC1259.15C     | 5/middle              | chromosome segregation (S.p.) |  |
| DNA re       | pair          |           |                  | 1                     |                               |  |
| RAD23        | YEL037C       | rhp23     | SPBC2D10.12      | 4/middle              | DNA repair                    |  |
| EXO1         | YOR033C       | exo l     | SPBC29A10.05     | 5/middle              | DNA repair/recombination      |  |
| HRR25        | YPL204W       | hhp1      | SPBC3H7.15       | 5/middle              | DNA repair (casein kinase I)  |  |
| Others       |               |           |                  |                       |                               |  |
| HUL4         | YJR036C       |           | SPBP8B7.27       | 5/late                | putative ubiquitin ligase     |  |

| LEE1  | YPL054W | scp3  | SPAC3A11.02   | 2/middle            | zinc finger domains   |
|-------|---------|-------|---------------|---------------------|---|
| ENA2  | YDR039C | cta3  | SPBC839.06    | 2/middle            | P-type ATPase   |
| PMC1  | YGL006W |       | SPAPB2B4.04C  | 2/middle            | P-type ATPase   |
| CMK2  | YOL016C | cmk1  | SPACUNK12.02C | 3/late              | casein kinase   |
| CHS1  | YNL192W | chs1  | SPAC13G6.12C  | 3/middle            | chitin-synthase   |
|       | YGR273C |       | SPBC19C7.04C  | 5/early             | unknown function  |
| ISA1  | YLL027W |       | SPCC645.03C   | 6/middle            | iron metabolism(S.c.)   |
| HTZ1  | YOL012C | pht1  | SPBC11B10.10C | 6/early             | histone   |
| SPO73 | YER046W |       | SPAC1296.04   | 6/middle            | very low homology-best reciprocal hits                                      |
| AUT7  | YBL078C |       | SPBP8B7.24C   | 7/middle            | <i>S.c.</i> protein required for delivery of autophagic vesicles to vacuole |
| BAG7  | YOR134W |       | SPBC557.01    | 3/late              | rho-GAP protein   |
| ROM2  | YLR371W |       | SPAC1006.06   | 6/middle            | rho-GEF   |
| RAS2  | YNL098C | ras1  | SPAC17H9.09C  | 3/middle            | ras homologue   |
| GNA1  | YFL017C | gna1  | SPAC16E8.03   | 6/late              | glucosamine transferase   |
| SGA1  | YIL099W | meu17 | SPBC14C8.05C  | 5/middle            | glucosamylase   |
| CLG1  | YGL215W |       | SPBC1D7.03    | 6/middle            | cyclin-like protein   |
| CYB2  | YML054C |       | SPAPB1A11.03  | unclassified/late   | dehydrogenase   |
|       | YNR036C |       | SPAC4F8.06    | unclassified/middle | mitochondrial ribosomal protein   |
| ECM4  | YKR076W |       | SPCC1281.07C  | 7/late              | glutathione-S-transferase domain  |
| TOS7  | YOL019W |       | SPCC1739.10   | 3/early             | unknown function  |
| ARN2  | YHL047C |       | SPCC61.01C    | unclassified/middle | MFS transporter   |
| GTT1  | YIR038C |       | SPAC688.04C   | 7/late              | glutathione-S-transferase domain  |
| RIB5  | YBR256C |       | SPCC1450.13C  | 2/late              | riboflavin synthesis  |
| CHO1  | YER026C |       | SPCC1442.12   | 3/middle            | CDP-DAG phosphatidyl transferase  |
| XKS1  | YGR194C |       | SPCPJ732.02C  | unclassified/middle | xylulose kinase   |
| PCT1  | YGR202C |       | SPCC1827.02C  | 6/middle            | phosphatydil-choline matabolism   |
|       | YLL032C |       | SPBC9B6.13    | 5/middle            | unknown function  |
|       | YHR097C |       | SPBC6B1.03C   | 3/late              | unknown function  |
| ELC1  | YPL046C |       | SPBC1861.07   | 6/middle            | transcription elongation factor   |
| SYF2  | YGR129W |       | SPBC3E7.13C   | unclassified/middle | pre-mRNA splicing factor (S.c.)   |
| PGM2  | YMR105C |       | SPBC32F12.10  | 2/middle            | phosphoglucomutase  |
| RKI1  | YOR095C | ppi   | SPAC144.12    | 7/middle            | phosphatidyl-serine metabolism  |
| SUR4  | YLR372W |       | SPAC1B2.03C   | 5/middle            | fatty acid elongation   |
| PIB1  | YDR313C |       | SPBC36B7.05C  | 4/early             | ubiquitin ligase (S.c.)   |
| PIN3  | YPR154W | csh3  | SPBC119.05C   | 2/middle            | SH3-containg protein  |
| SSO2  | YMR183C | sso1  | SPCC825.03C   | 7/middle            | syntaxin  |
| FBP1  | YLR377C | fbp1  | SPBC1198.14C  | unclassified/early  | fructose biphosphatase  |
| GLG2  | YJL137C |       | SPBC4C3.08    | 4/middle            | unknown function  |
| ARE2  | YNR019W |       | SPAC13G7.05   | 4/middle            | cholesterol metabolism  |
|       | YIL125W |       | SPBC3H7.03C   | unclassfied/middle  | alpha-ketoglutarate dehydrogenase   |
|       | YOR223W |       | SPAC20H4.02   | 3/middle            | unknown function  |
|       | YPL221W |       | SPCC663.14C   | 1/late              | unknown function  |
|       | YNL115C |       | SPAC23C11.06C | 3/late              | unknown function  |
|       | YDR262W |       | SPBC146.10    | 3/middle            | unknown function  |
|       | YHR087W |       | SPBC21C3.19   | 3/late              | unknown function  |
| GDI1  | YER136W | gdi1  | SPAC22H10.12C | 2/late              | secretion   |
|       | YPL170W |       | SPAC26H5.15   | 6/middle            | steroid -binding domain   |

| PDC1 | YLR044C | SPAC3H8.01  | 2/late   | pyruvate decarboxylate |
|------|---------|-------------|----------|------------------------|
| OXR1 | YPL196W | SPAC8C9.16C | 3/middle | unknown function       |
|      | YHR121W | SPBC9B6.12C | 3/middle | unknown function       |

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