

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

Note that ~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 7²⁶. Cell cycle genes, APC components and recombination genes tend to belong to the corresponding clusters in both species.

| <i>S.cerevisiae</i> | | <i>S. pombe</i> | | Cluster (<i>S.c./S.p</i>) | Function |
|--|---------|------------------|--|---------------------------------------|--|
| Anaphase-promoting complex | | | | | |
| <i>CDC27</i> | YBL084C | <i>nuc2</i> | SPAC1851.01 | 5/middle | APC component |
| <i>APC4</i> | YDR118W | <i>cut20</i> | SPAC19G12.01C | 5/middle | APC component |
| <i>CDC16</i> | YKL022C | <i>cut9</i> | SPAC6F12.15C | 6/middle | APC component |
| <i>APC1</i> | YNL172W | <i>cut4</i> | SPBC106.09 | 7/middle | APC component |
| <i>APC5</i> | YOR249C | <i>apc5</i> | SPAC959.09C | 5/middle | APC component |
| <i>CDC23</i> | YHR166C | <i>cut23</i> | SPAC6F12.14 | 6/middle | APC component |
| <i>CDC26</i> | YFR036W | <i>hcn1</i> | SPAC23C11.12 | 6/middle | APC component |
| <i>HCT1</i> | YGL003C | <i>ste9</i> | SPAC144.13c | 5/early(SPCC1620.04C) | APC regulator (<i>CDC20/fizzy</i>) |
| <i>CDC20</i> | YGL116W | <i>mfr1/fzr1</i> | SPBC660.02 | middle(SPAC13G6.08C, | |
| <i>AMA1</i> | YGR225W | <i>slp1s</i> | SPAC821.08C SPAC13G6.08 SPCC1620.04C | <i>slp1,mfr1</i> /late(<i>ste9</i>) | |
| Septins | | | | | |
| <i>CDC10</i> | YCR002C | <i>spn2</i> | SPAC821.06 | 5/middle | septins |
| <i>CDC3</i> | YLR314C | <i>spn5</i> | SPAC24C9.15C | | |
| <i>SPR3</i> | YGR059W | <i>spn6</i> | SPCC188.12 | | |
| <i>SPR28</i> | YDR218C | <i>spn7</i> | SPBC21.08C | | |
| Cell cycle regulators | | | | | |
| <i>CDC14</i> | YFR028C | <i>clp1/flp1</i> | SPAC1782.09C | 5/middle | protein phosphatase |
| <i>CDC5</i> | YMR001C | <i>pol1</i> | SPAC23C11.16 | 5/middle | polo kinase |
| <i>CLB1</i> | YGR108W | <i>cig2</i> | SPAPB2B4.03 | 5-6/middle | B-tpe cyclin |
| <i>CLB3</i> | YDL155W | <i>cdc13</i> | SPBC582.03 | | |
| <i>CLB4</i> | YLR210W | | | | |
| <i>CLB5</i> | YPR120C | | | | |
| <i>CLB6</i> | YGR109C | | | | |
| Recombination/chromosome cohesion | | | | | |
| <i>REC114</i> | YMR133W | <i>rec7</i> | SPCC1753.03C | 4/early | recombination protein |
| <i>DMC1</i> | YER179W | <i>dmc1</i> | SPAC8E11.03C | 4/early | recombination protein |
| <i>MND1</i> | YGL183C | | SPAC13A11.03 | 4/early | recombination protein |
| <i>HOP2</i> | YGL033W | <i>meu13</i> | SPAC222.15 | 4/early | recombination protein |
| <i>SMC3</i> | YJL074C | <i>smc3</i> | SPAC10F6.09C | 4/early | cohesin |
| <i>REC8</i> | YPR007C | <i>rec8</i> | SPC29A10.14 | 4/early | cohesin |
| Chromosome segregation | | | | | |
| <i>STU1</i> | YLR045C | <i>dis1</i> | SPCC736.14 | 5/middle | spindle pole body component |
| <i>TID3</i> | YIL144W | <i>ncd10</i> | SPBC11C11.03 | 6/middle | chromosome segregation |
| <i>UBC11</i> | YOR339C | <i>ubc11</i> | SPCC1259.15C | 5/middle | chromosome segregation (<i>S.p.</i>) |
| DNA repair | | | | | |
| <i>RAD23</i> | YEL037C | <i>rhp23</i> | SPBC2D10.12 | 4/middle | DNA repair |
| <i>EXO1</i> | YOR033C | <i>exo1</i> | SPBC29A10.05 | 5/middle | DNA repair/recombination |
| <i>HRR25</i> | YPL204W | <i>hhp1</i> | SPBC3H7.15 | 5/middle | DNA repair (casein kinase I) |
| Others | | | | | |
| <i>HUL4</i> | YJR036C | | SPBP8B7.27 | 5/late | putative ubiquitin ligase |

| | | | | | |
|--------------|---------|--------------|---------------|---------------------|---|
| <i>LEE1</i> | YPL054W | <i>scp3</i> | SPAC3A11.02 | 2/middle | zinc finger domains |
| <i>ENA2</i> | YDR039C | <i>cta3</i> | SPBC839.06 | 2/middle | P-type ATPase |
| <i>PMC1</i> | YGL006W | | SPAPB2B4.04C | 2/middle | P-type ATPase |
| <i>CMK2</i> | YOL016C | <i>cmk1</i> | SPACUNK12.02C | 3/late | casein kinase |
| <i>CHS1</i> | YNL192W | <i>chs1</i> | SPAC13G6.12C | 3/middle | chitin-synthase |
| | YGR273C | | SPBC19C7.04C | 5/early | unknown function |
| <i>ISA1</i> | YLL027W | | SPCC645.03C | 6/middle | iron metabolism(<i>S.c.</i>) |
| <i>HTZ1</i> | YOL012C | <i>pht1</i> | SPBC11B10.10C | 6/early | histone |
| <i>SPO73</i> | YER046W | | SPAC1296.04 | 6/middle | very low homology-best reciprocal hits |
| <i>AUT7</i> | YBL078C | | SPBP8B7.24C | 7/middle | <i>S.c.</i> protein required for delivery of autophagic vesicles to vacuole |
| <i>BAG7</i> | YOR134W | | SPBC557.01 | 3/late | rho-GAP protein |
| <i>ROM2</i> | YLR371W | | SPAC1006.06 | 6/middle | rho-GEF |
| <i>RAS2</i> | YNL098C | <i>ras1</i> | SPAC17H9.09C | 3/middle | ras homologue |
| <i>GNA1</i> | YFL017C | <i>gna1</i> | SPAC16E8.03 | 6/late | glucosamine transferase |
| <i>SGA1</i> | YIL099W | <i>meu17</i> | SPBC14C8.05C | 5/middle | glucosamylase |
| <i>CLG1</i> | YGL215W | | SPBC1D7.03 | 6/middle | cyclin-like protein |
| <i>CYB2</i> | YML054C | | SPAPB1A11.03 | unclassified/late | dehydrogenase |
| | YNR036C | | SPAC4F8.06 | unclassified/middle | mitochondrial ribosomal protein |
| <i>ECM4</i> | YKR076W | | SPCC1281.07C | 7/late | glutathione-S-transferase domain |
| <i>TOS7</i> | YOL019W | | SPCC1739.10 | 3/early | unknown function |
| <i>ARN2</i> | YHL047C | | SPCC61.01C | unclassified/middle | MFS transporter |
| <i>GTT1</i> | YIR038C | | SPAC688.04C | 7/late | glutathione-S-transferase domain |
| <i>RIB5</i> | YBR256C | | SPCC1450.13C | 2/late | riboflavin synthesis |
| <i>CHO1</i> | YER026C | | SPCC1442.12 | 3/middle | CDP-DAG phosphatidyl transferase |
| <i>XKS1</i> | YGR194C | | SPCPJ732.02C | unclassified/middle | xylulose kinase |
| <i>PCT1</i> | YGR202C | | SPCC1827.02C | 6/middle | phosphatidyl-choline matabolism |
| | YLL032C | | SPBC9B6.13 | 5/middle | unknown function |
| | YHR097C | | SPBC6B1.03C | 3/late | unknown function |
| <i>ELC1</i> | YPL046C | | SPBC1861.07 | 6/middle | transcription elongation factor |
| <i>SYF2</i> | YGR129W | | SPBC3E7.13C | unclassified/middle | pre-mRNA splicing factor (<i>S.c.</i>) |
| <i>PGM2</i> | YMR105C | | SPBC32F12.10 | 2/middle | phosphoglucomutase |
| <i>RK11</i> | YOR095C | <i>ppi</i> | SPAC144.12 | 7/middle | phosphatidyl-serine metabolism |
| <i>SUR4</i> | YLR372W | | SPAC1B2.03C | 5/middle | fatty acid elongation |
| <i>PIB1</i> | YDR313C | | SPBC36B7.05C | 4/early | ubiquitin ligase (<i>S.c.</i>) |
| <i>PIN3</i> | YPR154W | <i>csb3</i> | SPBC119.05C | 2/middle | SH3-containg protein |
| <i>SSO2</i> | YMR183C | <i>ssol</i> | SPCC825.03C | 7/middle | syntaxin |
| <i>FBP1</i> | YLR377C | <i>fbp1</i> | SPBC1198.14C | unclassified/early | fructose biphosphatase |
| <i>GLG2</i> | YJL137C | | SPBC4C3.08 | 4/middle | unknown function |
| <i>ARE2</i> | YNR019W | | SPAC13G7.05 | 4/middle | cholesterol metabolism |
| | YIL125W | | SPBC3H7.03C | unclassified/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 |
| <i>GDI1</i> | YER136W | <i>gdi1</i> | SPAC22H10.12C | 2/late | secretion |
| | YPL170W | | SPAC26H5.15 | 6/middle | steroid -binding domain |

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