

Appendix I

Table 1: Information about the proteins encoded by the genes depicted in Figure 3. For each gene, the *Saccharomyces* Genome Database (SGD) description, Gene Ontology (GO) terms and InterPro protein domains are listed (when available).

Name	Description
RAD54 (YGL163C)	SGD DNA-dependent ATPase, stimulates strand exchange by modifying the topology of double-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; member of the SWI/SNF family. GO DNA topoisomerase activity, DNA-dependent ATPase activity, ATP binding, DNA binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding. chromatin remodeling, heteroduplex formation, telomerase-independent telomere maintenance, double-strand break repair via synthesis-dependent strand annealing, DNA repair, response to DNA damage stimulus. Nucleus. Interpro DEAD/DEAH box helicase, N-terminal; The DEAD box helicases are involved in various aspects of RNA metabolism, including nuclear transcription, pre-mRNA splicing, ribosome biogenesis, nucleocytoplasmic transport, translation, RNA decay and organellar gene expression. Helicase, C-terminal; SNF2-related; SNF2 functions as the ATPase component of the SNF2/SWI multisubunit complex, which utilises energy derived from ATP hydrolysis to disrupt histone-DNA interactions, resulting in the increased accessibility of DNA to transcription factors.
DOA1 (YKL213C)	SGD WD repeat protein required for ubiquitin-mediated protein degradation, forms complex with Cdc48p, plays a role in controlling cellular ubiquitin concentration; also promotes efficient NHEJ in postdiauxic/stationary phase. GO double-strand break repair via nonhomologous end-joining; ubiquitin-dependent protein catabolism. cytoplasm; nucleus. Interpro WD-40 repeats (also known as WD or beta-transducin repeats) are short ~ 40 amino acid motifs, often terminating in a Trp-Asp (W-D) dipeptide. The underlying common function of all WD-repeat proteins is coordinating multi-protein complex assemblies, where the repeating units serve as a rigid scaffold for protein interactions.
RAD27 (Ykl113cp)	SGD 5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member of the <i>S. pombe</i> RAD2/FEN1 family. GO Nucleus. protein binding; 5'-flap endonuclease activity. DNA repair; DNA replication; DNA synthesis during DNA repair; double-strand break repair via non homologous end joining; replicative cell aging; telomere maintenance. Interpro The helix-hairpin-helix (HhH) motif is an around 20 amino acids domain present in prokaryotic and eukaryotic non-sequence-specific DNA binding proteins. These HhH motifs are observed in DNA repair enzymes and in DNA polymerases.
HHF1 (YBR009C)	SGD One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity. GO DNA binding. chromatin assembly or disassembly. nuclear nucleosome. Interpro Histone-fold/TFIID-TAF/NF-Y; Histone core; Histone H4.
RPB5 (YBR154C)	SGD RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III; contacts DNA and affects transactivation. GO DNA-directed RNA polymerase activity. transcription from RNA polymerase I promoter; transcription from RNA polymerase II promoter; transcription from RNA polymerase III promoter. DNA-directed RNA polymerase I complex; DNA-directed RNA polymerase II, core complex; DNA-directed RNA polymerase III complex. Interpro RNA polymerase Rpb5, N-terminal; RNA polymerase subunit, RPB5.
POL12 (YBL035C)	SGD B subunit of DNA polymerase α -primase complex, required for initiation of DNA replication during mitotic and premeiotic DNA synthesis; also functions in telomere capping and length regulation. GO α DNA polymerase activity. DNA replication initiation; DNA replication, synthesis of RNA primer; lagging strand elongation. α DNA polymerase:primase complex; nuclear membrane; nucleus. Interpro DNA polymerase α subunit B.

Name	Description
GAT1 (Yf021wp)	SGD Transcriptional activator of genes involved in nitrogen catabolite repression, member of the GATA family of DNA binding proteins; activity and localization regulated by nitrogen limitation and Ure2p GO cytosol; nucleus. specific RNA polymerase II transcription factor activity; transcriptional activator activity. positive regulation of transcription; regulation of nitrogen utilization; transcription initiation from RNA polymerase. Interpro A number of transcription factors (including erythroid-specific transcription factor and nitrogen regulatory proteins), specifically bind the DNA sequence (A/T)GATA(A/G) in the regulatory regions of genes.
RPL40A (YIL148W)	SGD Fusion protein, identical to Rpl40Bp, that is cleaved to yield ubiquitin and a ribosomal protein of the large (60S) ribosomal subunit with similarity to rat L40; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes. GO protein tag; structural constituent of ribosome. protein biosynthesis; protein ubiquitination; ribosome biogenesis and assembly. cytosolic large ribosomal subunit (sensu Eukaryota). Interpro Ubiquitin.
CHS2 (YBR038W)	SGD Chitin synthase II, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for the synthesis of chitin in the primary septum during cytokinesis. GO chitin synthase activity. cytokinesis. bud neck. Interpro Chitin synthase; Glycosyl transferase, family 2.
PIG2 (Yil045wp)	SGD Putative type-1 protein phosphatase targeting subunit that tethers Glc7p type-1 protein phosphatase to Gsy2p glycogen synthase. GO cytoplasm. protein phosphatase type 1 regulator activity. regulation of glycogen biosynthetic process. Interpro This family consists of several eukaryotic proteins that are thought to be involved in the regulation of glycogen metabolism.
CWP1 (YKL096W)	SGD Cell wall mannoprotein, linked to a β -1,3- and β -1,6-glucan heteropolymer through a phosphodiester bond; involved in cell wall organization. GO structural constituent of cell wall. cell wall organization and biogenesis. cell wall. Interpro Yeast PIR protein repeat.
MNN1 (YER001W)	SGD α -1,3-mannosyltransferase, integral membrane glycoprotein of the Golgi complex, required for addition of α 1,3-mannose linkages to N-linked and O-linked oligosaccharides, one of five <i>S. cerevisiae</i> proteins of the MNN1 family. GO α -1,3-mannosyltransferase activity. N-glycan processing; protein amino acid O-linked glycosylation. Golgi apparatus.
NCE102 (YPR149W)	SGD Protein of unknown function; contains transmembrane domains; involved in secretion of proteins that lack classical secretory signal sequences; component of the detergent-insoluble glycolipid-enriched complexes (DIGs). GO molecular function unknown. protein secretion. cytoplasm; endoplasmic reticulum; integral to membrane; mitochondrion.
DIP5 (YPL265W)	SGD Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate and L-aspartate; also a transporter for Gln, Asn, Ser, Ala, and Gly. GO amino acid permease activity; amino acid transporter activity. amino acid transport. plasma membrane. Interpro Amino acid/polyamine transporter I; Amino acid permease; Amino acid permease-associated region; Yeast amino acid permease.
CDC5 (YMR001C)	SGD Polo-like kinase with similarity to <i>Xenopus</i> Plx1 and <i>S. pombe</i> Plo1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through phosphorylation of substrates; may be a Cdc28p substrate. GO protein serine/threonine kinase activity. DNA-dependent DNA replication; protein amino acid phosphorylation. Cellular Component: bud neck; nucleus; spindle pole. Interpro POLO box duplicated region; Protein kinase; Serine/threonine protein kinase, active site; Serine/threonine protein kinase.

Name	Description
SR04/AXL2 (YIL140W)	SGD Integral plasma membrane protein required for axial budding in haploid cells, localizes to the incipient bud site and bud neck; glycosylated by Pmt4p; potential Cdc28p substrate. GO molecular function unknown. axial bud site selection; bud site selection. bud neck; integral to plasma membrane; septin ring. Interpro Dystroglycan-type cadherin-like; Putative Ig - This alignment represents the conserved core region of a ~ 90 residue repeat found in several haemagglutinins and other cell surface proteins.
HSL1 Ykl101w	SGD <i>Nim1p</i> -related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with <i>Hsl7p</i> for bud neck recruitment, phosphorylation, and degradation of <i>Swe1p</i> GO bud neck; septin ring. protein kinase activity. cell morphogenesis checkpoint; G2/M transition of mitotic cell cycle; protein amino acid phosphorylation; septin checkpoint. Interpro Protein kinases catalyze the phospho-transfer reaction fundamental to most signalling and regulatory processes in the eukaryotic cell.
CLN2 (YPL256C)	SGD G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p). GO cyclin-dependent protein kinase regulator activity. re-entry into mitotic cell cycle after pheromone arrest; regulation of cyclin dependent protein kinase activity. cytoplasm; nucleus. Interpro Cyclin, N-terminal; Cyclin.
SWE1 (YJL187C)	SGD Protein kinase that regulates the G2/M transition by inhibition of Cdc28p kinase activity; localizes to the nucleus and to the daughter side of the mother-bud neck; homolog of <i>S. pombe</i> Wee1p; potential Cdc28p substrate. GO protein kinase activity. G2/M transition of mitotic cell cycle; G2/M transition size control checkpoint; cell morphogenesis checkpoint; regulation of cyclin dependent protein kinase activity; regulation of meiosis. bud neck; nucleus. Interpro Serine/threonine protein kinase, active site; Serine/threonine protein kinase.
BEM1 (YBR200W)	SGD Protein containing SH3-domains, involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p. GO protein binding. cellular morphogenesis during conjugation with cellular fusion; establishment of cell polarity. bud neck; bud tip; incipient bud site; mating projection tip. Interpro Neutrophil cytosol factor 2; Octicosapeptide/Phox/Bem1p; Phox-like; SH3.
POL30 (YBR088C)	SGD Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase δ ; may function as a docking site for other proteins required for mitotic and meiotic chromosomal DNA replication and for DNA repair. GO DNA polymerase processivity factor activity. base-excision repair; lagging strand elongation; leading strand elongation; mismatch repair; mutagenesis; nucleotide-excision repair; postreplication repair. nucleus; replication fork. Interpro Proliferating cell nuclear antigen, PCNA.