

Table 1

Strain	Genetic Background	Genotype	Related Figures
DLY640	W303	MAT α	4, S1, S3
DLY1195	W303	MAT α cdc13-1	4
DLY1255	W303	MAT α rad9::HIS3 cdc13-1	S2
DLY1256	W303	MAT α rad9::HIS3 cdc13-1	S2
DLY1273	W303	MAT α exo1::LEU2	5
DLY1296	W303	MAT α exo1::LEU2 cdc13-1	4
DLY1543	W303	MAT α tel1::TRP1 cdc13-1	S3
DLY1544	W303	MAT α tel1::TRP1 cdc13-1	S3
DLY1585	W303	MAT α rad9::KANMX	S1
DLY2234	W303	MAT α rad9::LEU2	S1, S2
DLY2787	W303	MAT α yku70::LEU2	4
DLY2988	W303	MAT α cdc13-1 rad53::HIS3 sml1::KANMX	5
DLY3001	W303	MAT α	S1, S2
DLY4528	W303	MAT α nmd2::HIS3	S1
DLY4557	W303	MAT α cdc13-1 int	5
DLY4625	W303	MAT α cdc13-1 int nmd2::HIS3	4
DLY4647	W303	MAT α cdc13-1 rad9::HIS3	5, S3
DLY4921	W303	MAT α cdc13-1 int exo1::LEU2	5
DLY4922	W303	MAT α cdc13-1 rad9::HIS3 exo1::LEU2	5
DLY4931	W303	MAT α cdc13-1 rad24::TRP1	5
DLY5007	W303	MAT α yku70::LEU2 nmd2::HIS3	4
DLY5097	W303	MAT α cdc13-1 exo1::LEU2 rad24::TRP1	5
DLY5255	W303	MAT α rad9::LEU2 nmd2::HIS3 cdc13-1 int	4
DLY5260	W303	MAT α cdc13-1 cdc15-2 bar1::hisG	6
DLY5261	W303	MAT α cdc13-1 cdc15-2 bar1::hisG	6
DLY5266	W303	MAT α cdc13-1 cdc15-2 bar1::hisG exo1::LEU2	6
DLY5386	S288C	MAT α LEU2::cdc13-1 int::HPHMX rad9::NATMX lyp1 Δ can1::MFA1pr-HIS3 ura3 leu2 his3 LYS2+	2, S4
DLY5688	S288C	MAT α LEU2::cdc13-1 int::HPHMX lyp1 Δ can1::MFA1pr-HIS3 ura3 leu2 his3 LYS2+	1, 2, S4
DLY6720	S288C	MAT α LEU2::cdc13-1 int::HPHMX exo1::NATMX lyp1 Δ can1::STE2pr-his5 ura3 leu2 his3 LYS2+	2, S4
DLY7106	W303	MAT α chk1::HIS3	5
DLY7108	W303	MAT α exo2::LEU2 chk1::HIS3	5
DLY7110	W303	MAT α cdc13-1 chk1::HIS3	5
DLY7112	W303	MAT α cdc13-1 exo1::LEU2 chk1::HIS3	5
DLY7143	W303	MAT α cdc13-1 cdc15-2 bar1::hisG chk1::HIS3	6
DLY7145	W303	MAT α cdc13-1 cdc15-2 bar1::hisG exo1::LEU2 chk1::HIS3	6
DLY7146	W303	MAT α cdc13-1 cdc15-2 bar1::hisG exo1::LEU2 chk1::HIS3	6
DLY7747	W303	MAT α exo1::LEU2 nmd2::URA3 cdc13-1	4
DLY8460	W303	MAT α	5
DLY8767	S288C	MAT α LEU2::stn1-13::HPHMX lyp1::NATMX can1::STE2pr-his5 ura3 leu2 his3 met15 LYS2+	1
DLY9181	S288C	MAT α LEU2::rfa3-313::HPHMX lyp1::NATMX can1::STE2pr-his5 ura3 leu2 his3 met15 LYS2+	1

DLY9326	S288C	MAT α lyp1::HPHMX::LEU2::NATMX can1::STE2pr-his5 ura3 leu2 his3 met15 LYS2+	1
DLY9866	W303	MAT α rad9::LEU2 cdc13-1	4, S3
DLY11098	W303	MAT α stn1-13	S1
DLY11099	W303	MAT α stn1-13	S1
DLY11100	W303	MAT α stn1-13 rad9::LEU2	S1
DLY11101	W303	MAT α stn1-13 rad9::LEU2	S1
DLY11102	W303	MAT α stn1-13 rad24::TRP1	S1
DLY11103	W303	MAT α stn1-13 rad24::TRP1	S1
DLY11104	W303	MAT α stn1-13 rad17::TRP1	S1
DLY11105	W303	MAT α stn1-13 rad17::TRP1	S1
DLY11215	W303	MAT α nmd2::URA3 stn1-13	4
DLY11216	W303	MAT α stn1-13	4
DLY11637	W303	MAT α rfa3-313::KANMX	S2
DLY11696	W303	MAT α rfa3-313::KANMX nmd2::HIS3	S2
DLY11697	W303	MAT α rfa3-313::KANMX nmd2::HIS3	S2
DLY11729	W303	MAT α rfa3-313::KANMX rad9::HIS3	S2
DLY11730	W303	MAT α rfa3-313::KANMX rad9::HIS3	S2
DLY11182	W303	MAT α rad9::HIS3 tel1::TRP1 cdc13-1	S3
DLY11183	W303	MAT α rad9::HIS3 tel1::TRP1 cdc13-1	S3

Table 2

Quantitative Fitness Analysis Screens

Screen no.	Query Strain	Spotting	Media	Temperature
QFA0141	<i>ura3</i>	dilute	SDM_rhk_CTGN	27°C, UD_X3
QFA0132	<i>lyp1</i>	concentrated	SDM_rhIk_CTGNH	30°C, 33°C
QFA0140	<i>cdc13-1</i>	dilute	SDM_rhIk_CTGH	27°C, UD_X3
QFA0142	<i>rad9Δ cdc13-1</i>	dilute	SDM_rhIk_CTGNH	27°C, UD_X1
QFA0051	<i>exo1Δ cdc13-1</i>	dilute	SDM_rhIk_CTGNH	27°C, 30°C
QFA0136	<i>stn1-13</i>	concentrated	SDM_rhIk_CTGNH	33°C
QFA0131	<i>rfa3-313</i>	concentrated	SDM_rhIk_CTGNH	30°C

Table 3

List of genes highlighted in the QFA screens

Standard Name	Comple	Description from Saccharomyces Genome Database
Ddc1	911 sliding clamp	DNA damage checkpoint protein; part of a PCNA-like complex required for DNA damage response, required for pachytene checkpoint to inhibit cell cycle in response to unrepaired recombination intermediates; potential Cdc28p substrate; forms nuclear foci upon DNA replication stress
Rad17	911 sliding clamp	Checkpoint protein; involved in the activation of the DNA damage and meiotic pachytene checkpoints; with Mec3p and Ddc1p, forms a clamp that is loaded onto partial duplex DNA; homolog of human and <i>S. pombe</i> Rad1 and <i>U. maydis</i> Rec1 proteins
Rad24	911 sliding clamp	Checkpoint protein; involved in the activation of the DNA damage and meiotic pachytene checkpoints; subunit of a clamp loader that loads Rad17p-Mec3p-Ddc1p onto DNA; homolog of human and <i>S. pombe</i> Rad17 protein
Mre11	MRX complex	Nuclease subunit of the MRX complex with Rad50p and Xrs2p; complex functions in repair of DNA double-strand breaks and in telomere stability; Mre11p associates with Ser/Thr-rich ORFs in premeiotic phase; nuclease activity required for MRX function; widely conserved; forms nuclear foci upon DNA replication stress
Rad50	MRX complex	Subunit of MRX complex with Mre11p and Xrs2p; complex is involved in processing double-strand DNA breaks in vegetative cells, initiation of meiotic DSBs, telomere maintenance, and nonhomologous end joining; forms nuclear foci upon DNA replication stress
Xrs2	MRX complex	Protein required for DNA repair; component of the Mre11 complex, which is involved in double strand breaks, meiotic recombination, telomere maintenance, and checkpoint signaling
Nam7	Nonsense Mediated mRNA decay	ATP-dependent RNA helicase of the SFI superfamily; involved in nonsense mediated mRNA decay; required for efficient translation termination at nonsense codons and targeting of NMD substrates to P-bodies; binds to the small ribosomal subunit via an interaction with Rps26; forms cytoplasmic foci upon DNA replication stress
Nmd2	Nonsense Mediated mRNA decay	Protein involved in the nonsense-mediated mRNA decay (NMD) pathway; interacts with Nam7p and Upf3p; involved in telomere maintenance
Upf3	Nonsense Mediated mRNA decay	Component of the nonsense-mediated mRNA decay (NMD) pathway; along with Nam7p and Nmd2p; involved in decay of mRNA containing nonsense codons; involved in telomere maintenance
Yku70	Ku heterodimer	Subunit of the telomeric Ku complex (Yku70p-Yku80p); involved in telomere length maintenance, structure and telomere position effect; required for localization of telomerase ribonucleoprotein to nucleus via interaction with the TLC1 guide RNA; relocates to sites of double-strand cleavage to promote nonhomologous end joining during DSB repair

Yku80	Ku heterodimer	Subunit of the telomeric Ku complex (Yku70p-Yku80p); involved in telomere length maintenance, structure and telomere position effect; required for localization of telomerase ribonucleoprotein via interaction with the TLC1 guide RNA; relocates to sites of double-strand cleavage to promote nonhomologous end joining during DSB repair
Est1	Telomerase	TLC1 RNA-associated factor involved in telomere length regulation; recruitment subunit of telomerase; has G-quadruplex promoting activity required for telomere elongation; possible role in activating telomere-bound Est2p-TLC1-RNA; EST1 has a paralog, EBS1, that arose from the whole genome duplication
Est2	Telomerase	Reverse transcriptase subunit of the telomerase holoenzyme; essential for telomerase core catalytic activity, involved in other aspects of telomerase assembly and function; mutations in human homolog are associated with aplastic anemia.
Est3	Telomerase	Component of the telomerase holoenzyme; involved in telomere replication
Rif1	Rap1 interacting factor	Protein that binds to the Rap1p C-terminus; acts synergistically with Rif2p to help control telomere length and establish telomeric silencing; involved in control of DNA replication; contributes to resection of DNA double strand breaks (DSBs); deletion results in telomere elongation
Rif2	Rap1 interacting factor	Protein that binds to the Rap1p C-terminus; acts synergistically with Rif1p to help control telomere length and establish telomeric silencing; deletion results in telomere elongation; RIF2 has a paralog, ORC4, that arose from the whole genome duplication
Rad9		DNA damage-dependent checkpoint protein; required for cell-cycle arrest in G1/S, intra-S, and G2/M, plays a role in postreplication repair (PRR) pathway; transmits checkpoint signal by activating Rad53p and Chk1p; hyperphosphorylated by Mec1p and Tel1p; multiple cyclin dependent kinase consensus sites and the C-terminal BRCT domain contribute to DNA damage checkpoint activation; Rad9p Chk1 Activating Domain (CAD) is phosphorylated at multiple sites by Cdc28p/Clb2p
Chk1		Serine/threonine kinase and DNA damage checkpoint effector; mediates cell cycle arrest via phosphorylation of Pds1p; phosphorylated by checkpoint signal transducer Mec1p; homolog of <i>S. pombe</i> and mammalian Chk1 checkpoint kinase
Tel1		Protein kinase primarily involved in telomere length regulation; contributes to cell cycle checkpoint control in response to DNA damage; acts with Red1p and Mec1p to promote interhomolog recombination by phosphorylation of Hop1; functionally redundant with Mec1p; regulates P-body formation induced by replication stress; homolog of human ataxia-telangiectasia mutated (ATM) gene
Exo1		5'-3' exonuclease and flap-endonuclease; involved in recombination, double-strand break repair, MMS2 error-free branch of the post replication (PRR) pathway and DNA mismatch repair; role in telomere maintenance; member of the Rad2p nuclease family, with conserved N and I nuclease domains; relative distribution to the nucleus increases upon DNA replication stress; EXO1 has a paralog, DIN7, that arose from the whole genome duplication