Table S1 60 genes tested by liquid senescence assay

Gene	*Senescence phenotype	**Telomere length screens	Gene ontology annotation	***References
EST3	AERS	VS	telomerase component	*est2Δ est3Δ/est1Δ est3Δ/tlc1Δ est3Δ* showed normal senescence (LENDVAY *et al.* 1996)
RIF1	AERS	VL	telomere binding protein	*rif1Δ est2Δ* showed normal senescence (ANBALAGAN S *et al.* 2011); *rif1Δ est2Δ* accelerated entry to /recovery from senescence (CHANG *et al.* 2011)
RIF2	AERS	VL	telomere binding protein	*rif2Δ est2Δ* accelerated entry to/recovery from senescence (CHANG *et al.* 2011)
EST1	AS	VS	telomerase component	
MRE11	AS	VS	DNA repair/ MRX complex	Normal (LE *et al.* 1999)
XRS2	AS	VS	DNA repair/MRX complex	Normal (LE *et al.* 1999)
RAD52	AS		recombinational repair of double-strand breaks in DNA	*rad52Δ est1Δ and rad52Δ tlc1Δ* accelerated senescence (ABDALLAH *et al.* 2010; LE *et al.* 1999; LEBEL *et al.* 2009; LEE *et al.* 2007; LUNDBLAD and BLACKBURN 1993)
RAD54	AS		recombinational repair of double-strand breaks in DNA	*rad54Δ tlc1Δ* has severe growth defect (LE *et al.* 1999)
RAD55	AS		recombinational repair of double-strand breaks in DNA	
RAD57	AS		recombinational repair of double-strand breaks in DNA	*rad57Δ tlc1Δ* has severe growth defect (LE *et al.* 1999)
UPF1 (NAM7)	AS	VS	nonsense mediated deccay	*upf1Δ* with *tlc1Δ/est1Δ/est2Δ/est3Δ* delayed senescence measured by a different method (ENOMOTO *et al.* 2004)
UPF2 (NMD2)	AS	S	nonsense mediated deccay	*upf2Δ* with *tlc1Δ/est1Δ/est2Δ/est3Δ* delayed senescence measured by a different method (ENOMOTO *et al.* 2004)
UPF3	AS	S	nonsense mediated deccay	*upf3Δ* with *tlc1Δ/est1Δ/est2Δ/est3Δ* delayed senescence measured by a different method (ENOMOTO *et al.* 2004)

DCC1	AS	ss	Sister chromatid cohesion	
CTF18	AS	Literature reported	Sister chromatid cohesion	
CTF8	AS	ss	Sister chromatid cohesion	
ELG1	AS	L	RFC complex	
RTT101	AS		Histone acetyltransferase/involved in NHEJ	
RTT109	AS		Histone acetyltransferase/involved in NHEJ	
RTT107	AS		Mms22-dependent DNA repair during S phase/interacts with Mms22p and Slx4p	
MMS1	AS		Subunit of an E3 ubiquitin ligase complex/resolving replication intermediates	*mms1Δ tlc1Δ* accelerated senescence and failed to recover (ABDALLAH *et al.* 2010)
MMS22	AS		Ubiquitin-conjugating enzyme variant involved in error-free post replication repair	
CDC73	AS	S	PAF1 complex	
RTF1	AS	ss	PAF1 complex	
SLX8	AS	sl,	Subunit of the Slx5-Slx8 SUMO-targeted ubiquitin ligase (STUbL) complex	*slx8Δ tlc1Δ* accelerated senescence (AZAM *et al.* 2006)
SLX5 (HEX3)	AS		Subunit of the Slx5-Slx8 SUMO-targeted ubiquitin ligase (STUbL) complex	*slx5Δ tlc1Δ* accelerated senescence (AZAM *et al.* 2006)

RRP8	AS	L	pre-rRNA processing/methyltransferase	
SPT21	AS	ss	regulator of histone gene transcription	
POL32	AS	sl	Polymerase delta subunit	*pol32Δ tlc1Δ* accelerated senescence (LYDEARD *et al.* 2007)
SGS1	AS		Nucleolar DNA helicase of the RecQ family	*sgs1Δ tlc1Δ* accelerated senescence (AZAM *et al.* 2006; LEE *et al.* 2007)
RAD27	AS	VL	flap-endonuclease	*rad27Δ* with *est1Δ/tlc1Δ/est3Δ/cdc13-2* accelerated senescence (PARENTEAU and WELLINGER 2002)
HMO1	AS	L	HMG-box protein	
TEL1	AS	VS	PIK homologue	*tel1Δ tlc1Δ showed* normal senescence (ENOMOTO *et al.* 2002) ; *tel1Δ tlc1Δ* delayed senescence (RITCHIE *et al.* 1999), *tel1Δ tlc1Δ mec1Δ sml1Δ* is normal (CHAN *et al.* 2001); *tel1Δ tlc1Δ* delayed senescence (ABDALLAH *et al.* 2010)
KEM1	AS	S	RNA degradation	
YDL118	AS	ss	Unknown	
LEA1	AS	L	RNA splicing	
SUM1	AS	S	SUM1/RFM1 repressor complex	
RFM1	AS	S	SUM1/RFM1 repressor complex	
TSA1	AS		Thioredoxin peroxidase/ribosome-associated and free cytoplasmic antioxidant	
ASF1	AS		Nucleosome assembly factor/chromatin assembly and disassembly	
SLA1	AS		Cytoskeletal binding protein	

RHO4	AS		Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins	
EDE1	AS		Key endocytic protein	
EXO1	Normal	Literature reported	5'-3' exonuclease and flap-endonuclease	*exo1Δ tlc1Δ* delayed senescence (MARINGELE and LYDALL 2004)
EBS1	Normal	ss	nonsense mediated decay	
RAD9	Normal	Literature reported	DNA damage checkpoint effector	*rad9Δ tlc1Δ* had less G2/M arrested cells (IJPMA and GREIDER 2003)
RAD17	Normal	Literature reported	DNA damage checkpoint effector	
DDC1	Normal	Literature reported	DNA damage checkpoint effector	
RAD24	Normal	Literature reported	DNA damage checkpoint effector	*rad24Δ tlc1Δ* had less G2/M arrested cells (IJPMA and GREIDER 2003)
CHK1	Normal		DNA damage checkpoint effector	
BMH1	Normal	Literature reported	14-3-3 protein	
BMH2	Normal	Literature reported	14-3-3 protein	
MRPL44	Normal	ss	mitochondrial ribosomal protein	
MOT3	Normal	ss	POLII transcription	
HST3	Normal		Member of the Sir2 family of NAD(+)-dependent protein deacetylases	
CSM3	Normal		Replication fork associated factor	
BNR1	Normal		Formin	
HIS3	Normal		Imidazoleglycerol-phosphate dehydratase	Control strain
MAK3	Normal	L	N-terminal acetyltransferase complex	
MAK10	Normal	L	N-terminal acetyltransferase complex	
MAK31	Normal	L	N-terminal acetyltransferase complex	

Legend: Examining of the 60 genes selected for the liquid procedure in this study. The references quoted were indicated in the table and included below.

*Senescence phenotype abbreviations: AS- accelerated senescence, AERS-accelerated entry to and recovery from senescence.
Normal: normal entry to and recovery from senescence.
** Telomere phenotype abbreviations (ASKREE *et al.* 2004; GATBONTON *et al.* 2006; SHACHAR *et al.* 2008): VS - very short, S - short, ss - slightly short, sl - slightly long, L - long, VL - very long.
*** Conflicts in data may be due to differences in ways senescence was measured.

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