Hiraga et al., http://www.jcb.org/cgi/content/full/jcb.200806065/DC1

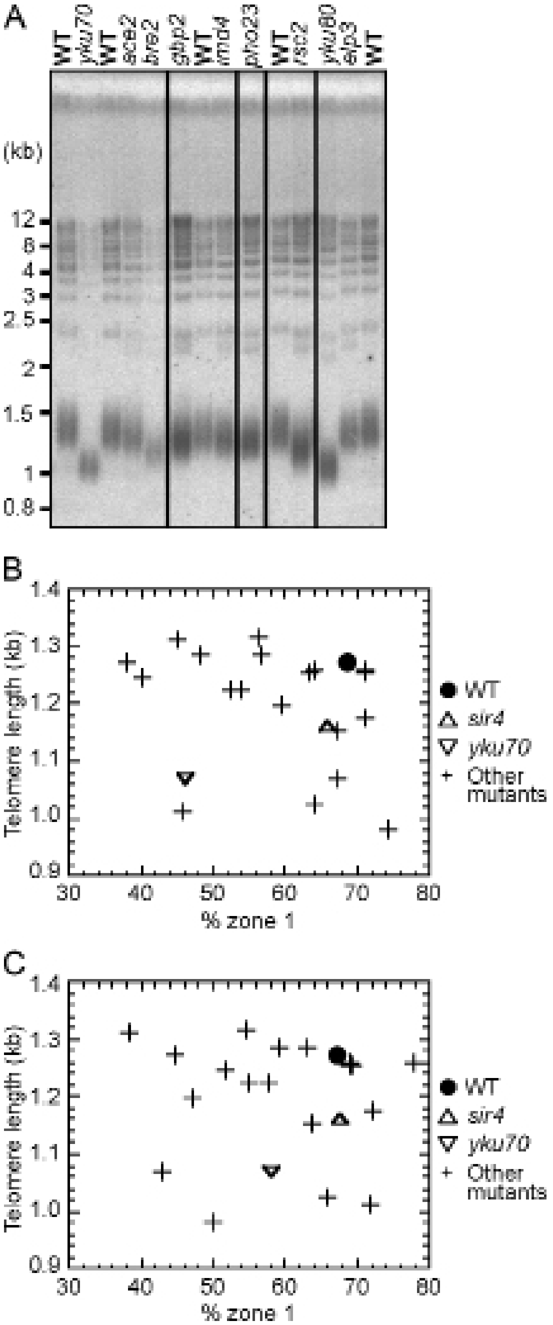

Figure S1. **No correlation between telomere length and positioning.** (A) Telomere length analyzed, as in Fig. 3, in mutants proficient for telomere positioning. Note that this composite image consists of several different portions of a single gel, not a composition from multiple gels. Black lines indicate that intervening lanes have been spliced out. (B) Telomere length versus telomere position during G1 phase is plotted, as in Fig. 3 B, for all Rap1 organization mutants listed in Table I. (C) Telomere length versus telomere position during S phase is plotted, as in Fig. 3 B, for identical set of mutants as in B.

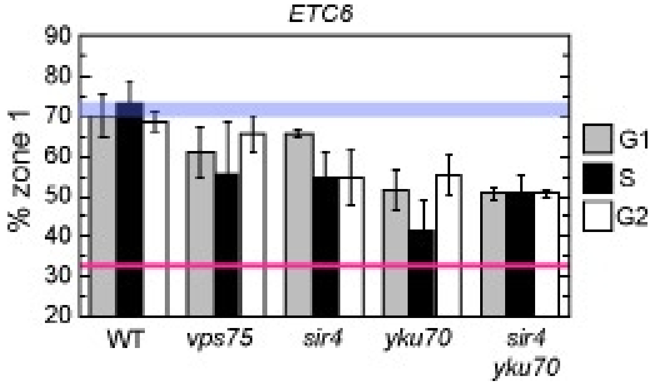

Figure S2. **Effect of *vps75*Δ, *sir4*Δ, and *yku70*Δ on perinuclear localization of the *ETC6* locus.** Localization of *ETC6* was tested as in Fig. 6 in the following strains: *vps75*Δ, *sir4*Δ, *yku70*Δ, and *sir4*Δ *yku70*Δ. WT and random localization values are indicated by blue and red lines, respectively.

Table S1. **Summary of Rap1 screening**

Gene	ORF name	Category	Known function.	Known complex	Rap1 phenotype	Score	Notes
ASF1	YJL115W	cd	Anti-silencing protein; histone chaperone; histone deposition		B	3	
BRE2	YLR015W	cl	Histone-lysine N-methyltransferase, cohesion	Set1/COMPASS complex	B	3	Aberrant nuclear morphology
CHL1 (CTF1)	YPL008W	d	Rad3p-like ATP-dependent DNA helicase subfamily. cohesion		C	3	
CTF18	YMR078C	cdl	Alternative RFC; Protein required for accurate chromosome transmission in mitosis and maintenance of normal telomere length	Ctf18-RLC	B	3	Most cells are large and sick-looking
CTF4	YPR135W	d	Protein required for DNA synthesis, binds DNA pol alpha; cohesion		B	3	Many enlarged cells. Rap1 clusters diminished in all cells and almost absent in enlarged cells
CTF8	YHR191C	cdl	Subunit of a complex with Ctf18p that shares some subunits with Replication Factor C and is required for sister chromatid cohesion	Ctf18-RLC	B	3	Most cells are large and sick-looking
DCC1	YCL016C	cdl	Part of an alternative RFC complex	Ctf18-RLC	B	3	Most cells are large and sick-looking
HNT3	YOR258W	r	Member of the third branch of the histidine triad (HIT) superfamily of nucleotide-binding proteins		C	3	Most cells are enlarged

NHP10	YDL002C	cl	Transcription, DNA maintenance, and/or chromatin structure as part of Ecm16p-associated complex	INO80 complex, Isw1-associated complex, Ecm16-associated complex	C	3	
PGD1	YGL025C	l	Telomeric silencing. Affects DNA supercoiling in vivo	RNA polymerase II mediator complex	B	3	Nucleolus enlarged
RRM3	YHR031C	cdlr	DNA helicase involved in rDNA replication and Ty1 transposition; promotes replication fork progression through replication pausing sites		B	3	
RSC1	YGR056W	c	Component of the abundant RSC complex involved in chromatin remodelling	RSC	C	3	
SIR3	YLR442C	cl	Silencing regulatory and DNA-repair protein	SIR	B	3	
SIR4	YDR227W	cl	Silencing regulatory and DNA-repair protein	SIR	B	3	
YAL049C	YAL049C	r	Protein of unknown function localized to cytoplasm and nucleus		C	3	
YKU80	YMR106C	cdl	Telomere binding, telomere length, telomeric silencing	yKu	B	3	
ACE2	YLR131C	d	Metallothionein expression activator. Expression of G1-specific genes		A	2	Partially defective in cytokinesis

CSM4	YPL200W		Protein required for accurate chromosome segregation during meiosis. Required for telomere positioning during meiosis		B	2	
ELP3	YPL086C	c	Histone acetyltransferase (HAT) that is part of the six-subunit Elongator complex, which is a major component of the RNA polymerase II holoenzyme responsible for transcriptional elongation	Elongator complex	B	2	
ELP4	YPL101W	c	A subunit of the six-subunit Elongator complex, which is a major histone acetyltransferase component of the RNA polymerase II holoenzyme responsible for transcriptional elongation	RNA pol II elongator holoenzyme	B	2	
GBP2	YCL011C		Protein involved in mRNA export, binds poly(A)+ RNA and single-stranded G-strand telomere sequence. Required for Rap1 localization		A	2	Aberrant nuclear shape with enlarged nucleolus
HDA1	YNL021W	c	Histone deacetylase A		C	2	
IMD4	YML056C	t	Complex of Imd2p, Imd3p, and Imd4p that binds a C-rich portion of telomeric DNA forms independently of Sir1p, Sir3p, Sir4p, and Rap1p		A	2	Defect mainly observed in small-budded cells

JJJ1	YNL227C	r	Co-chaperone that stimulates the ATPase activity of Ssa1p, required for a late step of ribosome biogenesis		A/C	2	Defect mainly observed in small-budded cells
MRE11	YMR224C	dl	DNA repair and meiotic recombination protein	MRX	B	2	
PHO23	YNL097C	c	Probable component of the Rpd3 histone deacetylase complex, involved in transcriptional regulation of PHO5	Rpd3-Sin3 histone deacetylase complex	B	2	
RAD16	YBR114W	l	Nucleotide excision repair protein		C	2	
RAD27	YKL113C	dl	ssDNA endonuclease and 5`-3`exonuclease; Fen-1 flap endonuclease		B	2	Most cells sick-looking
RSC2	YLR357W	cd	Component of the abundant RSC complex involved in chromatin remodelling. Cohesion	RSC	B	2	
SCP160	YJL080C	c	Mutant reported to be defective in telomere clustering		C	2	Most cells are enlarged
SIC1	YLR079W	d	P40 inhibitor of Cdc28p–Clb protein kinase complex		A/B	2	
SPE1	YKL184W	r	Ornithine decarboxylase; spermine biosynthesis		A	2	Slow growth
SWI3	YJL176C	d	Transcription regulatory protein	SWI–SNF complex	B	2	
TDP1	YBR223C	cd	Tyrosyl-DNA phosphodiesterase, involved in DNA repair. Telomeric, mating-type, and rDNA silencing		C	2	

TEL1	YBL088C	l	ATM homolog; Telomere length control protein		B	2	
UFD2	YDL190C	r	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3		C	2	
ABM1	YJR108W	r	Protein required for normal microtubule structure	Myo3p-Bee1p-Vrp1p actin assembly complex	B	1	
ADA2	YDR448W	c	Component of nucleosomal histone acetyltransferase complexes SAGA and ADA, also a component of SLIK complex	SAGA, ADA, SLIK	B	1	
APN1	YKL114C	r	Major Apurinic/Apyrimidinic endonuclease. 3′-repair diesterase.		B	1	
ARP6	YLR085C	c	Nuclear actin-related protein involved in chromatin remodeling	SWR1 complex	B/C	1	
ASF2	YDL197C	cn	GFP fusion forms perinuclear foci. Over-expression interfere with mating-type silencing		B	1	
BIO2	YGR286C	r	Biotin synthase		A	1	

BSC5	YNR069C	n	Binds phosphoinositol 3,4,5-triphosphate in vitro. Overproduced protein tagged with V5 epitope at the C terminus localizes to cytoplasm and nucleus, and shows some concentrated staining around the nuclear rim in budded, unbudded cells.		C	1	
CAC2	YML102W	c	Chromatin assembly complex subunit 1, involved in nucleosome assembly linked with DNA replication	CAF-1 (p60 subunit)	B	1	Most cells are enlarged
CDC73	YLR418C	c	DNA-directed RNA polymerase II accessory protein; involved in telomeric silencing		B	1	
DHH1	YDL160C	r	Putative RNA helicase of the DEAD box family.		B	1	
DOA1	YKL213C	c	WD repeat protein required for ubiquitin-mediated protein degradation		B	1	
EAF3	YPR023C	c	Component of NuA4 histone acetyltransferase complex	NuA4	B	1	Unusually variable brightness of GFP-Rap1 foci in single cells. Nucleolus enlarged
EBS1	YDR206W	l	Protein with similarity to Est1p, involved in maintenance of telomeres. Null mutant has shortened telomeres		B	1	
ESC2	YDR363W	c	Protein involved in chromatin silencing, has a SUMO domain		A	1	

FKH2	YNL068C	c	Homolog of fly forkhead, involved in transcriptional silencing, cell morphology and cell cycle		A	1	
GCN5	YGR252W	c	Catalytic component of two nucleosomal histone acetyltransferase complexes: SAGA and ADA	SAGA, ADA	A	1	
GRE2	YOL151W	n	Null mutant displays defective localization of nuclear pore component Nup49p and nucleolar marker Nop1p		B	1	
GSP2	YOR185C	n	Nuclear trafficking		A	1	
HEK2	YBL032W	cl	RNA binding protein with similarity to hnRNP-K that localizes to the cytoplasm and to subtelomeric DNA		B	1	Defect mainly observed in small-budded cells. Most cells are enlarged, sometimes unusual shape
HIR2	YOR038C	c	Involved in replication-independent histone deposition together with Asf1	Hir	A	1	
HMO1	YDR174W	c	May be involved in higher-order chromatin structure		B	1	
HOS3	YPL116W	c	member of histone deacetylase family.		A	1	
HSN1	YHR127W	n	Protein of unknown function localized to nucleus; purifies with the nuclear pore complex		B	1	Defect mainly observed in small-budded cells
HST1	YOL068C	c	NAD-dependent histone deacetylase of the Sir2 family. Component of Set3p complex	Set3 complex	B	1	

IDH1	YNL037C	r	NAD-dependent histone deacetylase of the Sir2 family. Component of Set3p complex		A	1	
IML3	YBR107C	t	Complex of Imd2p, Imd3p, and Imd4p that binds a C-rich portion of telomeric DNA forms independently of Sir1p, Sir3p, Sir4p, and Rap1p		A/C	1	
IWR1	YDL115C	cl	Interacts with RNA polymerase II		B	1	Most cells are large and sick-looking. Possibly defective in mitosis
KAP122	YGL016W	n	GFP-Pdr6p displays a punctate nuclear envelope staining typical of a nuclear pore complex component		C	1	
LSM1	YJL124C	cn	Null mutant displays defective localization of nuclear pore component Nup49p and nucleolar marker Nop1p. Null mutant exhibits defective mating type and rDNA gene silencing, compared to wild type		A	1	Nucleolus enlarged
MCM22	YJR135C	d	Protein required for maintenance of chromosomes and minichromosomes		B	1	Large sick-looking cells
MGS1	YNL218W	d	yWHIP. A member of the AAA family ATPases, DNA-dependent ATPase required for genome stability, appears to be a DNA replication accessory factor that is specific fro pol delta		A	1	

MSI1	YBR195C	c	Chromatin assembly complex, subunit 3, involved in both nucleosome assembly linked with DNA replication and negative regulation of the RAS pathway	CAF-1	C	1	
NPT1	YOR209C	c	Required for telomeric and rDNA gene silencing		A	1	
NUP53	YMR153W	rn	Component of the karyopherin docking complex of the nuclear pore complex; has similarity to Asm4p	Karyopherin docking complex of the nuclear pore complex	C	1	
PIF1	YML061C	l	5′-3′ helicase required to regulate telomere length		C	1	Abnormally bright foci. Possibly due to longer telomeres (ref)?
RAD52	YML032C	cd	Recombination and DNA repair protein		A	1	
RAD6	YGL058W	c	E2 ubiquitin-conjugating enzyme; involved in telomeric silencing		C	1	Defect mainly observed in small and medium-budded cells
RAD7	YJR052W	c	Interact with Sir3		C	1	
RFM1	YOR279C	c	Protein that interact with Hst1p-Sum1p complex which has histone deacetylase activity	Hst1p–Sum1p complex	B	1	Defect mainly observed in unbudded cells
RLF2 (CAC1)	YPR018W	c	Chromatin assembly complex, subunit p90	CAF-1 (p90 subunit)	B	1	Most cells are enlarged
SAS5	YOR213C	c	Component of SAS complex, involved in silencing at telomeres and the silent mating-type loci	SAS complex	A/C	1	
SIR2	YDL042C	c	Silencing regulatory protein and DNA-repair protein		B	1	

SIZ1	YDR409W	d	SUMO ligase that conjugates Smt3p with septins, also conjugates Smt3p to Pol30p (PCNA), which may be antagonistic to nonproteolytic ubiquitination of Pol30p in the Rad6-dependent DNA repair pathway		B	1	Defect mainly observed in small-budded cells
SNF5	YBR289W	d	SWI–SNF complex; may be involved in initiation of DNA replication	SWI–SNF	B	1	
SPO69	YPR007C	d	sister chromatid cohesion during meiosis both at centromere and the arms near telomeres		C	1	
SPO77	YML066C	r	Probably ATP-powered Ca^{2+} pump, possible role in sporulation		A	1	
SPT23	YKL020C	n	GFP-Spt23p fusion protein localizes to the nucleus uniformly and may interact with the nuclear membrane		A	1	
SUM1	YDR310C	c	Interacts with Hst1p and Rfm1p in a complex with histone deacetylase activity		A	1	
TRF4	YOL115W	d	Catalytic subunit of TRAMP (Trf4/Pap2p-Mtr4p-Air1p/2p), a nuclear poly (A) polymerase complex		A/B	1	

UPF3	YGR072W	cl	Protein involved with Nam7p and Nmd2p in decay of mRNA containing nonsense codons; telomere length and telomeric silencing		B	1	
VTC2	YFL004W	r	Putative polyphosphate synthetase		B	1	
VTC3	YPL019C	r	Putative polyphosphate synthetase, transcription regulated by the PHO system. Either ULP1 or VTC3 is responsible for the phonotype		A/C	1	
WTM2	YOR229W	cn	Transcriptional modulator involved in meiotic regulation and silencing		A	1	
YCK3	YER123W	n	Protein randomly tagged with HA epitope localizes to nuclear rim and ER in budded and unbudded cells, and also shows some diffuse, faint nuclear staining		A	1	Nucleolus enlarged?
YCR101C	YCR101C	n	Overproduced protein tagged with V5 epitope at the C terminus localizes to nucleus, and shows staining of the nuclear rim in budded and unbudded cells		A	1	
YKR045C	YKR045C	r	Conserved hypothetical protein		A	1	
YLR271W	YLR271W		Yku80-associated		C	1	Defect less apparent in unbudded cells.
AHC1	YOR023C	c	Component of the ADA histone acetyltransferase complex	ADA	W		

ARX1	YDR101C	n	Weak similarity to S. pombe Cdb4p, which is a DNA-binding protein that preferentially binds curved DNA. Interact with Nup42 and Nup100		W		
ASM4	YDL088C	dn	Component of the karyopherin docking complex of the nuclear pore complex, has a similarity to Nup53p.Suppressor of temperature-sensitive mutations in Cdc2p DNA polymerase Δ	Karyopherin docking complex of the nuclear pore complex	W		
BDF1	YLR399C	c	Protein required for sporulation, contains two bromodomain motifs and interacts with histones H3 and H4, antagonizes SIR function and limits heterochromatin spreading		W		
BMH1	YER177W	d	Cruciform-binding. Associate with cruciform DNA at ARS307 in vivo	Cruciform DNA-Binding Protein (Bmh1 and Bmh2)	W		
BMH2	YDR099W	d	Cruciform-binding. Associate with cruciform DNA at ARS307 in vivo	Cruciform DNA-Binding Protein (Bmh1 and Bmh2)	W		

BOI2	YER114C	r	Protein which binds Bem1p and contains a proline-rich sequence, an SH3 domain, and a pleckstrin homology domain. Defects in bud formation and maintenance of polarity		W		
BRE1	YDL074C	c	Required for ubiquitination of histone H2B (Htb1p and Htb2p), silencing at the telomere, and histone H3 (Hht1p and Hht2p) methylation at lys4 and lys79		W		
BUB1	YGR188C	d	Ser/Thr protein kinase		W		
CAP1	YKL007W	r	Addition of actin subunits; mutant has aberrant cell morphology		W		
CBF1	YJR061W	r	Basic helix-loop-helix (bHLH) kinetochore protein which binds to centromeric element CDEI, required for chromosome stability and for methionine prototrophy		W		
CKA1	YIL035C	d	Phosphorylates Top2 and modify its activity		W		
CKA2	YOR061W	d	Phosphorylates Top2 and modify its activity		W		
CKB1	YGL019W	d	Phosphorylates Top2 and modify its activity		W		
CKB2	YOR039W	d	Phosphorylates Top2 and modify its activity		W		
CLB6	YGR109C	d	Cyclin, B-type		W		

CSM3	YMR048W	d	Checkpoint; partially defective in cohesion.		W		
CUE1	YMR264W	y	Ubiquitination		W		
DDC1	YPL194W	d	Subunit of 9-1-1 checkpoint specific molecular clamp	9-1-1 complex	W		
DIN7	YDR263C	r	DNA damage induced; endonuclease located in the mitochondrial inner membrane; stabilizes mitochondrial genome; homology to Exo1p		W		
DLS1	YJL065C	c	Subunit of ISW2–yCHRAC chromatin accessibility complex along with Itc1p, Isw2p, and Dpb4p; involved in inheritance of telomeric silencing; telomeric silencing is enhanced in dls1Δmutant; has a weak similarity to Dpb3p	ISW2/yCHRAC	W		
DOT1	YDR440W	c	Histone H3 methyltransferase specific for Lys79 that is involved in silencing at telomeres and others.		W		
DOT5	YIL010W	c	Nuclear thio-peroxidase involved in derepression of telomeric silencing		W		
DOT6	YER088C	c	Protein involved in derepression of telomeric silencing		W		

DPB3	YBR278W	cd	Third-largest subunit of DNA polymerase II (DNA polymerase epsilon), required to maintain fidelity of chromosomal replication and also for inheritance of telomeric silencing	DNA polymerase II (DNA polymerase epsilon)	W		
DPB4	YDR121W	cd	Shared subunit of DNA polymerase (II) epsilon and of ISW2/yCHRAC chromatin accessibility complex; involved in both chromosomal DNA replication and in inheritance of telomeric silencing	DNA polymerase II (DNA polymerase epsilon)	W		
DSE2	YHR143W	rn	Daughter cell–specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother; expression is repressed by cAMP		W		
DUN1	YDL101C	c	Cell cycle checkpoint serine-threonine kinase		W		
ECM11	YDR446W	d	Nonessential protein apparently involved in meiosis, GFP fusion protein is present in discrete clusters in the nucleus throughout mitosis; may be involved in maintaining chromatin structure; interact with Cdc6 in2-hybrid		W		

EMP70	YLR083C	r	Protein whose 24-kD cleavage product is found in endosome-enriched membrane fractions, predicted to be a transmembrane protein		W		
EPS1	YIL005W	r	Pdi1p (protein disulfide isomerase)-related protein involved in endoplasmic reticulum retention of resident ER proteins		W		Poor culture growth with many dead cells
ESC1	YMR219W	cn	Protein localized to the nuclear periphery, involved in telomeric silencing; interacts with PAD4-domain of Sir4p		W		
ESC8	YOL017W	c	Protein involved in telomeric and mating-type locus silencing, interacts with Sir2p and also interacts with the Gal11p, which is a component of the RNA pol II mediator complex		W		
EST2	YLR318W	t	Catalytic subunit of the telomerase		W		Very sick
EXG1	YLR300W	r	Exo-β-1,3-glucanase (I/II), major isoform		W		
FKH1	YIL131C	cd	Forkhead protein, involved in transcriptional silencing, cell morphology and cell cycle		W		
FUN30	YAL019W	cd	Protein important for chromosome integrity and segregation; Snf2 homolog		W		

GDE1	YPL110C	r	Glycerophosphocholine (GroPCho) phosphodiesterase		W		
GFD1	YMR255W	n	Protein of the nuclear pore complex		W		
GPB1	YOR371C	r	G protein subunit mimic and signalling effector		W		Some sick-looking cells had abnormal nuclear morphology. Could be (partially) defective in mitosis.
GTT3	YEL017W	n	Protein of unknown function with a possible role in glutathione metabolism; localizes to nuclear periphery		W		
HAT2	YEL056W	c	Subunit of the major yeast histone acetyltransferase		W		
HCS1	YKL017C	d	DNA helicase A		W		
HFI1	YPL254W	r	Transcriptional coactivator		W		
HHO1	YPL127C	c	Histone H1 protein		W		
HIR1	YBL008W	c	Histone transcription regulator	Hir	W		
HOP2	YGL033W	d	Protein required for pairing of homologous chromosomes		W		
HOS1	YPR068C	c	Putative class I histone deacetylase (HDAC), involved in histone deacetylation at rDNA repeats		W		
HOS2	YGL194C	c	Putative histone deacetylase	Set3 complex	W		
HOS4	YIL112W	c	Subunit of SET3 complex including two histone deacetylases, Hos2 and Hst1, meiotic-specific repressor of sporulation	Set3 complex	W		
HPC2	YBR215W	cd	Cell cycle regulatory protein		W		
HST3	YOR025W	c	Silencing protein		W		

HST4	YDR191W	c	Member of the Sir2p family of putative NAD-dependent histone deacetylases		W		
HTZ1	YOL012C	c	Evolutionarily conserved member of the histone H2A F/Z family of histone variants		W		
IMD3	YLR432W	t	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis		W		
IPK1	YDR315C	n	Inositol 1,3,4,5,6-pentakisphosphate 2-kinase (IP5 2-kinase)		W		
ISW1	YBR245C	c	ATPase component of a four subunit chromatin remodeling complex	Isw1 complex	W		
ISW2	YOR304W	c	ATPase component of a two subunit chromatin remodeling complex	Isw2 complex	W		Most cells had aberrant nuclear morphology
ITC1	YGL133W	c	Subunit of Isw2 chromatin remodeling complex	Isw2 complex	W		
KAR3	YPR141C	d	Kinesin-related protein; required for establishment of cohesion		W		Most cells are enlarged. In addition, nuclear shape is aberrant in dumbbell-shaped cells
LIF1	YGL090W	d	DNA ligase IV interacting factor		W		
LOS1	YKL205W	cn	Pre-tRNA splicing protein; localizes to nuclear pore		W		
MAD2	YJL030W	d	Spindle-assembly checkpoint protein		W		
MAF1	YDR005C	r	Protein required for sorting of Mod5p		W		

MDL1	YLR118W	r	Half-size ABC transporter, mitochondrial		W		
MDT1 (PIN4)	YBL051C	d	FHA1 domain-interacting protein modulates DNA damage tolerance and G(2)/M cell cycle progression; synthetic growth defect with ctf18		W		
MGA2	YIR033W	c	May be involved in the remodeling chromatin structure		W		
MLP1	YKR095W	d	Myosin-like protein related to Uso1p; reported to be required for telomere position		W		
MLP2	YIL149C		Protein involved in translocation of macromolecules between the nucleoplasm and the NPC; reported to be required for telomere position		W		
MRC1	YCL061C	d	Mediator of the replication checkpoint; partially defective in cohesion		W		
MSB1	YOR118W	r	Morphogenesis-related protein		W		
MUP1	YGR055W	r	High affinity methionine permease		W		
NAT1	YDL040C	c	Protein N-acetyltransferase subunit; weak similarity to Tetrahymena telomerase component p95		W		
NDJ1	YOL104C	r	Meiotic telomere protein		W		
NEM1	YHR004C	n	Protein required for nuclear morphology		W		Enlarged nucleolus

NFI1	YOR156C		Interacts with Cdc12p in 2-hybrid assay; Protein involved in SUMO/Smt3p conjugation of a subset of yeast proteins, potential in vivo target of Ulp2p		W		
NGG1	YDR176W	c	General transcriptional adaptor or coactivator		W		
NHP6A	YPR052C	c	Nonhistone chromosomal protein related to mammalian HMG1		W		
NMA2	YGR010W	c	Nicotinate-nucleotide adenylyltransferase		W		
NPY1	YGL067W	r	NADH pyrophosphatase I of the Nudix family of hydrolases, has a peroxisomal targeting signal		W		
NUP2	YLR335W	cn	Nuclear pore protein		W		
NUT1	YGL151W	c	Negative transcription regulator from artificial reporters	RNA polymerase II mediator complex	W		
PBP2	YBR233W	cl	PAB1-binding protein		W		
PCL6	YER059W	r	Cyclin-like protein interacting with Pho85p		W		
PES4	YFR023W	d	DNA-directed DNA polymerase epsilon suppressor		W		
PEX19	YDL065C		Protein required for biogenesis of peroxisomes - peroxin; interact with Yku70		W		
PHB1	YGR132C	r	Prohibitin, antiproliferative protein		W		
PHB2	YGR231C	r	Prohibitin		W		

PHO4	YFR034C	c	Transcription factor		W		Perhaps defective in cytokinesis
PNC1	YGL037C	c	NAD(+) salvage pathway gene, pyrazinamidase and nicotinamidase		W		
PPR1	YLR014C	c	Transcription factor regulating pyrimidine pathway		W		
PRM3	YPL192C	n	Pheromone-regulated protein required for karyogamy		W		
PSD2	YGR170W	r	Phosphatidylserine decarboxylase 2		W		
PSP1	YDR505C	d	High copy suppressor of ts mutations in DNA polymerase alpha		W		
PTK2	YJR059W	cn	Protein involved in polyamine uptake		W		
PUS6	YGR169C	r	tRNA:Psi 31-synthase		W		
QRI8	YMR022W	c	E2 ubiquitin-conjugation enzyme		W		
RAD17	YOR368W	dlr	DNA damage checkpoint control protein	9-1-1 complex	W		
RAD18	YCR066W	c	DNA repair protein		W		
RAD24	YER173W	dr	Cell cycle checkpoint protein		W		
RAD30	YDR419W	d	DNA repair protein		W		
RAD50	YNL250W	dl	DNA repair protein	MRX	W		
RDR1	YOR380W	c	Transcriptional repressor (zinc cluster protein), Repressor of drug resistance; subtelomeric gene		W		
RPD3	YNL330C	c	Histone deacetylase B	Rpd3-Sin3p histone deacetylase	W		

RSN1	YMR266W	r	Over-expression rescues sro7/sop1 in NaCl		W		
RUB1	YDR139C	d	Ubiquitin-like protein		W		
SAC7	YDR389W	c	Suppressor of actin mutation		W		
SAG1	YJR004C	r	α-agglutinin		W		
SAP30	YMR263W	c	Subunit of the histone deacetylase B complex	Rpd3-Sin3p histone deacetylase	W		
SAS2	YMR127C	c	Protein involved in silencing at HMR	SAS complex	W		
SAS3	YBL052C	c	Silencing protein	SAS complex	W		
SAS4	YDR181C	c	Protein involved in silencing at telomeres	SAS complex	W		
SDS3	YIL084C	c	Transcriptional regulator	Rpd3p-Sin3p histone deacetylase complex	W		Nucleolus enlarged
SET2	YJL168C	c	Histone methyltransferase with a role in transcriptional elongation		W		
SET3	YKR029C	c	SET3 complex includes two histone deacetylases, Hos2 and Hst1, and is a meiotic-specific repressor of the sporulation gene program	Set3 complex	W		
SGS1	YMR190C	dr	DNA helicase		W		
SIF2	YBR103W	c	Sir4p interacting protein		W		
SIM1	YIL123W	dy	Protein involved in cell cycle regulation and aging		W		
SKN7	YHR206W	dr	Transcription factor		W		

SNF11	YDR073W	d	Component of SWI–SNF transcription activator complex	SWI–SNF global transcription activator complex	W		
SNF2	YOR290C	d	Component of SWI–SNF global transcription activator complex	SWI–SNF global transcription activator complex	W		
SNF6	YHL025W	d	Global transcription activator	SWI–SNF global transcription activator complex	W		
SNG1	YGR197C	r	Probable transporter conferring resistance to nitrosoguanidine (MNNG) when over-expressed - unknown biological function		W		
SNO2	YNL334C	r	Protein is related with B(1) biosynthesis during the exponential phase		W		
SNT1	YCR033W	r	Component of meiotic-specific repressor of the sporulation	Set3 complex	W		Most cells have large aberrant shape; nucleolus could be also enlarged
SOH1	YGL127C	cl	Allows hpr1 null mutant to grow at 37 deg; mutant has shorter telomeres	RNA polymerase II mediator complex	W		
SPP1	YPL138C	c	Subunit of the Set1/COMPASS complex, which methylates histone H3 on lysine 4	Set1–COMPASS complex	W		

SPT20	YOL148C	c	Member of the TBP class of SPT proteins that alter transcription site selection		W		
SPT3	YDR392W	c	General transcriptional adaptor or co-activator	SAGA and SLIK.	W		Cells accumulate as dumbbell shape.
SPT8	YLR055C	c	Transcriptional adaptor or co-activator	SAGA	W		Cells accumulate as dumbbell shape.
SRS2 (HPR5)	YJL092W	dr	ATP-dependent DNA helicase		W		
SSM4	YIL030C	n	Protein involved in mRNA turnover		W		
STM1	YLR150W	dl	Specific affinity for guanine-rich quadruplex nucleic acids		W		
STO1	YMR125W	r	Large subunit of the nuclear cap-binding protein complex CBC; Suppressor of Top1; plasmid DNA isolated from the mutant is significantly more negatively supercoiled than normal		W		
SWD1	YAR003W	c	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres	Set1/COMPASS complex	W		
SWD3	YBR175W	c	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4	Set1/COMPASS complex	W		
SWR1	YDR334W	r	DEAH-box protein, putative RNA helicase		W		
SXM1	YDR395W	cn	Putative beta-karyopherin		W		

TCO89 (SHD7)	YPL180W	dr	TOR complex 1, 89-kD subunit		W		
TEA1	YOR377W	r	TY1 enhancer activator		W		
TOF1	YNL273W	cd	Topoisomerase I interacting factor 1, DNA replication and damage checkpoint		W		
TOP1	YOL006C	d	DNA topoisomerase I		W		
TOP3	YLR234W	d	DNA topoisomerase III		W		
TPA1	YER049W	c	Protein of unknown function; localized to nucleus; has a role in translation termination efficiency, mRNA poly(A) tail length and mRNA stability		W		
TPO2	YGR138C	r	Proposed vacuolar polyamine transporter		W		
TRF5	YNL299W		Nuclear division protein		W		
TRM3	YDL112W	r	tRNA (guanosine-2`-O-)-methyltransferase		W		Some swollen cells have aberrant nuclear shape.
UIP5	YKR044W	r	Ulp1 Interacting integral membrane protein		W		
UME1	YPL139C	cn	Negative regulator of meiosis		W		
WTM1	YOR230W	cn	Transcriptional modulator		W		
XRS2	YDR369C	dl	DNA repair protein	MRX	W		
YAP5	YIR018W	d	Protein involved in transcription activation		W		
YBR063C	YBR063C	d	Conserved hypothetical protein; interact with MRX		W		
YBR242W	YBR242W	r	Protein of unknown function localized to cytoplasm and nucleus		W		

YDC1	YPL087W	r	Alkaline dihydroceramidase		W		
YDR128W	YDR128W	d	Protein of unknown function localized to vacuolar membrane; Yku80-associated		W		
YEA4	YEL004W	r	Uridine diphosphate-N-acetylglucosamine transporter localized to ER		W		
YGL080W	YGL080W	r	Found in mitochondrial proteome		W		
YGR111W	YGR111W	r	Protein of unknown function localized to cytoplasm and nucleus		W		
YGRCTy1-2	YGRCTy1-2	r	Full length Ty1		W		
YHL046C	YHL046C	n	Strong similarity to members of the Srp1p/Tip1p family		W		
YKE2	YLR200W	dn	Gim complex component; synthetic growth defect with ctf18		W		
YLR247C	YLR247C	c	Protein involved in DNA topology		W		
YNG1	YOR064C	c	Component of NuA3 histone acetyltransferase complex	NuA3	W		
YNL022C	YNL022C	n	Protein of unknown function localized to cytoplasm and nucleus		W		
YNR063W	YNR063W	r	Weak similarity to CYC1/CYP3 transcription activator		W		
YOR051C	YOR051C	n	Protein of unknown function localized to nucleus		W		
YOR154W	YOR154W	c	Protein of unknown function; putative SUN-like domain protein		W		

YTA6	YPL074W	r	Putative ATPase of the CDC48/PAS1/SEC18 (AAA) family, localized to the cortex of mother cells but not to daughter cells		W		

c, chromatin organization (remodeling, assembly, histone modification, and silencing); d, DNA maintenance; l, telomere length; n, localization to nuclear rim, pore-related; r, recombination control; t, telomere binding protein (experimentally confirmed or putative); y, other cell cycle–related (including cohesion).

Table S2. Result of telomere localization screening

Type	**Strain**	**G1**				**S**			
		% zone 1	*n*	P-value against		% zone 1	*n*	P-value against	
				Random	WT			Random	WT
Control	WT	68.5	295	6.3×10^{-11}	1.000	67.2	336	1.9×10^{-10}	1.000
	*sir4*Δ	46.0	124	0.010	1.5×10^{-5}	58.0	91	1.8×10^{-6}	0.008
	*yku70*Δ	54.0	184	3.4×10^{-10}	1.5×10^{-4}	55.0	87	3.5×10^{-6}	2.5×10^{-5}
A	*ace2*Δ[a]	ND				ND			
	*gbp2*Δ	71.0	31	5.0×10^{-5}	0.772	77.8	36	1.0×10^{-7}	0.406
	*imd4*Δ	71.0	31	1.6×10^{-5}	0.103	69.4	36	1.5×10^{-5}	0.571
	*spe1*Δ[b]	ND				ND			
B	*asf1*Δ	67.4	46	2.3×10^{-6}	0.052	43.1	51	0.113	4.7×10^{-4}
	*bre2*Δ	71.0	24	3.8×10^{-4}	0.559	72.0	29	4.2×10^{-5}	0.507
	*csm4*Δ	56.8	37	0.008	0.315	59	39	3.0×10^{-3}	0.258
	*ctf4*Δ[c]	ND				ND			
	*ctf18*Δ	40.2	247	4.3×10^{-5}	3.1×10^{-73}	51.9	212	1.2×10^{-21}	1.2×10^{-18}
	*mre11*Δ	59.4	32	0.007	0.409	47.3	55	0.009	0.001
	*pgd1*Δ	37.9	112	0.076	3.5×10^{-11}	44.8	95	0.123	$6.2 x 10^{-7}$
	*pho23*Δ	63.5	52	2.4×10^{-5}	0.927	69.0	29	2.5×10^{-4}	0.983
	*rad27*Δ[d]	ND				ND			
	*rrm3*Δ	45.2	62	0.161	0.002	38.4	86	0.141	2.0×10^{-8}
	*rsc2*Δ	67.4	43	2.9×10^{-4}	0.354	63.6	44	9.6×10^{-5}	0.515
	*sir3*Δ	56.5	46	0.004	0.312	54.5	44	0.004	0.070
	*swi3*Δ[e]	ND				ND			
	*tel1*Δ	48.1	54	0.029	0.002	63.0	46	9.3×10^{-5}	0.800
	*yku80*Δ	63.9	152	5.1×10^{-14}	0.084	65.8	196	6.0×10^{-21}	0.461
A/B	*sic1*Δ	74.2	31	8.0×10^{-6}	0.487	50.0	42	0.017	0.002
A/C	*jjj1*Δ	52.3	65	0.003	0.031	57.6	39	0.012	0.477
B/C	*elp3*Δ	63.9	36	3.1×10^{-4}	0.423	69.0	29	2.5×10^{-4}	0.752
	*elp4*Δ	45.7	35	0.105	0.008	71.9	32	2.2×10^{-5}	0.680

ND, not determined.

[a] Because of the cytokinesis defect of the *ace2*Δ mutant in the W303 strain background (Voth, W.P., A.E. Olsen, M. Sbia, K.H. Freedman, and D.J. Stillman. 2005. *Eukaryot. Cell.* 4:1018–1028.), the mutant strain was not suitable for microscopic analysis.

[b] The GFP-tagged *spe1*Δ mutant strain ceased to grow in the culture for microscopic observation as unbudded cells. The phenotype resembled the known phenotype of *spe1*Δ mutant under polyamine starvation (Balasundaram, D., C.W. Tabor, and H. Tabor. 1991. *Proc. Natl. Acad. Sci. USA.* 88:5872–5876.).

[c] We did not examine the *ctf4*Δ mutant because the mutant cells were too sick to be examined under a microscope. The *ctf4*Δ mutant is known to have a shorter life span than WT (Hoopes, L.L., M. Budd, W. Choe, T. Weitao, and J.L. Campbell. 2002. *Mol. Cell. Biol.* 22:4136–4146.). In fact, the *ctf4*Δ culture contained large number of dead cells (unpublished data).

[d] In the *rad27*Δ mutant, the copy number of the *lacO* operator array, which is essential for chromosomal GFP dot observation, seemed to decline very rapidly during cultivation, probably due to the hyper-recombination phenotype of the *rad27*Δ mutant (Tishkoff, D.X., N. Filosi, G.M. Gaida, and R.D. Kolodner. 1997. *Cell.* 88:253–263.).

[e] We were not able to construct the *swi3*Δ mutant in the chromosomal GFP dot strain. *SWI3* may be required for expression of the marker gene (*kanMX4*) from the *TEF* promoter.

Table S3. **Yeast strains**

Name	**Relevant genotype**	**Reference**
BY4741	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0*	Brachmann et al., 1998
GA-1320	W303-1A *his3-11,15::GFP-LacI-HIS3 NUP49-GFP*	Heun et al., 2001
GA-1459	GA-1320 *TELVI-R::lacO-lexA-TRP*	Hediger et al., 2002
GA-1985	GA-1420 *TELXIV-L::lacO-lexA-TRP1*	Hediger et al., 2002
GA-1986	GA-1320 *TELVIII-L::lacO-lexA-TRP*	Hediger et al., 2002
HMY57	W303-1A *(hht2-hhf2)Δ::kanMX3*	Masumoto et al., 2005
HMY133	W303-1A *(hht1-hhf1)Δ::LEU2 (hht2-hhf2)Δ::kanMX* [pHM027 (*HHT1 HHF1 TRP1*)]	Masumoto et al., 2005
HMY135	W303-1A *(hht1-hhf1)Δ::LEU2 (hht2-hhf2)Δ::kanMX* [pHM147 (*hht1-K56Q HHF1 TRP1*)]	Masumoto et al., 2005
HMY140	W303-1A *trp1-1::(hht1-K56R HHF1)::TRP1 (hht1-hhf1)Δ::LEU2 (hht2-hhf2)Δ::kanMX3*	Masumoto et al., 2005
HMY152	W303-1A *trp1-1::(HHT1 HHF1)::TRP1 (hht1-hhf1)Δ::LEU2 (hht2-hhf2)Δ::kanMX*	Masumoto et al., 2005
SHY114	GA-1985 *ctf18Δ::kanMX*	Hiraga et al., 2006
SHY155	GA-1985 *yku70Δ::URA3*	This study
SHY158	GA-1985 *sir4Δ::kanMX*	This study
SHY173	GA-1985 *asf1Δ::kanMX*	This study
SHY174	GA-1985 *bre2Δ::kanMX*	This study
SHY176	GA-1985 *rrm3Δ::kanMX*	This study
SHY179	GA-1985 *sic1Δ::kanMX*	This study
SHY180	GA-1985 *rsc2Δ::kanMX*	This study
SHY182	GA-1985 *sir3Δ::kanMX*	This study
SHY184	GA-1985 *mre11Δ::kanMX*	This study
SHY185	GA-1985 *ace2Δ::kanMX*	This study
SHY186	GA-1985 *jjj1Δ::kanMX*	This study
SHY187	GA-1985 *yku80Δ::kanMX*	This study
SHY188	GA-1985 *elp4Δ::kanMX*	This study
SHY189	GA-1985 *tel1Δ::kanMX*	This study
SHY191	GA-1985 *csm4Δ::kanMX*	This study
SHY192	GA-1985 *elp3Δ::kanMX*	This study
SHY193	GA-1985 *gbp2Δ::kanMX*	This study
SHY194	GA-1985 *imd4Δ::kanMX*	This study
SHY195	GA-1985 *pho23Δ::kanMX*	This study
SHY196	GA-1985 *rtt109Δ::kanMX4*	This study
SHY219	GA-1985 *pgd1Δ::kanMX*	This study
SHY227	GA-1985 *vps75Δ::nat1*	This study
SHY229	GA-1985 *asf1Δ:kanMX4 vps75Δ::nat1*	This study
SHY234	W303-1B (*hht2 hhf2*)*Δ::kanMX his3-11,15::GFP-LacI-HIS3 TELXIV-L::(256x lacO)::ADE2*	This study
SHY247	HMY140 *his3-11,15::GFP-LacI-HIS3 TELXIV-L::(256x lacO)::ADE2* [pSH115 (*GFP-NUP49 URA3*)]	This study
SHY248	HMY152 *his3-11,15::GFP-LacI-HIS3 TELXIV-L::(256x lacO)::ADE2* [pSH115 (*GFP-NUP49 URA3*)]	This study
SHY296.2	SHY234 [pSH115 (GFP-*NUP49 URA3*)]	This study
SHY298	GA-1459 *rtt109Δ::kanMX*	This study
SHY299	GA-1986 *rtt109Δ::kanMX*	This study
SHY304	HMY135 *his3-11,15::GFP-LacI-HIS3 TELXIV-L::(256x lacO)::ADE2* [pSH115 (GFP-*NUP49 URA3*)]	This study
SHY310	HMY133 *his3-11,15::GFP-LacI-HIS3 TELXIV-L::(256x lacO)::ADE2* [pSH115 (GFP-*NUP49 URA3*)]	This study
SBY1	GA-1320 *BCP1-(256x lacO)::TRP1-TFC6* (chromosome VI-R)	This study
SBY2	Identical to SBY1. Different isolate	This study
SBY6	Identical to SBY1. Different isolate	This study
SBY39	SBY1 *sir4Δ::kanMX*	This study
SBY40	SBY1 *vps75Δ::kanMX*	This study
SBY41	Identical to SBY40. Different isolate	This study
SBY42	Identical to SBY40. Different isolate	This study
SBY43	SBY1 *yku70Δ::kanMX*	This study
SBY44	Identical to SBY43. Different isolate	This study

SBY45	Identical to SBY43. Different isolate	This study
SBY46	SBY1 *sir4Δ::kanMX yku70Δ::URA3*	This study
SBY47	Identical to SBY46. Different isolate	This study
SBY48	Identical to SBY46. Different isolate	This study
RGY1	SBY1 *rtt109Δ::kanMX*	This study
RGY2	Identical to RGY1. Different isolate	This study
RGY5	SBY1 *asf1Δ::kanMX*	This study
RGY6	Identical to RGY5. Different isolate	This study

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Table S4. **Plasmids**

Name	**Relevant feature**	**Reference**
pAF52	256x *lacO*, *TRP1*	Straight et al., 1996
pAF59	256x *lacO*, *LEU2*	Straight et al., 1996
pAFS135	GFP-*lacI*, *HIS3*	Straight et al., 1996
pAG25	*natMX4*	Goldstein and McCusker, 1999
pGVH30	*ADE2*	Bystricky et al., 2004
pHM027	*HHT1 HHF1 TRP1*	Masumoto et al., 2005
pHM147	*hht1-K56Q HHF1 TRP1*	Masumoto et al., 2005
pSH114	Chromosome XIV:18831-19853, 256x *lacO*, *ADE2*	This study
pSH115	YCplac33 GFP-*NUP49, URA3*	This study
pUN100-GFP-NUP49	GFP-*NUP49*, *LEU2*	Belgareh and Doye, 1997
YCp-GFP-Rap1	YCplac33, GFP-*RAP1*, *URA3*	Hiraga et al., 2006

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