Table 1. Activity of the genes analyzed

Deleted yeast gene	Human homolog	Biological function	Associated mammalian syndome	Yeast mutator genetic assays: CAN1^r [rate ($\times10^{-7}$)*]	Yeast mutator genetic assays: GCR assay [rate ($\times10^{-9}$)*,†]
WT	—	—	—	2.80 (1)	0.35 (1)
CAC1 and CAC3	CAF1 subunits	Chromatin-assembly factor	CAF-1 is overexpressed in breast tumors	1.16 (0.4)	690 (1971)
PIF1	*hPIF1*	Helicase with telomerase inhibitor activity; involved in maintenance of mitochondrial genome	Unknown	20.41 (7)	353 (1,009)
POL32	*POLD3*	Subunit of polymerase δ involved in DNA replication	Unknown	2.81 (1)	0.65 (2)
TSA1	*PRDX1*	Thioredoxin peroxidase involved in oxidative stress response	Lymphoma, carcinoma, and sarcoma	19.25 (7)	6 (17)
MSH2	*hMSH2*	Protein playing a key role in the mismatch repair process	Hereditary nonpolyposis colorectal cancer	59.60 (21)	4 (11)
RAD27	*FEN1*	Flap endonuclease involved in DNA replication and repair	Lung adenoma and adenocarcinoma	95.87 (34)	320 (914)
MEC1 and *TEL1*‡	*ATR* and *ATM*	DNA damage/S-phase checkpoints	Ataxia telangiectasia	482.49 (172)	4,500 (12,857)
CLB5	*CCNB1*	B-type cyclin involved in DNA replication during S-phase	Unknown	2.28 (0.8)	0.22 (6)
MRE11	*hMRE11*	Protein involved in DSB repair, NHEJ, and telomere metabolism	Ataxia telangiectasia-like disorder (ATLD)	20.81 (7)	220 (629)

Mammalian orthologs and diseases associated with their deficiencies are indicated.
*Average mutation rate of the WT and parental mutator strains (G_0) in the CAN^r (present results) and GCR (6) reporter assays. The relative fold increase over the WT strain is reported in parentheses.
†See refs. 6, 12, 15, 32, 33, and 44–46.
‡The *sml1*Δ mutation is necessary to suppress the lethality of the *mec1*Δ mutation (47). In the text, the *mec1*Δ *tel1*Δ *sml1*Δ genotype is abbreviated to *mec1*Δ *tel1*Δ.

6. Chen C, Kolodner RD (1999) Gross chromosomal rearrangements in Saccharomyces cerevisiae replication and recombination defective mutants. *Nat Genet* 23(1):81–85.

12. Huang ME, Rio AG, Nicolas A, Kolodner RD (2003) A genomewide screen in Saccharomyces cerevisiae for genes that suppress the accumulation of mutations. *Proc Natl Acad Sci USA* 100(20):11529–11534.

15. Myung K, Datta A, Kolodner RD (2001) Suppression of spontaneous chromosomal rearrangements by S phase checkpoint functions in Saccharomyces cerevisiae. *Cell* 104(3):397–408.

32. Myung K, Chen C, Kolodner RD (2001) Multiple pathways cooperate in the suppression of genome instability in *Saccharomyces cerevisiae*. *Nature* 411(6841):1073–1076.
33. Myung K, Pennaneach V, Kats ES, Kolodner RD (2003) Saccharomyces cerevisiae chromatin-assembly factors that act during DNA replication function in the maintenance of genome stability. *Proc Natl Acad Sci USA* 100(11):6640–6645.

44. Motegi A, Kuntz K, Majeed A, Smith S, Myung K (2006) Regulation of gross chromosomal rearrangements by ubiquitin and SUMO ligases in Saccharomyces cerevisiae. *Mol Cell Biol* 26(4):1424–1433.
45. Myung K, Datta A, Chen C, Kolodner RD (2001) SGS1, the Saccharomyces cerevisiae homologue of BLM and WRN, suppresses genome instability and homeologous recombination. *Nat Genet* 27(1):113–116.
46. Putnam CD, et al. (2012) Bioinformatic identification of genes suppressing genome instability. *Proc Natl Acad Sci USA* 109(47):E3251–E3259.