

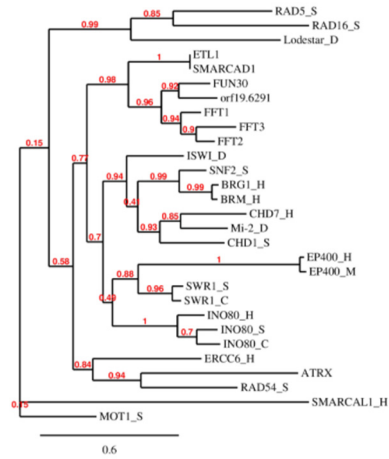
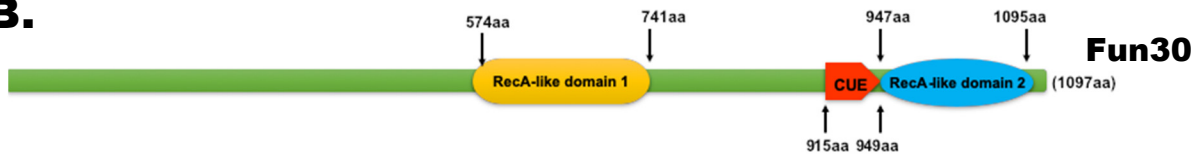
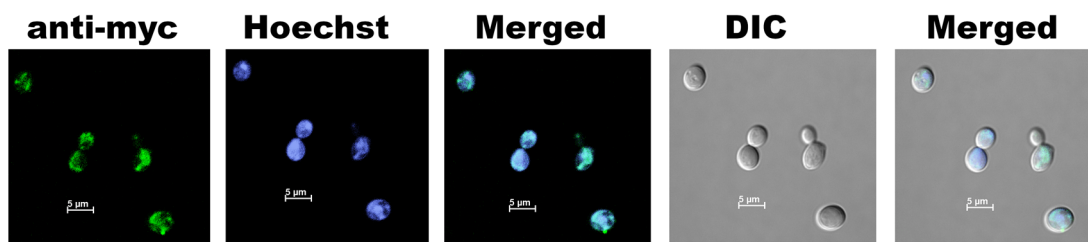
A.**B.****C.**

Figure S1. The orf19.6291 encodes for Fun30, a member of the ATP-dependent chromatin remodeling protein family. (A) Phylogenetic analysis of orf19.6291 protein from *C. albicans* was done with Rad5 from *S. cerevisiae* (RAD5_S), Rad16 from *S. cerevisiae* (RAD16_S), Lodestar from *D. melanogaster* (Lodestar D), Etl1 from *M. musculus* and SMARCAD1 from *H. sapiens*, Fun30 from *S. cerevisiae*, Fft1, Fft2, and Fft3 from *S. pombe* (FFT1, FFT2, and FFT3 respectively), Iswi from *D. melanogaster* (ISWI_D), Snf2 from *S. cerevisiae* (SNF2_S), BRG1, BRM, and CHD7 from *H. sapiens* (BRG1_H, BRM_H, CHD7_H respectively), Mi-2 from *D. melanogaster* (Mi-2_D), CHD1 from *S. cerevisiae* (CHD1_S), EP400 from *H. sapiens* and *M. musculus* (EP400_H and EP400_M respectively), SWR1 from *S. cerevisiae* and *C. elegans* (SWR1_S and SWR1_C respectively), Ino80 from *H. sapiens*, *S. cerevisiae* and *C. elegans* (INO80_H, INO80_S, and INO80_C respectively), ERCC6 from *H. sapiens* (ERCC6_H), ATRX from *H. sapiens*, Rad54 from *S. cerevisiae* (RAD54_S), SMARCAL1 from *H. sapiens* (SMARCAL1_H) and Mot1 from *S. cerevisiae* (MOT1_S). (B) Domain architecture of Fun30 (orf19.6291) from *C. albicans*. (C) Localization of Fun30 protein from *C. albicans* was monitored using immunofluorescence. Fun30 was tagged with myc and localization was monitored using anti-myc antibody. The nucleus was stained using Hoechst.

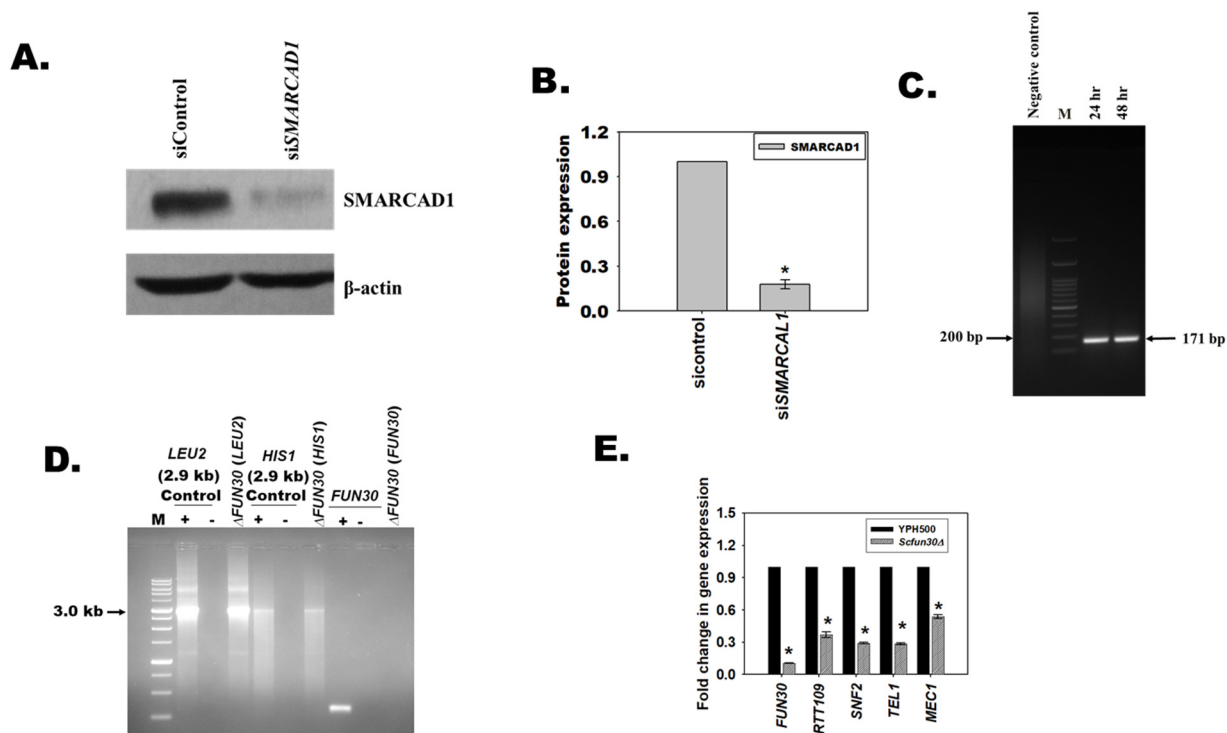


Figure S2. Confirmation of *FUN30* homozygous null mutant. **A.** Expression of SMARCAD1 was analyzed by western blot in siSMARCAD1 cells. β -actin was used as the internal control. **B.** Quantification of the western blots. The data is represented as average \pm s.d of two independent experiments. **C.** Expression of *C. albicans* *FUN30* was analyzed in siSMARCAD1 cells at 24 hr and 48 hr. **D.** Confirmation of Δ *FUN30* mutant was done using PCR. **E.** Expression of *FUN30*, *RTT109*, *SNF2*, *TEL1*, and *MEC1* was analyzed by qPCR in YPH500 and *S. cerevisiae* Δ fun30 Δ mutants. Star indicates $p < 0.5$.

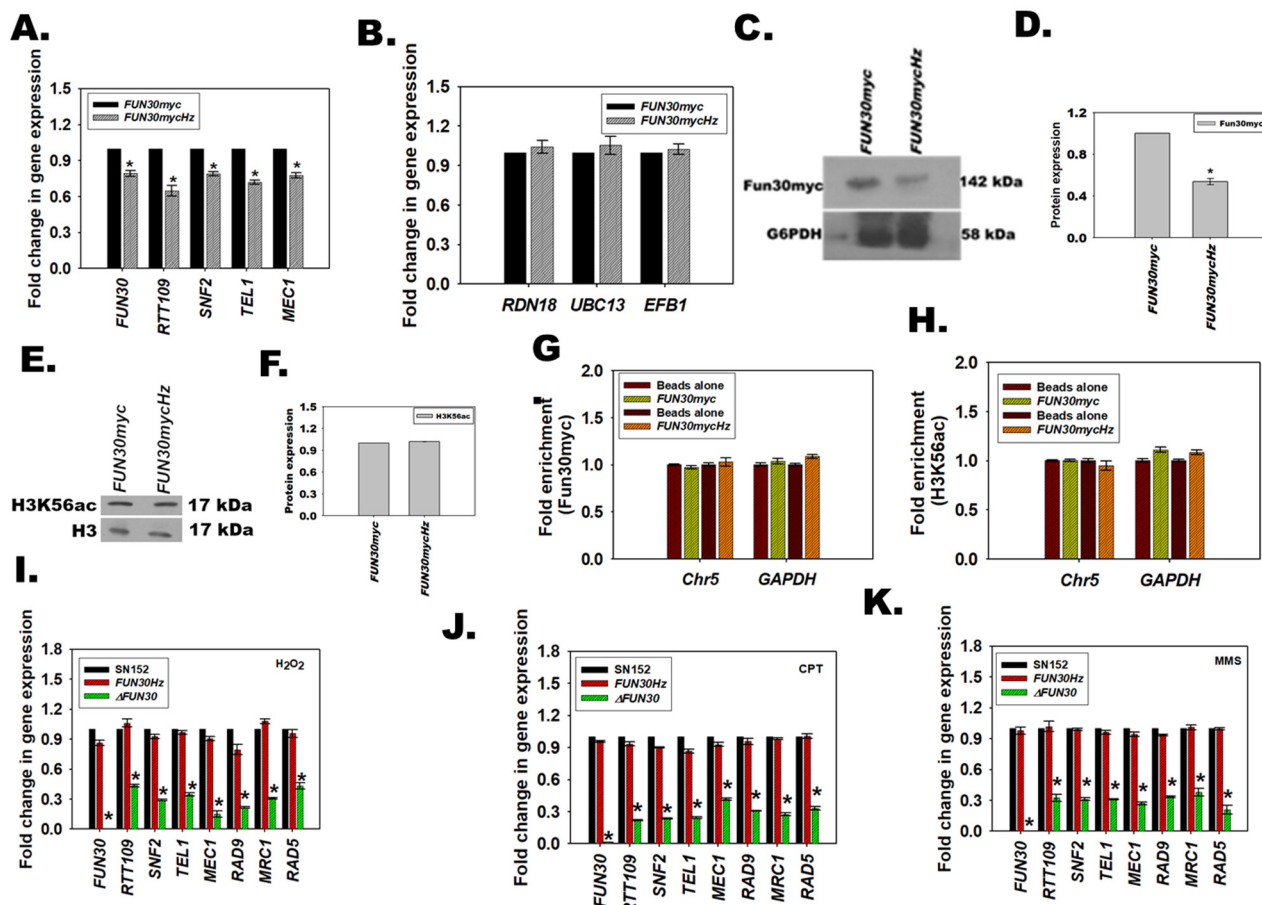


Figure S3. Expression of *RTT109*, *SNF2*, *TEL1*, and *MEC1* is regulated by Fun30. **A.** Expression of *FUN30*, *RTT109*, *SNF2*, *TEL1*, and *MEC1* was analyzed by qPCR in *FUN30myc* and *FUN30mycHz* mutants. **B.** Expression of *RDN18*, *UBC13*, and *EFB1* was analyzed by qPCR in *FUN30myc* and *FUN30mycHz* mutants. **C.** Western blots showing the expressing of Fun30 in *FUN30myc* and *FUN30mycHz* strains. G6PDH was used as loading control. **D.** Quantitation of Fun30myc expression in *FUN30myc* and *FUN30mycHz* strains from the western blots. **E.** Western blot showing the levels of H3K56ac in *FUN30myc* and *FUN30mycHz* strains. H3 was used as the loading control. **F.** Quantitation of H3K56ac expression in *FUN30myc* and *FUN30mycHz* strains from the western blots. **G.** Occupancy of Fun30myc on the intergenic region of Chr5 as well as *GAPDH* promoter in *FUN30myc* and *FUN30mycHz* strains. **H.** Occupancy of H3K56ac on the intergenic region of Chr5 as well as *GAPDH* promoter in *FUN30myc* and *FUN30mycHz* strains. **I.** Comparison of expression of *FUN30*, *RTT109*, *SNF2*, *TEL1*, *MEC1*, *RAD9*, *MRC1* and *RAD5* between SN152, *FUN30Hz*, and Δ *FUN30* in the presence of 7.5 μ M H_2O_2 . **J.** Comparison of expression of *FUN30*, *RTT109*, *SNF2*, *TEL1*, *MEC1*, *RAD9*, *MRC1*, and *RAD5* between SN152, *FUN30Hz*, and Δ *FUN30* in the presence of 1000 μ M CPT. **K.** Comparison of expression of *FUN30*, *RTT109*, *SNF2*, *TEL1*, *MEC1*, *RAD9*, *MRC1*, and *RAD5* between SN152, *FUN30Hz*, and Δ *FUN30* in the presence of 0.02% MMS. Star indicates $p < 0.5$.

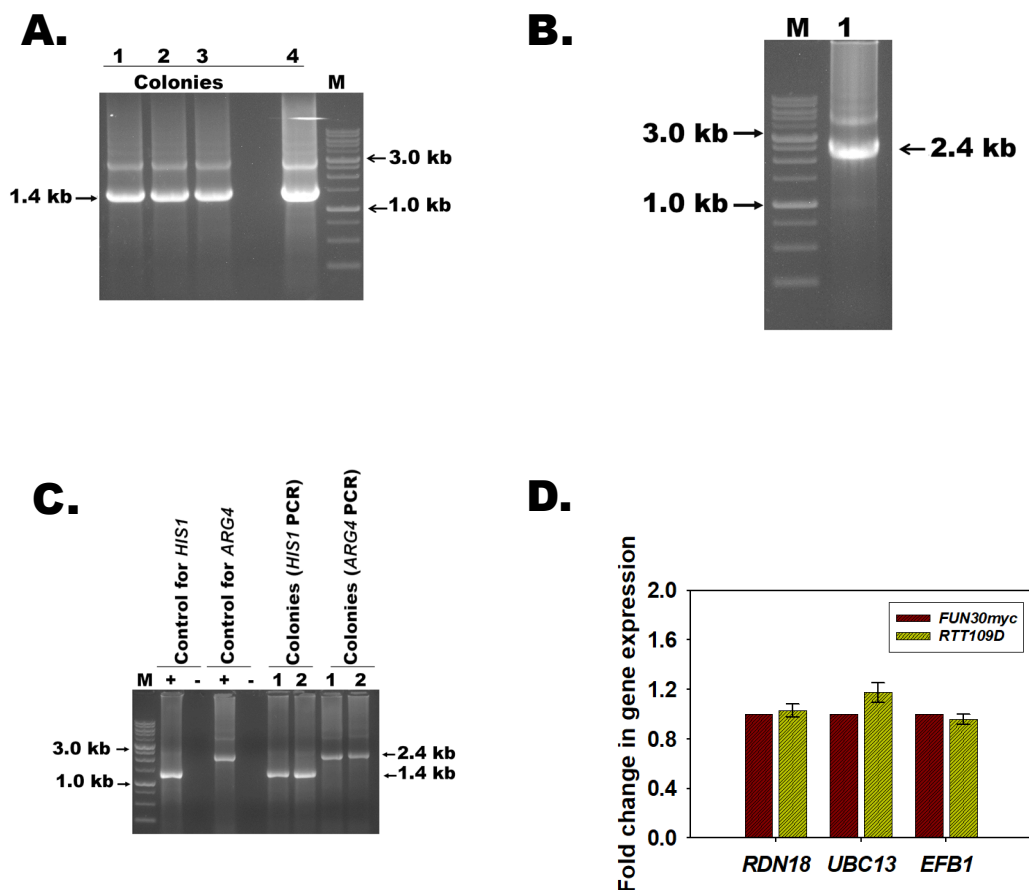


Figure S4. The *RTT109Hz* and *RTT109D* mutants were confirmed using PCR. **A.** One copy of *RTT109* was deleted in the BWP17 strain. Four colonies (# 1, 2, 3, and 4) were screened using *HIS1* specific primers and all the colonies gave the expected 1.4 kb product. **B.** The deletion of the second copy of *RTT109* in the *RTT109Hz* strain was confirmed by PCR using *ARG4* specific primers. The appearance of the expected 2.4 kb band confirmed the mutant strain. **C.** Deletion of the second copy of *RTT109* in *RTT109Hz* strain made in *FUN30myc* background was confirmed by PCR using *HIS1* and *ARG4* cassette specific primers. Two colonies (1 and 2) were screened. The appearance of the expected 1.4 kb and 2.4 kb confirmed the mutants. **D.** Expression of *RDN18*, *UBC13* and *EFB1* was analyzed by qPCR in *FUN30myc* and *RTT109D* strain.

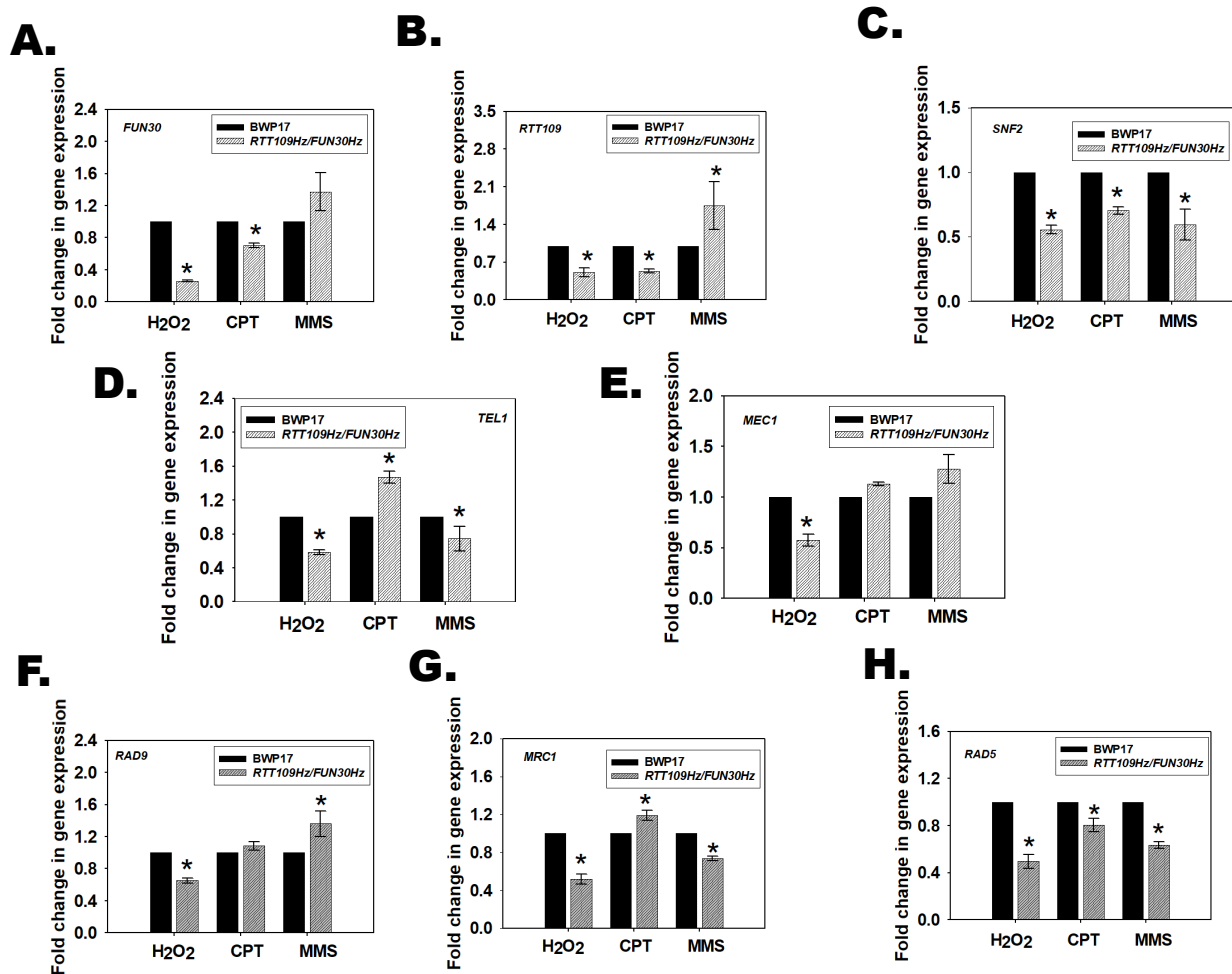


Figure S5. *Rtt109* and *Fun30* regulate the transcription of genes involved in DNA damage response pathways. Expression of **A.** *FUN30*; **B.** *RTT109*; **C.** *SNF2*; **D.** *TEL1*; **E.** *MEC1*; **F.** *RAD9*; **G.** *MRC1*; **H.** *RAD5* was analyzed in *BWP17* and *RTT109Hz/FUN30Hz* strains in the presence of H_2O_2 (7.5 mM), CPT (100 μ M), and MMS (0.02%). The qPCR data are presented as average \pm s.e.m. of three biological replicates. Star indicates $p < 0.05$.

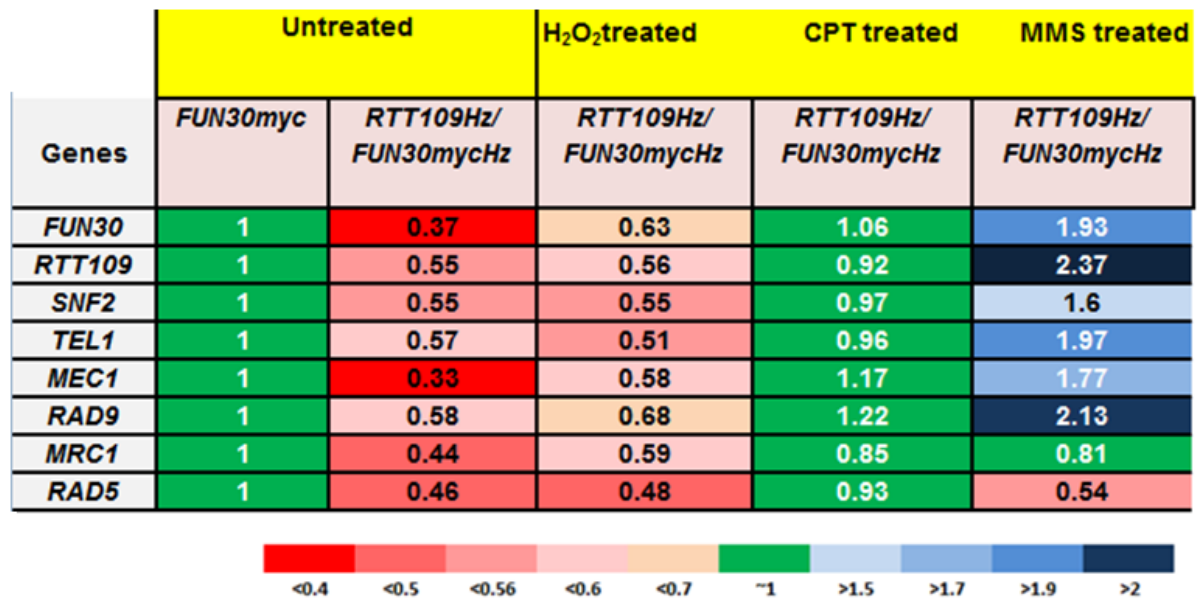


Figure S6. Expression (fold changes) of *FUN30*, *RTT109*, *SNF2*, *TEL1*, *MEC1*, *RAD9*, *MRC1*, and *RAD5* in *FUN30myc* and *RTT109Hz/FUN30mycHz* strains in untreated and treated conditions with H₂O₂ (7.5 mM), CPT (100 μ M), and MMS (0.02%).

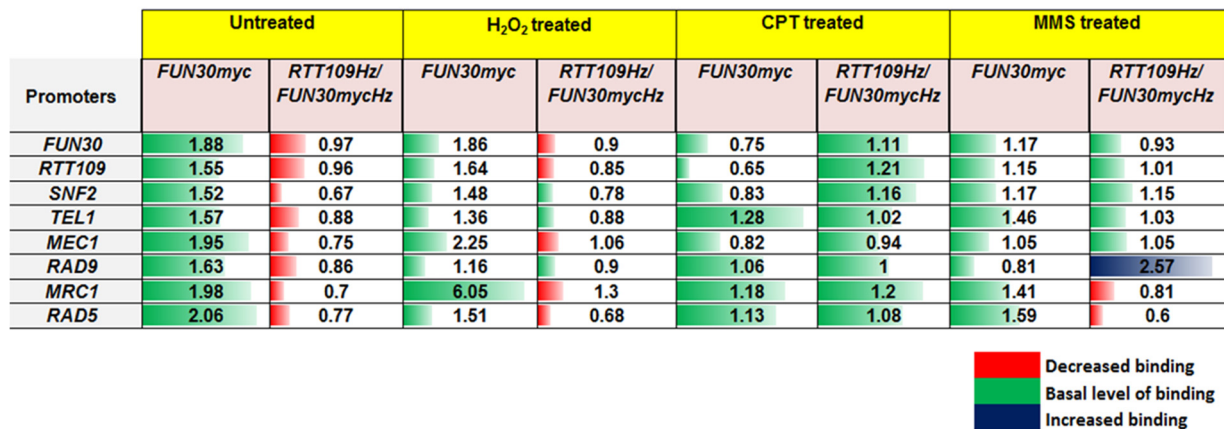


Figure S7. The occupancy (fold changes) of Fun30myc on *FUN30*, *RTT109*, *SNF2*, *TEL1*, *MEC1*, *RAD9*, *MRC1*, and *RAD5* promoters in *FUN30myc* and *RTT109Hz/FUN30mycHz* strains in untreated and treated conditions with H₂O₂ (7.5 mM), CPT (100 μ M) and MMS (0.02%).

	Untreated		H ₂ O ₂ treated		CPT treated		MMS treated	
Promoters	<i>FUN30myc</i>	<i>RTT109Hz/ FUN30mycHz</i>	<i>FUN30myc</i>	<i>RTT109Hz/ FUN30mycHz</i>	<i>FUN30myc</i>	<i>RTT109Hz/ FUN30myc</i>	<i>FUN30myc</i>	<i>RTT109Hz/ FUN30myc</i>
<i>FUN30</i>	153.1	102.45	17.11	18.67	6.69	10.42	40.09	53.03
<i>RTT109</i>	198.49	126.2	75.52	70.66	27.07	49.31	11.02	6.49
<i>SNF2</i>	133.98	58.63	22.4	32.55	10.62	15.6	25.21	14.1
<i>TEL1</i>	173.47	118.17	51.29	57.09	24.69	15.32	7.69	21.01
<i>MEC1</i>	12.92	7.33	101.31	145.04	3.92	6.14	1.44	2.66
<i>RAD9</i>	146.22	92	25.55	18.05	13.23	17.23	1.08	1.71
<i>MRC1</i>	213.1	132.46	290.12	253.48	23.55	23.31	17.11	4.79
<i>RAD5</i>	192.33	129.37	154.2	131.93	25.27	33.22	39.38	15.95

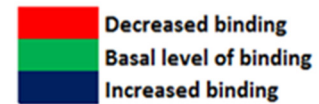


Figure S8. The occupancy (fold changes) of H3K56ac on *FUN30*, *RTT109*, *SNF2*, *TEL1*, *MEC1*, *RAD9*, *MRC1*, and *RAD5* promoters in *FUN30myc* and *RTT109Hz/FUN30mycHz* strains in untreated and treated conditions with H₂O₂ (7.5 mM), CPT (100 μ M) and MMS (0.02%).

Table S1. List of primers used for constructing mutants.

Primer Name	Primer Sequence (5'→ 3')
RTT109-HindIII-FP	GCGAAGCTTGATTCTTAAAATCGCGTCCTTTCA
RTT109-NheI-RP	GCGGCTAGCCTATTTTGATTTTCTATAATTACT
RTT109-HIS1-FP	ATGCTTCCTCCAGATATATTACAAAATGGTGAATTTGAAA CCATTTACTTCCAGACAAATCGGGGATCCTGGAGGATGAG
RTT109-HIS1 -RP	CTATTTTGATTTTCTATAATTACTTACAAAATTACTAACT TCAACACGATCACTAAAATCCGGAATATTTATGAGAACT
RTT109-ARG4-FP	ATGCTTCCTCCAGATATATTACAAAATGGTGAATTTGAAA CCATTTACTTCCAGACAAATTGTGGAATTGTGAGCGGAAG
RTT109-ARG4-RP	CTATTTTGATTTTCTATAATTACTTACAAAATTACTAACTT CAACACGATCACTAAAATCTTTCCAGTCACGACGTT
FUN30-PstI-FP	GCGCTGCAGATGAGTTGGTTTAGAAGAAATAAAC
FUN30-NheI-RP	GCGGCTAGCTCAACTATAAACTATTGACTCTAATG
FUN30-HIS1-FP	ATGAGTTGGTTTAGAAGAAATAAACCAACGGAGGAATCA TCTACAGCTGATCCAAACACACGGGGATCCTGGAGGATGAG
FUN30-HIS1-RP	TCAACTATAAACTATTGACTCTAATGTTGAAATCTTTTCG TCTAACTCTAATTTGTTTCTCGGAATATTTATGAGAGAACT
FUN30-ARG4-FP	ATGAGTTGGTTTAGAAGAAATAAACCAACGGAGGAATCA TCTACAGCTGATCCAAACACATGTGGAATTGTGAGCGGAAG
FUN30-ARG4-RP	TCAACTATAAACTATTGACTCTAATGTTGAAATCTTTTCG TCTAACTCTAATTTGTTTCTTTTCCAGTCACGACGTT
FUN30-MYC-FP	GAAACAAATTAGAGTTAGACGAAAAGATTTCACATTAGAGTCAATAGTTTATAGTCG- GATCCCCGGGTTAATTAACGG
FUN30-MYC-RP	TTACCAAAACAAGCGGGAAAATCAGCTTCAAATGTGTACATTTCTATTTT- GCGGCGGCCGCTCTAGAACTAGTGGATC
RAD9-URA3-FP	ATACAATTGCCAGAACTCAATCTCAAAGCTTATTATATTATGATTCACACTA- GAAGGACCACCTTTGATTG
RAD9-URA3-RP	TTTGGTGCTATAATTGGGATTATTTTCATCTGATTGTTTTTAGATTCTGATT- GTACAATTCATCCATAC
RAD5-HindIII-FP	CCCAAGCTTATGAAAGTTATAAAGAAAAGG
RAD5-NheI -RP	CTAGCTAGCCTATTCTCTCAAAAAGGATTTG
RPS1-RP	AATAGAGAGAACTATATTATACAC
FUN30 URA3 FP	TTGTCGTGAAAAATTGAGACACGACCTGCATTTTCAGTCGACGCGTGTTTTTCAATTCTA- GAAGGACCACCTTTGATTGT

FUN30 MET3 RP	TTCTCCGTTGGTTTATTCTTCTAAACCAACTCATATTGAATGAAAATAAGTAAA- GCCATTTTAATAAACGCGGATCC
FUN30-Xho1-FP	CCGCTCGAGATGAGTTGGTTTAGAAGAAATAAAC
FUN30-Xma1-RP	CCCCCGGGTCAACTATAAACTATTGACTCTAATG
FUN30-BamH1	CGCGGATCCATGAGTTGGTTTAGAAGAAATAAAC
FUN30-Mlu1-RP	CGACGCGTTCAACTATAAACTCCATTGACTCTAATG
ScFUN30 deletion-FP	ATGAGTGGTTCGCATTCAAATGATGAGGATGACGTAGTGCAAGTGCCCCGAGAC- GTCCTCTCTCCAGGAACCGAAATACA
ScFUN30 deletion-RP	TTATTCTTTGGTTCCCTTCGGTTTCGAGTTTTCATCATAAATTATATCCTCCAACATA- TCCTCAACCAAGTCATTCTGAG
ScDownFun30-FP	GATGAAAACCTCGAAACCGAAGGGAACCAAGAATAAATAAAAA- TATAGTAACTCCAGGAACCGAAATACA
ScDownFun30-RP	GCTATACATACTAACCTATGTATATATACACATATATGTATATTATACTCTA- GAACTCAACCAAGTCATTCTGAG
PHO5-FP	TACCATTCCCTTAGGCAAAC
PHO5-RP	CATGTCTACCAACCATTTGC
FUN30-GKT-FP	GCACGAGATGGGTCTTGGTGCAACTTGTCAAGTCATTGCA
FUN30-GKT-RP	TGCAATGACTTGACAAGTTGCACCAAGACCCATCTCGTCG
FUN30 Primer 1	ATCGCTAAGTATCGCCCGTT
FUN30 Primer 3	cacggcgcgctagcagcggTGGATGGAGATGGCTTGGTT
FUN30 Primer 4	gtcagcgggcgcatccctgcAGCTGATTTCCCGCTTGT
FUN30 Primer 6	TGTCAATCCACCACCACCAA
Universal Primer 2	ccgctgctaggcgcgccgtgACCAGTGTGATGGATATCTGC
Universal Primer 5	gcagggatgcggccgctgacAGCTCGGATCCACTAGTAACG

Table S2. List of plasmids used in this study.

Plasmids	Reference
pACT1-GFP	Alistair Brown, Aberdeen
pACT1-RTT109	This study
pACT1-FUN30	This study
pACT1-RAD5	This study
pmCherry-HIS1	Victoria et al. [1]
pRS-ARG4	Wilson et al. [2]
URA3-pMET3-GFP	Gerami-Nejad et al. [3]
YepHIS	Jain et al. [4]
pYES2	This study
eGFP-C2	This study
pSN40	This study
pSN52	This study

Table S3. List of strains used in this study.

Strains	Genotype	Referred in Manuscript	Reference
Mutants made using BWP17 strain			
BWP17	<i>ura3::imm434/ura3::imm434 iro1/iro1::imm434 his1::hisG/his1::hisGarg4/arg4</i>	BWP17	Wilson et al., 1999 [2]
BWP17-URA3	BWP17 with <i>RPS1/rps1Δ::pACT1-GFP::URA3</i>	BWP17-URA3	Jain et al., 2010 [4]
<i>VPS75/vps17-URA3</i>	BWP17with <i>VPS75/vps75Δ::ARG4</i> with <i>RPS1/rps1Δ::pACT1-GFP::URA3</i>	<i>VPS75Hz-URA3</i>	This study
<i>RTT109/rtt109</i>	BWP17 with <i>RTT109/rtt109Δ::HIS1</i>	<i>RTT109Hz</i>	This study
<i>RTT109/rtt109-URA3</i>	BWP17- <i>RTT109</i> heterozygous with <i>RPS1/rps1Δ::pACT1-GFP::URA3</i>	<i>RTT109Hz-URA3</i>	This study
<i>rtt109/rtt109-URA3</i>	BWP17- <i>RTT109</i> heterozygous <i>URA3</i> with <i>RTT109/rtt109Δ::ARG4</i>	<i>RTT109D-URA3</i>	This study
<i>rtt109/rtt109/pACT1-RTT109</i>	BWP17- <i>RTT109</i> deletion with <i>RPS1/rps1Δ::pACT1-RTT109</i>	<i>RTT109D/RTT109OE-URA3</i>	This study
<i>rtt109/rtt109/pACT1-FUN30</i>	BWP17- <i>RTT109</i> deletion with <i>RPS1/rps1Δ::pACT1-FUN30</i>	<i>RTT109D/FUN30OE-URA3</i>	This study
<i>FUN30/fun30</i>	BWP17 with <i>FUN30/fun30Δ::HIS1</i>	<i>FUN30Hz</i>	This study
<i>FUN30/fun30-URA3</i>	BWP17- <i>FUN30</i> heterozygous with <i>RPS1/rps1Δ::pACT1-GFP::URA3</i>	<i>FUN30Hz-URA3</i>	This study
<i>FUN30/fun30/pACT1-FUN30</i>	BWP17- <i>FUN30</i> heterozygous with <i>RPS1/rps1Δ::pACT1-FUN30</i>	<i>FUN30Hz/FUN30OE-URA3</i>	This study
<i>FUN30/fun30/pACT1-RTT109</i>	BWP17- <i>FUN30</i> heterozygous with <i>RPS1/rps1Δ::pACT1-RTT109</i>	<i>FUN30Hz/RTT109OE-URA3</i>	This study
<i>RTT109/rtt109/FUN30/fun30</i>	BWP17- <i>RTT109</i> heterozygous with <i>FUN30/fun30Δ::ARG4</i>	<i>RTT109Hz/FUN30Hz</i>	This study
<i>RTT109/rtt109/FUN30/fun30 -URA3</i>	BWP17- <i>RTT109</i> and <i>FUN30</i> heterozygous with <i>RPS1/rps1Δ::pACT1-GFP::URA3</i>	<i>RTT109Hz/FUN30Hz -URA3</i>	This study
<i>RTT109/rtt109/FUN30/fun30/RAD9/rad9-URA3</i>	BWP17- <i>RTT109</i> and <i>FUN30</i> heterozygous with <i>RAD9/rad9Δ::URA3</i>	<i>RTT109Hz/FUN30Hz/RAD9Hz-URA3</i>	This study
<i>RTT109/rtt109/FUN30/fun30/pACT1-RAD5</i>	BWP17- <i>RTT109</i> and <i>FUN30</i> heterozygous with <i>RPS1/rps1Δ::pACT1-RAD5</i>	<i>RTT109Hz/FUN30Hz/RAD5OE-URA3</i>	This study
Mutants made using SN152 strain			
SN152	<i>ura3::imm434::URA3/ura3::imm434 iro1::IRO1/iro1::imm434 his1::hisG/his1::hisG leu2/leu2 arg4/arg4</i>	SN152	Noble and Johnson, 2005 [5]
<i>SN152/fun30</i>	SN152 with <i>FUN30/fun30Δ::LEU2</i>	<i>FUN30Hz</i>	This study
<i>fun30/fun30</i>	SN152 with <i>fun30Δ::LEU2 /fun30Δ::HIS1</i>	<i>ΔFUN30</i>	This study
<i>FUN30myc</i>	SN152 with <i>FUN30-13X myc-FLP-SAT1</i>	<i>FUN30myc</i>	This study
<i>RTT109/rtt109</i>	<i>FUN30myc</i> with <i>RTT109/rtt109Δ::HIS1</i>	<i>RTT109Hz</i>	This study
<i>FUN30myc/fun30</i>	<i>FUN30myc</i> with <i>FUN30/fun30Δ::HIS1</i>	<i>FUN30mycHz</i>	This study
<i>rtt109/rtt109</i>	<i>FUN30myc-RTT109</i> heterozygous with <i>RTT109/rtt109Δ::ARG4</i>	<i>RTT109D</i>	This study
<i>RTT109/rtt109/FUN30myc/fun30</i>	<i>FUN30myc-RTT109</i> heterozygous with <i>FUN30/fun30Δ::ARG4</i>	<i>RTT109Hz/FUN30mycHz</i>	This study
Mutants made in <i>S. cerevisiae</i>			
YPH500	MATα <i>ura3-52 lys2-801_amber ade2-101_ochre trp1-Δ63 his1-Δ200 leu2-Δ1</i>	YPH500	Sikorski and Hieter, 1989 [6]
JKM179	MATα <i>ade1 leu2-3,112 lys5 trp1::hisG ura3-52 hml::ADE1 hmr::ADE1 ade3::GAL::HO</i>	JKM179	Eapen et al., 2012 [7]
<i>Scfun30Δ</i>	YPH500 with <i>fun30Δ::URA3</i>	<i>fun30Δ</i>	This study

<i>fun30Δ</i>	JKM179 with <i>fun30Δ::URA3</i>	<i>fun30Δ</i>	This study
YPH500- <i>URA3</i>	YPH500; intergenic region:: <i>URA3</i>	YPH500- <i>URA3</i>	This study
JKM179- <i>URA3</i>	JKM179; intergenic region:: <i>URA3</i>	JKM179- <i>URA3</i>	This study
YPH500- <i>URA3</i> - <i>YepHIS</i>	YPH500; intergenic region:: <i>URA3</i> with <i>YepHIS</i>	YPH500- <i>URA3</i> - <i>YepHIS</i>	This study
JKM179- <i>URA3</i> - <i>YepHIS</i>	JKM179; intergenic region:: <i>URA3</i> with <i>YepHIS</i>	JKM179- <i>URA3</i> - <i>YepHIS</i>	This study
<i>Scfun30Δ</i> - <i>YepHIS</i>	YPH500; <i>fun30Δ::URA3</i> with <i>YepHIS</i>	<i>fun30Δ</i> - <i>YepHIS</i>	This study
<i>fun30Δ</i> - <i>YepHIS</i>	JKM179; <i>fun30Δ::URA3</i> with <i>YepHIS</i>	<i>fun30Δ</i> - <i>YepHIS</i>	This study
<i>Scfun30Δ</i> - <i>YepHIS</i> - <i>CaFUN30</i>	YPH500; <i>fun30Δ::URA3</i> with <i>YepHIS</i> - <i>CaFUN30</i>	<i>fun30Δ</i> - <i>YepHIS</i> - <i>CaFUN30</i>	This study
<i>fun30Δ</i> - <i>YepHIS</i> - <i>CaFUN30</i>	JKM179; <i>fun30Δ::URA3</i> with <i>YepHIS</i> - <i>CaFUN30</i>	<i>fun30Δ</i> - <i>YepHIS</i> - <i>CaFUN30</i>	This study

Table S4. List of primers used for qPCR analysis.

	Forward Primer (5'→ 3')	Reverse Primer (5'→ 3')
<i>C. albicans</i>		
<i>RTT109</i>	TCGTTGATTGGATGCTGTAAGG	ACCAGCTTCAACAGGTTTCATAA
<i>FUN30</i>	GTGGAATTGAACCAAGTGTAGCTG	TGAGATTGCCTTCCGTTGTCTC
<i>TEL1</i>	ATTCTACCAGTTGGCTTGCGA	TCCAAAGTTGTTCTTTCCGGC
<i>MEC1</i>	GAGACACAGCAAGACCCATTA	CGAGCAACTTGTTCATCTTTCAG
<i>SNF2</i>	TGGAGGAGTATGGTCGTGGT	TCTTCGGCTTGGCTTCCATT
<i>RAD5</i>	GGCCATACGCATCTCAAAC	CGGCGTTTGGATAATCTTGT
<i>RAD9</i>	TCAAATTCATTGGTGGCTGA	TTCGTTTTCGTTCTCGTTCA
<i>MRC1</i>	TGACGAACAAGCCACTCAAG	TCATTTTACGACCACGACGA
<i>UBC13</i>	TCGGTCCTAATCAATCACCTT	TCTTTCAACACATCCAAACAAA
<i>RDN18</i>	CCACCACCCACAAAATCAA	CGGCACCTTACGAGAAATCA
<i>EFB1</i>	GCTTCTGGTTCTGCTGCTG	GCTGGTTTTGGACCTTTAGC
<i>VPS75</i>	CCAATGTATGCCAAAAGACG	AATGACCTGCCTCATCATCG
<i>GAPDH</i>	GTCCATCCCACAAGGACTGG	CAACGGAAACATCGGTGGTTGG
<i>S. cerevisiae</i>		
<i>RTT109</i>	GTACGCCAGCAAGAACTTA	AGAATCTGGGAAGAGGTACTG
<i>FUN30</i>	GCCTCACATAGGCCATATTC	CAGACTCAATTGCATTGTAACC
<i>TEL1</i>	GTTTCGATACGAGGCCTTTAG	TCAGGTCCGATTCTCTTTG
<i>MEC1</i>	GTTTCGATACGAGGCCTTTAG	TCAGGTCCGATTCTCTTTG
<i>SNF2</i>	ACGACGACGACAATTCTAAC	CTTAAGGTAGGAGCCCATTC
<i>ALG9</i>	GTGGCTTTGGTGAACAATTAC	CCTGGAAGAAGACCATCAAAT
Chr3 Primers used for Double-strand end resection		
<i>Distance (kb)</i>		
-56.59	CCAAAGCGTCATGGACATCT	AGGCCCATCATTCTACTACTGG
-48.148	CACGCCTAGTTTCAGTTGTTT	CTTCAAGACATAATCAACGACGC
-29.91	TCGTCGTCGCCATCATTTTC	GCCCAAGTTTGAGAGAGGTTGC
-16.712	CGTCTTCTCAGCGAACAACAGC	CGTCTTCTCAGCGAACAACAGC
-9.592	TCAGGGTCTGGTGAAGGAATG	CAAAGGTGGCAGTTGTTGAACC
-5.358	ATTGCGACAAGGCTTCAACC	CACATCACAGGTTTATTGGTTCCC
-0.186	CATACAGAAACACAGCGG	AGGAAGGAACAGGAATCTGG
0.183	CCTGGTTTTGGTTTTGTAGAGTGG	GAGCAAGACGATGGGGAGTTTC
5.453	GGACTGGTTATAGACGATGAAGTGT	AAGTCGTCCTTCTTCTTGCTCC
9.187	TGGATCATGGACAAGTCTCTAC	GGCGAAAACAATGGCACTCT
18.206	CGGTCCTCGATTTTGTACCTTC	GCAAGGATATTCCTGCCTTTTC
26.869	GGAAAGACTGGCTCATCAAAAC	ACATTCTCAGAGAGAACCTCCA
47.693	ACACCCTGAATGGGGAAAC	CTGCATGGGTGCTTGATG
61.721	ATCTCAGCCAGCTGCTGG	CCCTCTATCTGCTTCTGC
69.192	AACAACGGTGAACGGTGCTG	GCAGTAGAAACCTGGGATGTGG

Table S5. List of primers used for ChIP analysis.

Gene Promoter	Forward Primer (5'→ 3')	Reverse Primer (5'→ 3')
<i>FUN30</i>	AATCAGTTGTATAGGAAGGAGAT	GCAAAAGTTGGTTATTTGTACTAG
<i>SNF2</i>	GATGAGGGTGGTTGGAGATAT	GGATGAATACTATGTATTGGGTCG
<i>MEC1</i>	ATTATTCAAGAGACCCCTTAAATCCC	ATTTCTATCCTATTTCTGAGGAGGG
<i>TEL1</i>	GGTAGAGAGAGTGACAGTATCAACT	ATATCTGACGTAGACATGATTACG
<i>RTT109</i>	CCATCCCAGTTAATTGTTTACCATCTG	GAATACACCACAATAACAACACTTGCTAAT
<i>RAD5</i>	CCAACCTTCACTCTAACAAACATTTAG	TGGGAGAAGTGTTGTTTCTTC
<i>RAD9</i>	AGTGTGCACAACCTGAATGG	GTGAATTCCTTGATGAGGCAGAT
<i>MRC1</i>	GCAGATCCCAATTTGTAACACT	CGTACGGTTTAGCTTAGAAAGAAA
<i>Chr5 inter-genic region</i>	ATGGGTGTGCTGCTTTTGT	TAAGGAAGTTGTCGGGTCGA
<i>GAPDH</i>	CAGCTGTTTCAAATCCAGGCT	GTGGTTGAGTGGGTTGGTTG

Table S6. Doubling time for wild-type and mutant strains in the absence and presence of MMS.

Strain	Doubling Time (hr)	P-Value (Significance with Respect to BWP17-URA3)
Without MMS		
<i>BWP17-URA3</i>	1.8 ± 0.04	-
<i>RTT109Hz/FUN30Hz-URA3</i>	2.4 ± 0.004	5.68E-03
<i>RTT2109Hz/FUN30Hz/RAD5OE-URA3</i>	2.5 ± 0.02	5.04E-03
<i>RTT109Hz/FUN30Hz/RAD9Hz-URA3</i>	1.8 ± 0.02	0.06 (not significant)
With MMS		
<i>BWP17-URA3</i>	3.9 ± 0.04	-
<i>RTT109Hz/FUN30Hz-URA3</i>	2.4 ± 0.09	4.68E-03
<i>RTT2109Hz/FUN30Hz/RAD5OE-URA3</i>	3.2 ± 0.07	5.14E-03
<i>RTT109Hz/FUN30Hz/RAD9Hz-URA3</i>	3.8 ± 0.02	0.31 (not significant)

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