Supporting Information

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Fig. S1. The original *tah18-515* temperature-sensitive (ts) mutant is sensitive to hydroxyurea (HU). WT and mutant cells from log-phase cultures were dotplated in 10-fold serial dilution, starting at 10⁶ cells, on yeast extract/peptone/dextrose (YPD) plates or on YPD plates containing 25 mM or 50 mM HU and were incubated at 23 °C for 3 d before being imaged.



Fig. S2. Defects in cell-cycle progression in the original *tah18* ts mutant strains. WT, *tah18-515*, and *tah18-5H8* mutant cells from log-phase cultures were synchronized in G1 phase by α factor-mediated arrest at 23 °C before being shifted to 37 °C for 1 h. Cells were released into the cell cycle by washing off the α factor, and samples were taken at 10-min intervals and processed for flow cytometry.



Fig. S3. Comparison of tyrosyl radical (Y•) content in the original tah18-5H8 mutant and its isogenic WT strain. (A and B) EPR spectra of the WT cells without HU treatment (*Left*) or after incubation with 100 mM HU for 2 h (*Right*). (C and D) EPR spectra of the tah18-5H8 cells without HU treatment (*Left*) or after incubation with 100 mM HU for 2 h (*Right*). (C and D) EPR spectra of the tah18-5H8 cells without HU treatment (*Left*) or after incubation with 100 mM HU for 2 h (*Right*). (E) Comparison of WT (blue) and tah18-5H8 (red) EPR signals after the HU-treated spectra were subtracted from the untreated spectra.



Fig. 54. Instability of the Tah18-ts mutant proteins at the nonpermissive temperature. The $\Delta tah18$ mutant harboring a centromeric plasmid (one to three copies per cell) that expressed N-terminally Myc3-tagged *TAH18*, tah18-5H8, or tah18-5H5 was grown at 23 °C to log phase and shifted to 37 °C at time 0. Cells were harvested at 0.5 and 1 h after temperature shift, and the Myc3-Tah18 protein levels were monitored by Western blotting with the 9E10 monoclonal anti-Myc antibody. G6PDH was probed on the same blot as a loading control.



Fig. S5. Comparison of protein levels and activities of $\beta\beta'$ in $\Delta crt1$ *GalRNR4* TAH18 and $\Delta crt1$ *GalRNR4* tah18ts mutant cells before and after *GalRNR4* induction. (A) Comparison of Rnr2 (β) and Rnr4 (β') protein levels in W303, $\Delta crt1$ *GalRNR4* TAH18 (TAH18), $\Delta crt1$ *GalRNR4* tah18-5H8 (5H8), and $\Delta crt1$ *GalRNR4* tah18-5H5 (5I5) cells before (–) and 2 h after (+) β' induction. (B) Comparison of β and β' protein levels at the 2-h time point after β' induction. (C) Assays of $\beta\beta'$ activities at the 2-h time point after β' induction.

Table S1. Yeast strains used in this study

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Strain	Genotype	Source
BY4741	MATa his3 Δ 1 leu2 Δ 0 met15 Δ 0 ura3 Δ 0	(1)
BY4742	MAT α his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0	(1)
GalRNR4	BY4741, rnr4::HIS3MX6-P _{GAL1} -RNR4	(2)
∆aft1	BY4741, aft1::KanMX4	EUROSCARF
∆aft2	BY4741, aft2::KanMX4	EUROSCARF
∆crt1	BY4741, crt1::KanMX4	EUROSCARF
∆pmr1	BY4741, pmr1::KanMX4	EUROSCARF
∆dun1	BY4741, dun1::KanMX4	EUROSCARF
∆grx3∆grx4	BY4742, grx3::LEU2 grx4::KanMX4	(3)
GalDRE2∆crt1	BY4741, dre2::HIS3-P _{GAL1} -DRE2 crt1::KanMX4	This study
SPY122	BY4741, cth1::KanMX4 cth2::HIS3MX4	(4)
AXY1171	BY4741, dre2::HIS3-P _{GAL1} -DRE2	This study
AXY1195	BY4742, dre2::HIS3-P _{GAL1} -DRE2 pmr1::KanMX4	This study
AXY1493	BY4741, <i>tah18::KanMX4 pMH1712</i> (pRS415- P _{TAH18} -MYC3-TAH18)	This study
AXY1494	BY4741, tah18::KanMX4 pMH1713 (pRS415- P _{TAH18} -MYC3-tah18-5H8)	This study
AXY1495	BY4741, <i>tah18::KanMX4 pMH1714</i> (pRS415- P _{TAH18} -MYC3-tah18-5I5)	This study
AXY1542	BY4741, rnr4::HIS3MX6-P _{GAL1} -RNR4, tah18::KanMX4 pMH1712	This study
	(pRS415- P _{TAH18} -MYC3-TAH18)	
AXY1543	BY4741, rnr4::HIS3MX6-P _{GAL1} -RNR4, tah18::KanMX4 pMH1713	This study
	(pRS415- P _{TAH18} -MYC3-tah18-5H8)	
AXY1544	BY4741, rnr4::HIS3MX6-P _{GAL1} -RNR4, tah18::KanMX4 pMH1714	This study
	(pRS415- P _{TAH18} -MYC3-tah18-5I5)	
AXY1664	BY4741, tah18::KanMX4::MYC3-TAH18-LEU2	This study
AXY1668	BY4741, tah18::KanMX4::MYC3-tah18-5H8-LEU2	This study
AXY1696	BY4741, tah18::KanMX4::MYC3-tah18-5I5-LEU2	This study
AXY1860	BY4742, dre2::HIS3-P _{GAL1} -DRE2 cth1::KanMX4 cth2::HIS3MX4	This study
AXY2023	BY4741, dre2::HIS3-P _{GAL1} -DRE2 aft2::KanMX4	This study
AXY2026	BY4741, dre2::HIS3-P _{GAL1} -DRE2 dun1::KanMX4	This study
AXY2033	BY4741, dre2::HIS3-P _{GAL1} -DRE2 aft1::KanMX4	This study
AXY1767	BY4741, dre2::KanMX4, pMH1751 (pRS415-P _{DRE2} -MYC3-DRE2)	This study
Y300	MATa can1-100 ade2-1 his3-11,15 leu2-3,112 trp1-1 ura3-1	(5)
AXY1233	Y300, tah18-5H8	This study
AXY1235	Y300, tah18-515	This study
AXY1282	Y300, rnr4::HIS3MX6-P _{GAL1} -RNR4	This study
AXY1313	Y300, rnr4::HIS3MX6-P _{GAL1} -RNR4 tah18-5H8	This study
AXY1317	Y300, rnr4::HIS3MX6-P _{GAL1} -RNR4 tah18-5I5	This study
AXY1914	Y300, HIS3-P _{GAL1} -RNR4 crt1::LEU2	This study
AXY1916	Y300, HIS3-P _{GAL1} -RNR4 crt1::LEU2 tah18-5H8	This study
AXY1918	Y300, HIS3-P _{GAL1} -RNR4 crt1::LEU2 tah18-5I5	This study
MHY340	Y300, rnr2::KanMX6-P _{RNR2} -MYC3-RNR2	This study

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Table S2.	Plasmids	used	in	this	study
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Plasmid	Description	Source	
pMH1763	pRS415-P _{DIF1} -MYC3-DIF1	This study	
pMH1712	pRS415-P _{TAH18} -MYC3-TAH18	This study	
pMH1713	pRS415-P _{TAH18} -MYC3-tah18-5H8	This study	
pMH1714	pRS415-Р _{ТАН18} -МҮС3-tah18-5I5	This study	
pMH1751	pRS415-P _{DRE2} -MYC3-DRE2	This study	

Table S3. Oligos used in quantitative RT-PCR analyses

FET3 reverse 5'-TCAAGTCCGTGACCAAGTCGT-3' FET3 reverse 5'-GCCAAGTGCAGGAAACTCCCAA-3' CTH2 forward 5'-CCTTTAATTCGCCGAGTCCGT-3' RNR2 forward 5'-CCTTGAGAGAACCCCTTCCAAAG-3' RNR2 reverse 5'-GCCTCGCGCTGCTATTCAGCGTC-3' RNR3 forward 5'-GCCTCCGCTGCTATTCAA-3' RNR3 reverse 5'-CAGATGCCGCCTTTCATCGAG-3' RNR4 forward 5'-CATAAGGCTGCTTTCATCGAG-3' RNR4 reverse 5'-CTGTTGGCCATTGCTAAACC-3' ACT1 forward 5'-GTATGTGTAAAGCCGGTTTTG-3' ACT1 reverse 5'-CATGATACCTTGGTGTCTTGG-3'	FFT3 forward	5'- CTTCTTGACGCAATGTCCAA-3'
CTH2 forward5'-GCCAAGTGCAGGAAACTCCCAA-3'CTH2 reverse5'-CCTTTAATTCGCCGAGTCCGT-3'RNR2 forward5'-CCTTAAGAGACCCCTTCCAAAG-3'RNR3 forward5'-GCCTCGCTGCTATTCAA-3'RNR3 reverse5'-CAGATGCCGCCTTTTGTT-3'RNR4 forward5'-CATAAGGCTGCTTTCATCGAG-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTGG-3'	FET3 reverse	5'-TCAAGTCCGTGACCAAGTCGT-3'
CTH2 reverse5'-CCTTTAATTCGCCGAGTCCGT-3'RNR2 forward5'-CCTTAAGAGAGCCCCTTCCAAAG-3'RNR2 reverse5'-GCCTTGTGATTTTCAGCGTC-3'RNR3 forward5'-GCCTCCGCTGCTATTCAA-3'RNR4 forward5'-CAGATGCCGCCTTTTGTT-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	CTH2 forward	5'-GCCAAGTGCAGGAAACTCCCAA-3'
RNR2 forward5'-CCTAAAGAGACCCCTTCCAAAG-3'RNR2 reverse5'-GCCTTGTGATTTTCAGCGTC-3'RNR3 forward5'-GCCTCCGCTGCTATTCAA-3'RNR4 reverse5'-CAGATGCCGCCTTTTGTT-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTGG-3'	CTH2 reverse	5'-CCTTTAATTCGCCGAGTCCGT-3'
RNR2 reverse5'-GCCTTGTGATTTTCAGCGTC-3'RNR3 forward5'-GCCTCCGCTGCTATTCAA-3'RNR3 reverse5'- CAGATGCCGCCTTTTGTT-3'RNR4 forward5'-CATAAGGCTGCTTTCATCGAG-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	RNR2 forward	5'-CCTAAAGAGACCCCTTCCAAAG-3'
RNR3 forward5'-GCCTCCGCTGCTATTCAA-3'RNR3 reverse5'- CAGATGCCGCCTTTTGTT-3'RNR4 forward5'-CATAAGGCTGCTTTCATCGAG-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	RNR2 reverse	5'-GCCTTGTGATTTTCAGCGTC-3'
RNR3 reverse5'- CAGATGCCGCCTTTTGTT-3'RNR4 forward5'-CATAAGGCTGCTTTCATCGAG-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	RNR3 forward	5'-GCCTCCGCTGCTATTCAA-3'
RNR4 forward5'-CATAAGGCTGCTTTCATCGAG-3'RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	RNR3 reverse	5'- CAGATGCCGCCTTTTGTT-3'
RNR4 reverse5'-CTGTTGGCCATTGCTAAACC-3'ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	RNR4 forward	5'-CATAAGGCTGCTTTCATCGAG-3'
ACT1 forward5'-GTATGTGTAAAGCCGGTTTTG-3'ACT1 reverse5'-CATGATACCTTGGTGTCTTGG-3'	RNR4 reverse	5'-CTGTTGGCCATTGCTAAACC-3'
ACT1 reverse 5'-CATGATACCTTGGTGTCTTGG-3'	ACT1 forward	5'-gtatgtgtaaagccggttttg-3'
	ACT1 reverse	5'-CATGATACCTTGGTGTCTTGG-3'

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