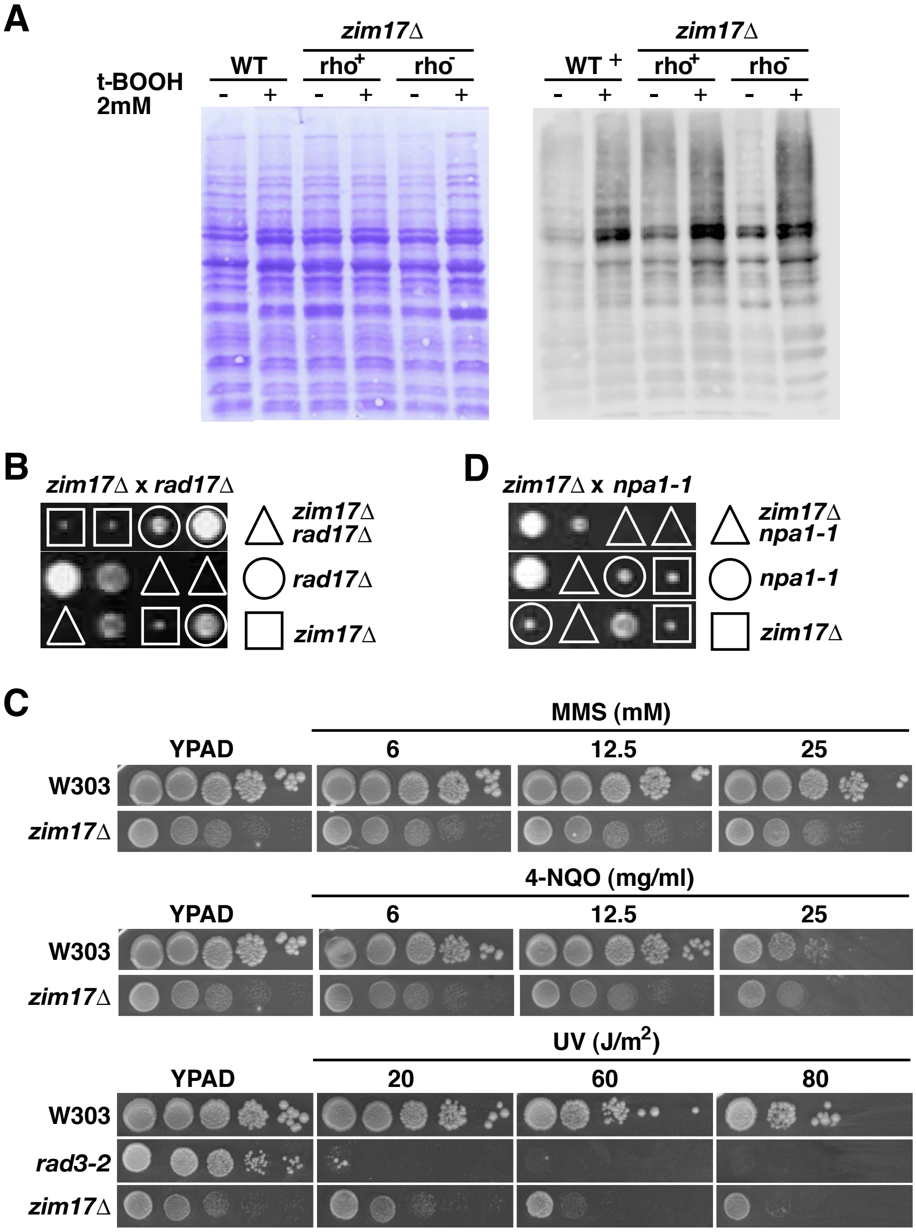
SUPPLEMENTAL DATA

Supplemental Data include one figure and two tables, and the microarray data in excel format.

Supplemental Figure S1. (A) Protein carbonylation in *zim17*Δ rho$^+$ and rho$^-$ strains grown in the absence (-) or presence of oxidative stress (+) induced by 2mM *t*-BOOH. Total protein content is shown (Coomassie staining, left) together with the immunodetection of carbonylated proteins (right). Relative intensity of protein carbonylation normalized to the signal obtained by Coomassie staining. (B) Tetrad analysis crossing *zim17*Δ with *rad17*Δ mutant cells. Note that viable *zim17*Δ*rad17*Δ spores could not be recovered. (C) Drop test analysis of serial 1:10 dilutions of WT and zim17Δ cells spotted onto media containing different concentrations of MMS and 4-NQO or of cells exposed to different doses of UV-irradiation (254nm). (D) Tetrad analysis crossing *zim17*Δ with *npa1-1* cells. For explanation see B above.

Supplemental Table S1. Yeast strains and plasmids used in this study.

Supplemental Table S2. Transcriptionally up- and down-regulated genes in *zim17*Δ mutants.



Supp. Figure 1

Supplemental Table S1. Yeast strains and plasmids used in this study.

strain	**genotype**	**source**
W303-1A	MAT a *ade2-1 trp1-1 ura3-1 his3-11 leu2-3,112 can1-100*	(65)
W303-1B	MAT α *ade2-1 trp1-1 ura3-1 his3-11 leu2-3,112 can1-100*	(65)
BY4741	MAT a *trp1-1 ura3Δ0 leu2Δ0 his3Δ0 met15Δ0*	(66)
BY4742	MAT α *trp1-1 ura3Δ0 leu2Δ0 his3Δ0 lys2Δ0*	(66)
FPAA001-09B	MAT *α ura3Δ0 leu2Δ0 zim17::KAN*	Euroscarf
WRK5-3C	W303-1A, *leu2-k::URA3-ADE2::leu2-k*	(24)
WFNL-5A	MAT α *ura3 leu2 leu2-k::URA3-ADE2::leu2-k*	this study
WFNL-5B	MATa *ura3 leu2 zim17::KAN leu2-k::URA3-ADE2::leu2-k*	this study
WZFN3D-1B	W303-1B *zim17::KAN*	this study
WZFN3D-1D	W303-1A *zim17::KAN*	this study
MCDY101	W303-1B *zim17::KAN leu2-k::URA3-ADE2::leu2-k*	this study
MCDY102	W303-1A *rad24::TRP1 leu2-k::URA3-ADE2::leu2-k*	this study
MCDY103	W303-1B *zim17::KAN rad24::TRP1 leu2-k::URA3-ADE2::leu2-k*	this study
KM84	*MAT a ade2-1 trp1-HIII ura3-52 his4-260 leu2-3,112 lys2::Bam, can1-100 URA3::rDNA ADE2::rDNA*	(25)
MCDY104	MAT a *ade2-1 trp1 ura3-52 leu2-3,112 his zim17:KAN URA3::rDNA ADE2::rDNA*	this study
WRS52-4B	MATa-inc *ade2-1 trp1-1 ura3-52 his3-11 ade3::GAL-HO LEU2::SFA1, rad52::KAN*	(67)
MCDY105	MAT a *ade2-1 trp1-1 ura3-52 leu2-3,11 his3-11 met15Δ0 lys2Δ0 zim17::KAN rad52::KAN*	this study
Y04222	BY4741 *mus81::KANMX4*	Euroscarf
MCDY106	MAT α *trp1 ura3 leu2 his3-11 met15Δ0 zim17::KAN mus81::KAN*	this study
Y10775	BY4742 *sgs1::KAN*	Euroscarf
MCDY107	MATa *ade2-1 trp1-1 leu2 his3 zim17::KAN sgs1::KAN*	this study
AMH5	*hoΔ MATa ade1-100 ura3-52 leu2-3 his4-519 ade3::GAL::HO cdc44-8::URA3*	(68)

strain	genotype	source
MCDY108	MAT a *ade trp1-1 ura3-52 leu2 his zim17::KAN cdc44-8::URA3*	this study
DD379	W303-1A *rad24::TRP1*	D. Durocher
MCDY109	*zim17::KAN rad24::TRP1*	this study
DD303	W303-1A *elg1::KAN*	D. Durocher
MCDY110	W303-1B *zim17::KAN elg1::KAN*	this study
DD377	W303-1A *elg1::KAN*	D. Durocher
MCDY111	W303-1A *zim17::KAN ctf18::HYG*	this study
AMH4	*hoΔ MATa ade1-100 ura3-52 leu2-3 his4-519 ade3::GAL::HO pol30-52*	(68)
MCDY112	MAT α *ade2-1 trp1-1 ura3 -52 leu2-3,112 his3-11 met15Δ0 lys2Δ0 zim17::KAN pol30-52*	this study
MC2_7B	MAT *α ade2 ura3 leu2 his3 leu2-k::URA3-ADE2::leu2-k cdc2-3*	this study
MCDY113	MAT a *ade2 ura3 trp1-1 leu2-3,112 his3-11 zim17::KAN cdc2-3*	this study
Y14963	BY4742 *rad27::KAN*	Euroscarf
MCDY114	MAT α *ade2-1 trp1-1 ura3 leu2 his3-11 zim17::KAN rad27::KAN*	this study
Y00994	BY4741 *rrm3::KAN*	Euroscarf
MCDY115	MAT α *ade2-1 trp1-1 ura3 leu2 his3-11 zim17::KAN rrm3::KAN*	this study
Y00509	BY4741 *pif1::KAN*	Euroscarf
MCDY116	MAT α *ade2-1 trp1-1 ura3 leu2 his3-11 zim17::KAN pif1::KAN*	this study
Y11171	BY4742 *tof1::KAN*	Euroscarf
MCDY117	MAT α *ade2-1 trp1-1 ura3 leu2 his3-11 zim17::KAN, tof1::KAN*	this study
JVY325	W303-1A *npa1-1*	(22)
DMP1913-11C	W303-1B *rad17::TRP1*	(69)
MMI-81	W303-1B RAD5 *rad3-102::HYG*	(62)

MCDY118	W303-1A *npa1-1 leu2-k::URA3-ADE2::leu2-k*	this study
strain	**genotype**	**source**
FLRA006-01B(A)	MAT α *ura3Δ0 leu2Δ0 YGL099w(154,1920)::KAN*	Euroscarf
Y02292 (acc. no.)	MAT α *ura3Δ0 leu2Δ0 rpl13::KAN*	Euroscarf
MCDY119	MATa *ura3 leu2 YGL099w(154,1920)::KAN leu2-k::URA3-ADE2::leu2-k*	this study
MCDY120	MATa *ura3 leu2 rpl13::KAN leu2-k::URA3-ADE2::leu2-k*	this study

plasmid	**description**	**source**
pWJ1344	*LEU2, RAD52::YFP::CYCt*	R.Rothstein, Columbia University
pRS316-RPS2-eGFP	*URA3, RPS2::GFP*	(50)
pRS316-RPL25-eGFP	*TRP1, RPL25::GFP*	(49)
pRS314-L	pRS314 containing two 598 bp *Cla*I–*Eco*RV *LEU2* fragments repeated in direct orientation separated by 31 bp of polylinker	(32)

Supplemental Table 2. Transcriptionally up-regulated and down-regulated genes (≥ 2 fold, Pvalues ≥ 0.05) that cluster within predictable GO-terms versus all *S. cerevisiae* ORFs.

Up-regulated genes	Fold increase
Iron metabolism (iron starvation adaptation)	
Siderophore transport	
FIT1	92.1
FIT2	88.2
FIT3	28.8
Iron ion homeostasis	
CAD1	2.8
CTH2	41.7
FRE8	2.6
HMX1	3.2
Iron transport	
ARN1	18.1
ARN2	41.1
ENB1	15.7
FET3	6.0
FET4	2.0
FET5	2.5
FMP23	5.8
FRE1	7.3
FRE2	19.3
FRE3	8.5
FRE4	21.2
FRE5	64.3
FRE6	4.0
FTH1	3.2
FTR1	6.8
MRS4	3.4
PCA1	3.2
SIT1	31.8
SMF3	2.9
Glycogen/glucan metabolism	
GAC1	2.6
GDB1	2.3
GIP2	2.8
GLC3	2.2
GPH1	2.2
GSC2	2.6
GSY2	2.1
PGM2	2.7
Transmembrane transport	
AGP2	2.0
ALP1	4.5
CCC2	8.3
COT1	2.5
NCA3	2.3
NFT1	6.9
PDR3	5.5
PDR5	3.9
PDR15	14.0
PDR16	2.3
RSB1	13.1
SNQ2	3.9
VBA3	6.4
VMR1	15.4
YCT1	2.0
YOR1	2.6

Down-regulated genes	Fold decrease
Electron transport chain	
ACO2	2.9
ATP17	2.2
ATP20	2.6
CCP1	2.9
COR1	2.5
COX4*	2.8
COX5A*	2.5
COX6*	3.0
COX7	2.3
COX8*	2.6
CYB5	2.6
CYC1*	3.7
CYT1	2.7
QCR10	2.1
QCR2	2.8
QCR6*	2.7
QCR7*	2.5
QCR9*	2.0
RIP1*	2.6
SDH1*	3.0
SDH2*	4.3
SDH3*	2.9
SDH4	2.4
Phosphate metabolism	
PHO11/12	10.9
PHO5	17.2
PHO84	7.2
VTC3	3.3
Cofactor metabolic processes	
Biotin metabolism	
BIO2	7.6
BIO4	2.5
Heme metabolism	
HEM3	2.1
HEM13	2.3
HEM15	2.1
Iron-sulfur cluster biosynthesis	
ISA1	2.5
NFU1	2.0
YFH1	2.2
Nitrogen compound metabolism	
AAH1	2.6
ARO9	5.4
ARO10	13.4
DAL3	2.0
DAL80	2.4
DUR3	3.6
GLT1	5.0
ILV3	2.6
LEU1	3.6
LEU9	2.4
LYS4	2.9
MEP2	3.7
MYS1	2.8
RKI1	2.3
SER3	3.1
URA7	2.0

Statistically relevant GO terms (biological processes) and the fold increase or decrease in respect to the WT are indicated. Omitted genes can be found in the Supplementary Data (microarray analysis).

* Target genes for CTH1/CTH2-dependent degradation

Supplementary References

66. Thomas, B.J. and Rothstein, R. (1989) Elevated recombination rates in transcriptionally active DNA. *Cell*, **56**, 619-630.
67. Brachmann, C.B., Davies, A., Cost, G.J., Caputo, E., Li, J., Hieter, P. and Boeke, J.D. (1998) Designer deletion strains derived from Saccharomyces cerevisiae S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications. *Yeast (Chichester, England)*, **14**, 115-132.
68. Gonzalez-Barrera, S., Cortes-Ledesma, F., Wellinger, R.E. and Aguilera, A. (2003) Equal sister chromatid exchange is a major mechanism of double-strand break repair in yeast. *Mol. Cell*, **11**, 1661-1671.
69. Holmes, A.M. and Haber, J.E. (1999) Double-strand break repair in yeast requires both leading and lagging strand DNA polymerases. *Cell*, **96**, 415-424.
70. Majka, J. and Burgers, P.M. (2005) Function of Rad17/Mec3/Ddc1 and its partial complexes in the DNA damage checkpoint. *DNA Repair (Amst)*, **4**, 1189-1194.