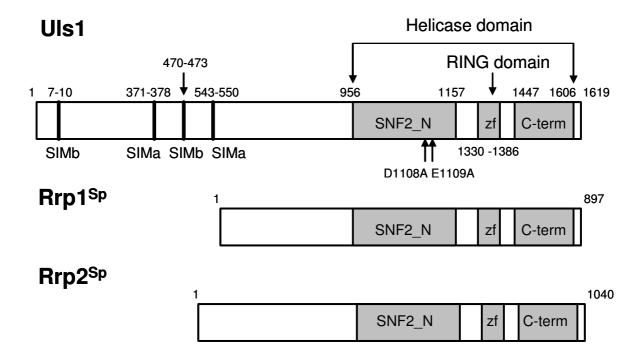
## **Supplementary Table S1**

Yeast strains used in this work.

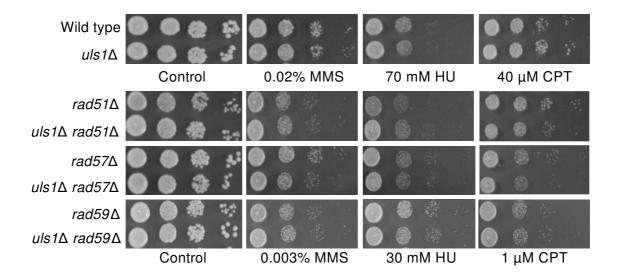
Strain	Genotype	Source
W303-1A	MAT <b>a</b> ade2-1 can1-100 ura3-1 his3-11,15 leu2-3,112 trp1-1 RAD5	R. Rothstein
MC001	MATa uls1Δ::TRP1	This study
MC002	MATa rad51Δ::kanMX6	This study
MC003	MATa uls1Δ::TRP1 rad51Δ::kanMX6	This study
MC004	MATa rad57Δ::kanMX6	This study
MC005	MATa uls1Δ::TRP1 rad57Δ::kanMX6	This study
MC006	MATa rad52Δ::kanMX6	This study
MC007	MATa uls1Δ::TRP1 rad52Δ::kanMX6	This study
MC008	MATa mus81Δ::kanMX6	This study
MC009	MATa uls1Δ::TRP1 mus81Δ::kanMX6	This study
MC010	MATa srs2Δ::kanMX6	This study
MC011	MATa uls1Δ::TRP1 srs2Δ::kanMX6	This study
MC012	MATa sgs1Δ::kanMX6	This study
MC013	MATa uls1Δ::TRP1 sgs1Δ::kanMX6	This study
MC012	MATa rmi1Δ::kanMX6	This study
MC013	$MATa$ uls $1\Delta$ :: $TRP1$ $rmi1\Delta$ :: $kanMX6$	This study
MC012	MATa yen1∆::kanMX6	This study
MC013	$MATa$ uls $1\Delta$ :: $TRP1$ yen $1\Delta$ :: $kanMX6$	This study
W1868-8B	MATa SUP4-o::URA3	R. Rothstein
MC014	MATa uls1Δ::TRP1 SUP4-o::URA3	This study
JJ001	MATa sgs1::kanMX6 SUP4-o::URA3	This study
JJ002	MATa uls1Δ::TRP1 sgs1::kanMX6 SUP4- <b>o</b> ::URA3	This study
W4314-2C	MATα rDNA::ADE2-CAN1	R. Rothstein
W6666-6D	MATa sgs1::HIS3 rDNA::ADE2-CAN1	R. Rothstein
JJ003	MATα uls1Δ::TRP1 rDNA::ADE2-CAN1	This study
JJ004	MATa uls1Δ::TRP1 sgs1::HIS3 rDNA::ADE2-CAN1	This study

MC015	MATa top3Δ::kanMX6	This study
MC016	MATa uls1Δ::TRP1 top3Δ::kanMX6	This study
MC017	MATa rad5Δ::kanMX6	This study
MC018	MATa uls1Δ::TRP1 rad5Δ::kanMX6	This study
MC019	MATa rad18Δ::kanMX6	This study
MC020	MATa uls1Δ::TRP1 rad18Δ::kanMX6	This study
MC021	MATa rev3Δ::kanMX6	This study
MC022	MATa uls1Δ::TRP1 rev3Δ::kanMX6	This study
MC023	MATa rad59Δ::kanMX6	This study
MC024	MATa uls1Δ::TRP1 rad59Δ::kanMX6	This study
MC025	MATa mph1Δ::kanMX6	This study
MC026	MATa uls1Δ::TRP1 mph1Δ::kanMX6	This study



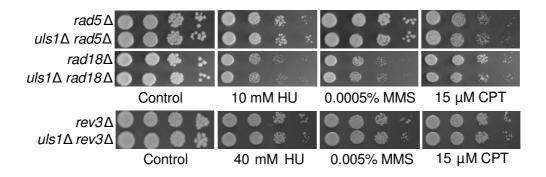
**Figure S1.** Schematic representation of Uls1, Rrp1<sup>Sp</sup> and Rrp2<sup>Sp</sup> domain structures and the sites of point mutations introduced in this study. SIMa, SUMO interacting motif, type a; SIMb, SUMO interacting motif, type b; SNF2\_N, SNF2 family N-terminal/helicase ATP-binding domain; zf, RING type zinc finger domain; C-term, C-terminal helicase domain.

## **Supplementary Figure S2**



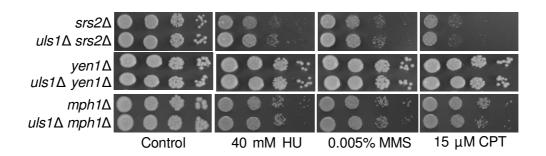
**Figure S2.** Epistasis analysis between *ULS1* and homologous recombination genes. Ten-fold serial dilutions of each strain were spotted onto YPD plates in the presence or absence of DNA damaging agents. Plates were photographed after 2 days at 28°C.

## **Supplementary Figure S3**



**Figure S3.** Epistasis analysis between *ULS1* and post-replication repair genes. Ten-fold serial dilutions of each strain were spotted onto YPD plates in the presence or absence of DNA damaging agents. Plates were photographed after 2 days at 28°C.

## **Supplementary Figure S4**



**Figure S4.** Epistasis analysis between *ULS1* and DNA repair genes. Ten-fold serial dilutions of each strain were spotted onto YPD plates in the presence or absence of DNA damaging agents. Plates were photographed after 2 days at 28°C.