

Supplemental Table 1

Yeast strains used in this study.

	Genotype	Source
W9100-12C [W303 RAD5+]	MAT alpha <i>ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	(1,2)
KBY673-3B	MAT α <i>ubp7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY673-9A	MAT a <i>ubp7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY218-3C	MAT a <i>rad51::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	S. Godin <i>submitted</i>
KBY784-9B	MAT a <i>rad4::hphNT1 ADE2 leu2-3,112 his3-11,15 ura3-1 TRP1 lys2Δ RAD5</i>	This study
KBY830-2A	MAT a <i>ubp7::natNT2 rad4::hph-NT1 ADE2 leu2-3,112 his3-11,15 ura3-1 TRP1 lys2Δ RAD5</i>	This study
KBY880-4C	MAT a <i>rad7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY895-8D	Mat a <i>rad7::natNT2 ubp7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY949-1B	Mat a <i>ADE2 leu2ΔEcoRI::URA3-HO::leu2ΔBstEII his3-11 lys2Δ RAD5</i>	This study
KBY950-12B	Mat alpha <i>ubp7::natNT2 ADE2 leu2ΔEcoRI::URA3-HO::leu2ΔBstEII his3-11 LYS2 trp1-1 RAD5</i>	This study
KBY987-10A	MAT alpha <i>CAN1 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY987-4B	MAT a <i>CAN1 ubp7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY987-5C	MAT alpha <i>CAN1 rad51::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY987-10D	MAT alpha <i>CAN1 rad51::natNT2 ubp7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY825-4B	MAT a <i>rad51::natNT2 ubp7::natNT2 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY51-3B	MAT a <i>sgs1::HIS3 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY826-21A	MAT a <i>ubp7::natNT2 sgs1::HIS3 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY1024-1D	MAT a <i>mus81::KanMX4 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY1024-8C	MAT a <i>ubp7::natNT2 mus81::KanMX4 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
W8196-6A	MAT a <i>RFA1-YFP RAD52-CFP ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	R. Rothstein
KBY776-4A	MAT a <i>ubp7::natNT2 RFA1-YFP RAD52-CFP ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY891-13C	MAT alpha <i>rad17::KanMX ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY891-3A	MAT a <i>rad17::KanMX ubp7::natNT2 ADE2 leu2-3,112 his3-</i>	This study

	<i>11,15 ura3-1 trp1-1 LYS2 RAD5</i>	
KBY726-2D	MAT alpha <i>mrc1::KanMX4 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	S. Godin <i>submitted</i>
KBY986-1D	MAT a <i>ubp7::natNT2 mrc1::KanMX4 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
KBY725-4A	MAT a <i>rad9::HIS3MX6 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	S. Godin <i>submitted</i>
KBY985-3B	MAT a <i>ubp7::natNT2 rad9::HIS3MX6 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY990-8A	MAT a <i>MRC1-9myc::HIS3MX6 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KBY990-4A	MAT a <i>ubp7::natNT2 MRC1-9myc::HIS3MX6 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
W9197-7A	MAT a <i>rad6::KanMX TRP1 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	R. Rothstein
KBY964-6A	Mat a <i>ubp7::NAT rad6::KanMX ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study
W9152-2D	MAT alpha <i>asf1::KanMX ADE2 leu2-3,112 his3-11,15 ura3-1 trp1Δ lys2Δ RAD5</i>	R. Rothstein
KBY980-14A	MAT a <i>ubp7::natNT2 asf1::KanMX ADE2 leu2-3,112 his3-11,15 ura3-1 trp1 lys2Δ RAD5</i>	This study
KBY912-1	MAT alpha <i>UBP7-3HA::hph-NT1 ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 LYS2 RAD5</i>	This study
KY1023*	MAT a <i>his3del200 trp1del63</i>	K. Arndt
KBY983-1*	MAT a <i>ubp7::hph-NT1 his3del200 trp1del63</i>	This study
KY2167*	MAT alpha <i>HTA1-htb1-K123R (hta2-htb2)del::KanMX ura3del0</i>	K. Arndt, (3)
KBY984-7B*	MAT a <i>ubp7::hph-NT1 HTA1-htb1-K123R (hta2-htb2) del::KanMX ura3del0</i>	This study
KBY254-2C	MAT a <i>ADE2 leu2-3,112 his3-11,15 ura3-1 trp1-1 lys2Δ RAD5</i>	This study

All strains are isogenic to W303 with exception of those denoted with *, which are derivatives of FY2 (4). Strain construction of KY2167 is essentially described in (3).

References

1. Thomas, B. J., and Rothstein, R. (1989) Elevated recombination rates in transcriptionally active DNA. *Cell* **56**, 619-630
2. Zhao, X., Muller, E. G., and Rothstein, R. (1998) A suppressor of two essential checkpoint genes identifies a novel protein that negatively affects dNTP pools. *Mol. Cell* **2**, 329-340
3. Tomson, B. N., Davis, C. P., Warner, M. H., and Arndt, K. M. (2011) Identification of a role for histone H2B ubiquitylation in noncoding RNA 3'-end formation through mutational analysis of Rtf1 in *Saccharomyces cerevisiae*. *Genetics* **188**, 273-289
4. Winston, F., Dollard, C., and Ricupero-Hovasse, S. L. (1995) Construction of a set of convenient *Saccharomyces cerevisiae* strains that are isogenic to S288C. *Yeast* **11**, 53-55