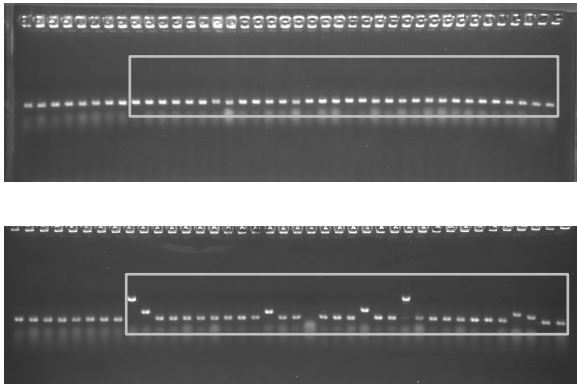
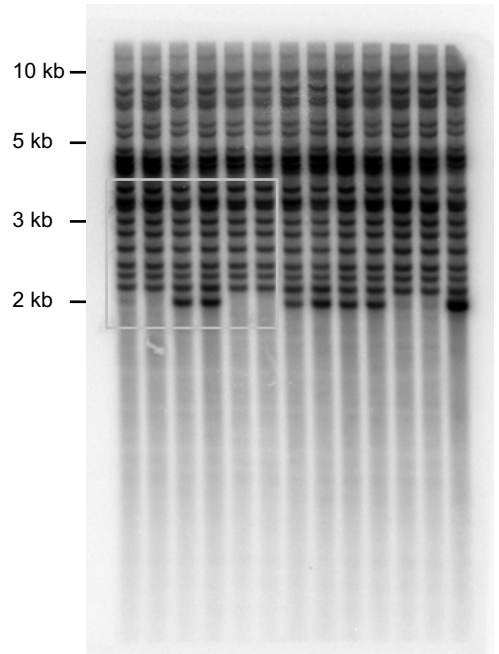


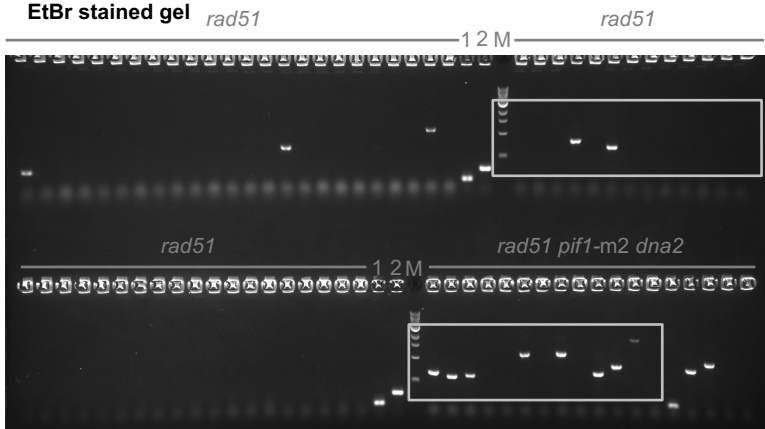
Gel source picture for Extended Fig. 1a. EtBr stained gel



Southern blot source picture for Figure 2c

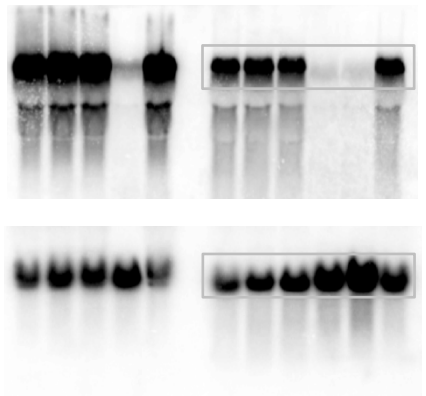


Gel source picture for Extended Fig. 1d
EtBr stained gel

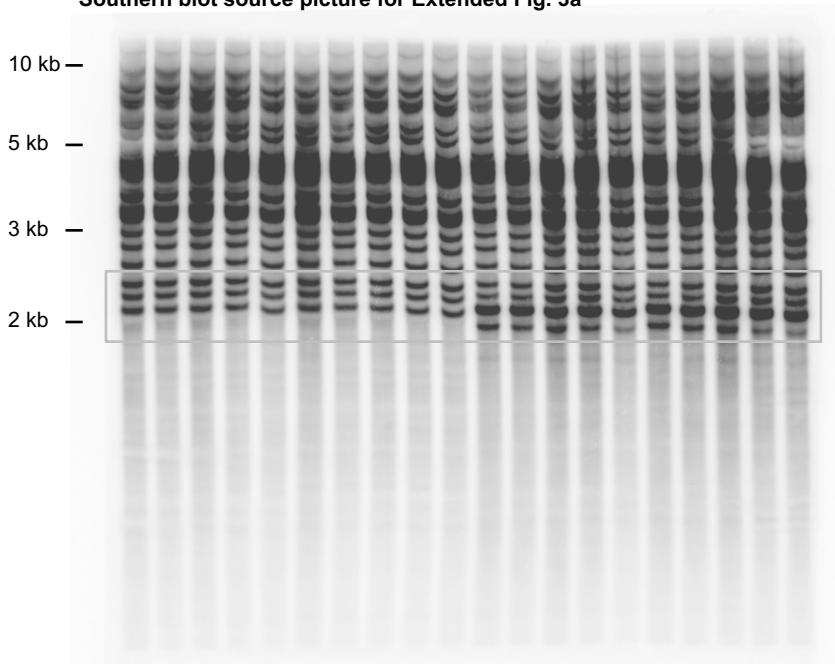


Note: 1 and 2 are two control samples. 1, without HO cleavage site in ACT1 intron. 2, with HO cleavage site in ACT1 intron. M, 1 kb DNA Ladder (the size of band from lower to upper: 0.5 kb, 1 kb, 1.5 kb, 2 kb, 3 kb, 4 kb, 5 kb, 6 kb, 8 kb, 10kb)

Northern blot source picture for Extended Fig. 3b



Southern blot source picture for Extended Fig. 3a



Supplementary Table 2. List of strains used in this study.

Strain name	Parental strain	Genotype	Source
JKM139		DELho <i>hml::ADE1 MATa hmr::ADE1 ade1 leu2-3,112 lys5 trp1::hisG ura3-52 ade3::GAL10::HO</i>	¹
yYY349	JKM139	<i>pif1-m2</i>	this study
yWH475	JKM139	<i>pif1-m2 dna2::kanMX</i>	²
yNP331	JKM139	<i>pif1-m2 dna2R1253Q</i>	this study
yNP490	JKM139	<i>pif1-m2 dna2E675A</i>	this study
yWH811	JKM139	<i>yku70::kanMX pif1-m2 dna2::URA3</i>	³
yYY393	JKM139	<i>lig4::klTRP1 pif1-m2 dna2::kanMX</i>	this study
yYY360	JKM139	<i>pol4::klTRP1 pif1-m2 dna2::kanMX</i>	this study
yYY381	JKM139	<i>rad51::natMX pif1-m2 dna2::kanMX</i>	this study
yAP481	JKM139	<i>rad51::kanMX</i>	this study
yNP590	JKM139	<i>rad52::kanMX pif1-m2 dna2::kanMX</i>	this study
yAP485	JKM139	<i>rad52::kanMX</i>	this study
yYY356	JKM139	<i>spt3::klTRP1 pif1-m2 dna2::kanMX</i>	this study
yYY398	JKM139	<i>rad27::klTRP1</i>	this study
yGI200	JKM139	<i>sgs1::kanMX</i>	²
yGI198	JKM139	<i>exo1::TRP1</i>	²
yYY408	JKM139	<i>fob1::klTRP1 pif1-m2 dna2::kanMX</i>	this study
yYY389	JKM139	<i>pif1::kanMX pol32::natMX dna2::klTRP1</i>	this study
yYY382	JKM139	<i>mus81::natMX pif1-m2 dna2::kanMX</i>	this study
yYY392	JKM139	<i>slx1::klTRP1 pif1-m2 dna2::kanMX</i>	this study
yYY430	JKM139	<i>mus81::natMX pif1-m2 dna2E675A</i>	this study
yNP98	JKM139	<i>yen1^{ON}</i>	this study
yNP128	JKM139	<i>yen1^{ON} dna2::kanMX</i>	this study
yYY422	JKM139	<i>pif1-m2 yen1^{ON} dna2::kanMX</i>	this study
DG1657		<i>MATa ura3-167 his3Δ-200 trp1-hisG leu2-hisG Ty1-270his3-AI Ty1-588neo Ty1-146[tyb1::lacZ]</i>	⁴
yNP495	DG1657	<i>pif1-m2</i>	this study
yNP503	DG1657	<i>pif1-m2 dna2::URA3</i>	this study
yNP513	DG1657	<i>spt3::klTRP1 pif1-m2 dna2::URA3</i>	this study
yYY379		DELho <i>hml::ADE1 MATa::hphMX hmr::ADE1 ade1 leu2-3,112 lys5 trp1::hisG URA3::ACT1 intron::HOcs ade3::GAL10::HO</i>	this study and ⁵
yYY395	yYY379	<i>rad51::natMX</i>	this study
yYY396	yYY379	<i>rad51::natMX pif1-m2</i>	this study
yYY397	yYY379	<i>rad51::natMX pif1-m2 dna2::kanMX</i>	this study
yYY457	JKM139	<i>MATa-inc bRA77-LYS2-2^w</i>	this study
yYY459	JKM139	<i>MATa-inc bRA77-LYS2-2^w pif1-m2 dna2::kanMX</i>	this study

- 1 Moore, J. K. & Haber, J. E. Cell cycle and genetic requirements of two pathways of nonhomologous end-joining repair of double-strand breaks in *Saccharomyces cerevisiae*. *Mol Cell Biol* **16**, 2164-2173 (1996).
- 2 Zhu, Z., Chung, W. H., Shim, E. Y., Lee, S. E. & Ira, G. Sgs1 helicase and two nucleases dna2 and exo1 resect DNA double-strand break ends. *Cell* **134**, 981-994 (2008).
- 3 Shim, E. Y. *et al.* *Saccharomyces cerevisiae* Mre11/Rad50/Xrs2 and Ku proteins regulate association of Exo1 and Dna2 with DNA breaks. *EMBO J* **29**, 3370-3380, doi:[emboj2010219](https://doi.org/10.1038/emboj.2010.219) [pii] [10.1038/emboj.2010.219](https://doi.org/10.1038/emboj.2010.219) (2010).
- 4 Sundararajan, A., Lee, B. S. & Garfinkel, D. J. The Rad27 (Fen-1) nuclease inhibits Ty1 mobility in *Saccharomyces cerevisiae*. *Genetics* **163**, 55-67 (2003).
- 5 Yu, X. & Gabriel, A. Patching broken chromosomes with extranuclear cellular DNA. *Mol Cell* **4**, 873-881 (1999).