Table SI Yeast strains used in this study

Strains	**Genotype**	**Source**
BY4741	*MAT **a** his3Δ1 leu2Δ0 met15Δ ura3Δ0*	Invitrogen
BY4742	*MAT α his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0*	Invitrogen
SC061	*MAT **a** lsm1::KanMX*	Invitrogen
SC062	*MAT α lsm1::KanMX*	Invitrogen
SC063	*rad52::KanMX*	Invitrogen
SC064	*yku80::KanMX*	Invitrogen
SC065	*lsm1::KanMX rad52::HIS3*	This study
SC066	*lsm1::KanMX yku80::HIS3*	This study
SC067	*yku80::KanMX rad52::HIS3*	This study
GA2321	*Mat α hml::ADE1 hmr::ADE1 ade3::GALHO MATinc-URA3*	Susan Gasser
GA2368	*Mat α hml::ADE1 hmr::ADE1 ade3::GALHO MATinc-URA3 rad52::LEU2*	Susan Gasser
SC070	*Mat α hml::ADE1 hmr::ADE1 ade3::GALHO MATinc-URA3 lsm1::KanMX*	This study
SC071	*MAT **a** his3Δ1 leu2Δ0 met15Δ ura3Δ0 trp1::HIS3*	This study
SC072	*lsm1::KanMX trp1::HIS3*	This study
SC073	*yku80::KanMX trp1::HIS3*	This study
SC074	*fob1::KanMX*	Invitrogen
SC075	*mus81::NAT*	S.Moreno
SC076	*mms4::NAT*	S.Moreno
SC077	*lsm1::KanMX mus81::NAT*	This study
SC078	*lsm1::KanMX mms4::NAT*	This study
SC079	*ski2::HIS3*	This study
SC080	*lsm1::KanMX ski2::HIS3*	This study
SC081	*hht2-hhf2::NAT*	This study
SC082	*lsm1::KanMX hht2-hhf2::NAT*	This study
SC083	*lsm1::KanMX ski2::HIS3 hht2-hhf2::NAT*	This study
SC084	*lsm1::KanMX hta1-htb1::HYG*	This study
SC085	*lsm1::KanMX ski2::HIS3 hta1-htb1::HYG*	This study

Table SII Plasmids used in this study

Plasmids	**Description**	**Source**
pWJ1213	*Rad52-YFP*	Felix Prado (Feng et al., 2007)
pMT116	*2µ (TRP1)*	Stanley Fields (Boulton and Jackson, 1996)
pRS316-SU	see experimental procedures	Felix Prado (Prado and Aguilera, 1995)
pARP02	*pYES2*	Alain Verreault
pARP19 (GAL-H3)	*pGAL-3xHA-Histone H3*	Alain Verreault
pARP23 (GAL-H4)	*pGAL-3xHA-Histone H4*	Alain Verreault
P67(GAL-H2A-H2B)	*pGAL-HTA2-HTB2-URA3*	Akash Gunjan (Gunjan and Verreault, 2003)

Materials and Methods

RNA isolation and Microarray analysis

Total RNA was extracted from yeast using RNeasy Mini Kit (Qiagen, Valencia, CA, USA) according to the manufacturer's instructions. The RNA integrity was assessed using Agilent 2100 Bioanalyzer (Agilent, Palo Alto, CA). Labelling and hybridizations were performed according to protocols from Affymetrix. Briefly, 7 μg of total RNA were labeled using the WT Double Stranded cDNA synthesis kit and DNA terminal labelling kit (Affymetrix Inc., Santa Clara, CA, USA), and then hybridized to Yeast Genome 2.0 array (Affymetrix). Washing and scanning were performed using *GeneChip* System of Affymetrix (GeneChip Hybridization Oven 640, GeneChip Fluidics Station 450 and GeneChip Scanner 7G). The robust microarray analysis (RMA) algorithm was used for background correction, intra- and inter-microarray normalization, and expression signal calculation (Bolstad et al., 2003; Irizarry et al., 2003a; Irizarry et al., 2003b). Ratios were calculated by dividing the expression signals corresponding to the *lsm1Δ* strain by the expression signals of the wild-type strain (Table S3). Values higher than 1 corresponds to genes upregulated in the *lsm1Δ* strain and those lower than 1 represents genes dowregulated in the mutant compared to the wild-type strain. The average value of two experiments was used.

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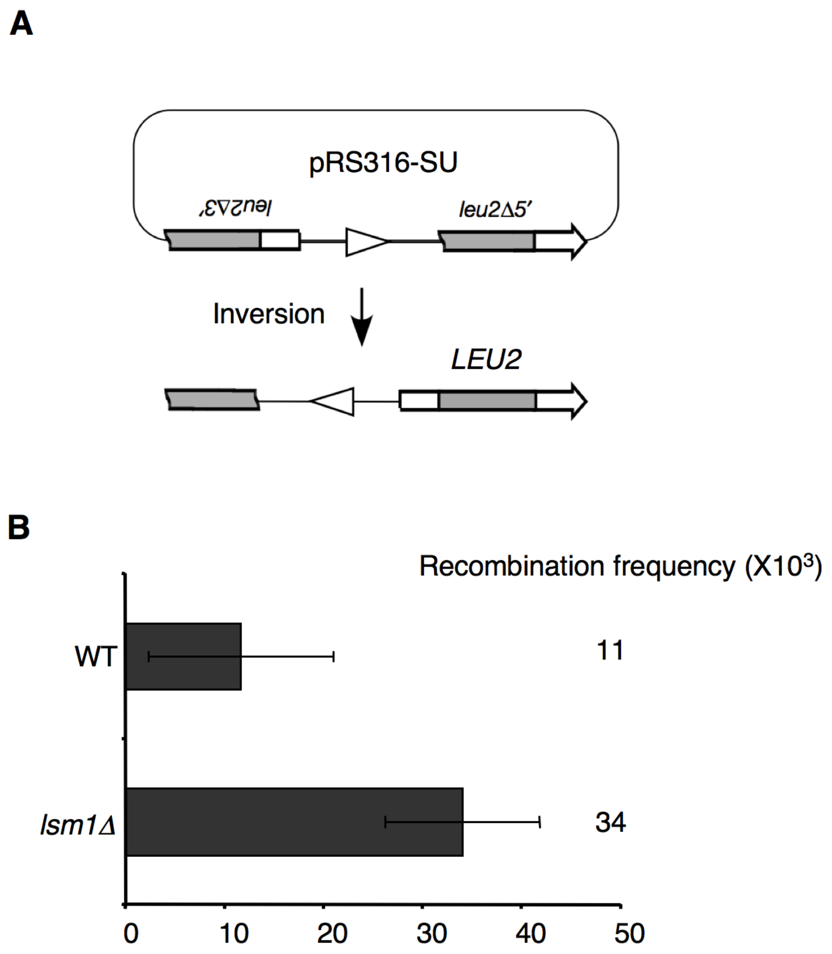

Figure S1 Frequency of homologous recombination. (**A**) Plasmid pRS316-SU carrying the inverted repeat system SU and its recombination product.(**B**) Frequency of Leu+ recombinants in wild-type and *lsm1Δ* cells.