SUPPLEMENTARY METHODS: Plasmid construction

Low (centromeric, pJNY347) and high (2μ, pJNY339) copy plasmids containing *LHP1* (with promoter and terminator regions, amplified from genomic DNA) were constructed in pRS315 (77) and pRS425 (78) respectively. *LHP1^{F51A}* was generated by PCR. 2 fragments were amplified from plasmid pJNY339 using T7 promoter primer plus BSAI51Aup (5'-CCAG*GGTCTC*GCGCAACGCCCTGTCATATGGAAAGTTG; BsaI site in italics altered codon 51 underlined) and T3 promoter primer plus BSAI51Ado (5'-CCAG*GGTCTC*TTGCGCACAACAGCG). These fragments were digested with BsaI, ligated and cloned into pRS425. Cloned fragments were sequenced to confirm accuracy.

SUPPLEMENTARY TABLE S1: Yeast strains used in this study.

Strain	Genotype	Reference/Source
JDY3	MATα, *trp1*, *ura3*, *ade2*, *his3*, *lys2*	(59)
JDY8	*sec65Δ::HIS3*, *[rho-]*, otherwise as JDY3	(79)
JDY44	*srp21Δ::HIS3*, *[rho-]*, otherwise as JDY3	(59)
JDY66	*srp14Δ::HIS3*, *[rho-]*, otherwise as JDY3	(59)
JDY97	*srp68Δ::HIS3*, *[rho-]*, otherwise as JDY3	(59)
JDY99	*srp72Δ::HIS3*, *[rho-]*, otherwise as JDY3	(59)
JDY103	*scr1Δ::HIS3*, *[rho-]*, otherwise as JDY3	(59)
JDY335	MATα, *srp14::HIS3*, *[rho-]*, *trp1-1*, *ura3-1*, *ade2-1*, *his3-11*, *-15, leu2-3, -112, can1-100*	This study
JDY483	MAT**a**, *trp1-1*, *ura3-1*, *ade2-1*, *his3-11*, *-15*, *leu2-3*, *-112*, *can1-100*, *scr1Δ::TRP1*, pRS316-*SCR1*	(57)
JDY596	*srp72::GFP-kanMX3*, otherwise as JDY3	This study
JDY618	MATα, *mtr4-1*, *ura3-52, lys2-801, pep4::HIS3, prb1-Δ1-6R, GAL+*	Alan Tartakoff
JDY721	MAT**a**, *ura3-1*, *ade2-1*, *his3-11*, *-15*, *leu2-3*, *-112*, *can1-100, trp1-1::*(*TRP1, GFP-MS2*)	This study
JDY726	MAT**a**, *ura3-1*, *ade2-1*, *his3-11*, *-15*, *leu2-3*, *-112*, *can1-100, trp1-1::*(*TRP1, GFP-MS2*), *scr1::MS2X6-HIS3*	This study
JDY895	MAT**a**, *his3Δ1*, *leu2Δ0*, *met15Δ0*, *ura3Δ0*	(80)
JDY898	*trf4Δ::kanMX6*, *HisMX6-pGAL-3HA::trf5*, otherwise as JDY895	(14)
JDY899	*air2Δ::kanMX4*, otherwise as JDY895	(11)

JDY900	*air1Δ::kanMX4*, otherwise as JDY895	(11)
JDY901	*air1Δ::kanMX4*, *air2Δ::natMX6*, otherwise as JDY895	(11)
JDY906	*rrp6Δ::HIS3MX6*, otherwise as JDY483	This study
JDY910	*lhp1Δ::HIS3MX6*, otherwise as JDY483	This study
JDY911	*trf4Δ::HIS3MX6*, otherwise as JDY483	This study
JDY912	*trf5Δ::HIS3MX6*, otherwise as JDY483	This study
JDY974	*rex1Δ::kanMX6* otherwise as JDY895	Euroscarf
JDY978	*lsm1Δ::kanMX4*, otherwise as JDY895	Jean Beggs
JDY981	*lsm6Δ:: hphMX6*, otherwise as JDY895	Jean Beggs
JDY982	*lsm7Δ::hphMX6*, otherwise as JDY895	Jean Beggs
JDY983	*lsm5Δ::hphMX6*, otherwise as JDY895	Jean Beggs
JDY984	*lsm4Δ::kanMX4*, otherwise as JDY895	Jean Beggs
JDY990	*natNT2-pGAL(S)::mtr4*, otherwise as JDY483	This study
JDY1015	*natNT2-pGAL(L)::rrp44*, otherwise as JDY483	This study
JDY1018	*natNT2-pGAL(L)::lhp1*, otherwise as JDY483	This study
JDY1028	*rex1Δ::natNT2*, otherwise as JDY483	This study
JDY1042	*lhp1Δ::HIS3MX6*, *rex1Δ::natMX6*, otherwise as JDY483	This study
JDY1058	*natNT2-pGAL(L)::lhp1*, *trf4Δ::HIS3MX6*, otherwise as JDY483	This study
JDY1083	*natNT2-pGAL(S)::mtr3*, otherwise as JDY483	This study
JDY1084	*natNT2-pGAL(L)::rrp42*, otherwise as JDY483	This study
JDY1093	*srp21::GFP-HIS3MX6*, otherwise as JDY895	This study
JDY1156	*air1Δ::kanMX6*, *air2Δ::natMX6*, *lhp1Δ::HIS3MX6*, otherwise as JDY895	This study
JDY1199	*lhp1Δ::natNT2* otherwise as JDY335	This study
JDY1201	*rrp6Δ::natNT2* otherwise as JDY335	This study
JDY1203	*trf4Δ::kanMX6* otherwise as JDY335	This study
JDY1239	*rex1Δ::kanMX4, srp14Δ::HIS3*, *[rho-]*, *ura3, his3, leu2 **	This study
JDY1241	*rrp44Δ::kanMX6*, pRS315-*rrp44-exo-HTP, srp14Δ:HIS3, ura3, his3, leu2 **	This study

CS-66	*rrp44Δ::kanMX6*, pRS315-*RRP44-HTP*, otherwise as JDY895	(3)
CS-77	*rrp44::kanMX6*, pRS315-*rrp44-exo-HTP*, otherwise as JDY895	(3)
CS-31	*trf4::HTP-URA3*, otherwise as JDY895	(50)

* The mating type of these strains has not been determined.

SUPPLEMENTAL TABLE S2 The 3' terminus of scR1.

The 3' terminus of scR1 was inferred by reverse transcription-PCR after ligating a 3'-blocked DNA oligonucleotide onto RNA isolated from the cells indicated. PCR products were sequenced directly and, where indicated, cloned and sequenced individually. The genomic sequence at the 3' end of *SCR1* is:
…CATATTTTTTAACA… the run of 6 thymidines comprising the pol III terminator

Genotype	RT-PCR product	Cloned RT-PCR products	No. of clones
wild type	…CAUAUUUU(U)*	…CAUAUUUU	11
		…CAUAUUUUU	6
		…CAUAUUUUUU	1
		…CAUAUUU	1
		…CAUA	1
lhp1Δ	…CAUAU(U/A)(U/A)(U/A)	…CAUAAAAA	2
		…CAUAU	2
		…CAUAUAAA	1
		…CAUAUU	3
		…CAUAUUA	2
		…CAUAUUAA	1
		…CAUAUUAAA	4
		…CAUAUUU	4
		…CAUAUUUAA	4
		…CAUAUUUU	1
lhp1^{F51A}	…CAUAU(U/A)(U/A)(U/A)		
rex1Δ	…CAUAUUUUU(U)	…CAUAUUUU	1
		…CAUAUUUUU	8
		…CAUAUUUUUU	4
lhp1Δ, rex1Δ	…CAUAUU(U/A)(U/A)	…CAUAU	6
		…CAUAUAAA	2
		…CAUAUAAAA	1
		…CAUAUU	2
		…CAUAUUU	1
		…CAUAUUUAA	1
trf4Δ	…CAUAU(UUUU)	…AAUUGUGC$_{(420)}$†	1
		…CCAUCAGG$_{(462)}$	1
		…UUGGCGGU$_{(453)}$	3
		…CAUAU	2
		…CAUAUA	1
		…CAUAUU	2
		…CAUAUUU	5
		…CAUAUUUU	6
		…CAUAUUUUU	2
		…CAUAUUUUUA	1
		…CAUAUUUUUU	2
		…CAUAUUUUUUAACAUUUU¶	1
lhp1Δ, *trf4Δ*	…CAUAU(U)(U)(U)	…CUCGCACA$_{(475)}$	1
		…GUGUGUC$_{(507)}$	1
		…CAUAAAA	1
		…CAUAU	10
		…CAUAUU	1
		…CAUAUUU	2
		…CAUAUUUU	4

lhp1Δ, rrp6Δ	…CAUAU(U)(U)	…CAUAA …CAUAAA …CAUAAAA …CAUAAAAA …CAUAU …CAUAUA …CAUAUAA …CAUAUAAA …CAUAUUU	3 1 1 1 1 1 1 1 1
air1Δ, air2Δ	…CAUAU	…CAU …CAUA …CAUAU …CAUAUAA …CAUAUU …CAUAUUU …CAUAUUUUU	1 4 10 1 2 1 3
air1Δ	…CAUAUUUU(U)		
air2Δ	…CAUAUUUU(U)		
rrp6Δ	…CAUAU(U/A)(U/A)	…CAUAAAAA …CAUAU …CAUAUAAA …CAUAUU …CAUAUUAA …CAUAUUU …CAUAUUUU	1 3 2 2 2 1 1
rrp6^{D238N}	…CAUAU(U/A)(U/A)	…CAUAAAAAA …CAUAU …CAUAUAAA …CAUAUUAAA …CAUAUUUUU …CAUAUUUUUU	1 4 2 1 1 1
rrp44-exo	…CAUAU(U)(U)	…CAU …CAUA …CAUAAAA …CAUAU …CAUAUU …CAUAUUAA …CAUAUUU …CAUAUUUU …CAUAUUUUAA …CAUAUUUUU	1 1 3 10 2 1 4 2 1 5
rrp44-endo	…CAUAUUUU(U)		
rrp44-exo, rrp6Δ	…CAUAU(U)(U)	…CAUA …CAUAU …CAUAUU …CAUAUUUU …CAUAUUUUU	1 1 1 1 1
lsm4Δ	…CAUAUUUU(U)		
lsm5Δ	…CAUAUUUU(U)		
lsm6Δ	…CAUAUUUU(U)		
lsm7Δ	…CAUAUUUU(U)		

* Bracketed nucleotides indicate heterogeneity of the 3’ end with either alternative nucleotides at a given position, or that the sequence indicated the presence of a

particular nucleotide (such as the 5th U in wild type scR1) in only part of the cDNA product.

†numbers in brackets refer to final nucleotide of scR1 present in the clone sequenced.

¶ this clone extends beyond the terminator of scR1 into the next stretch of T's in the template.

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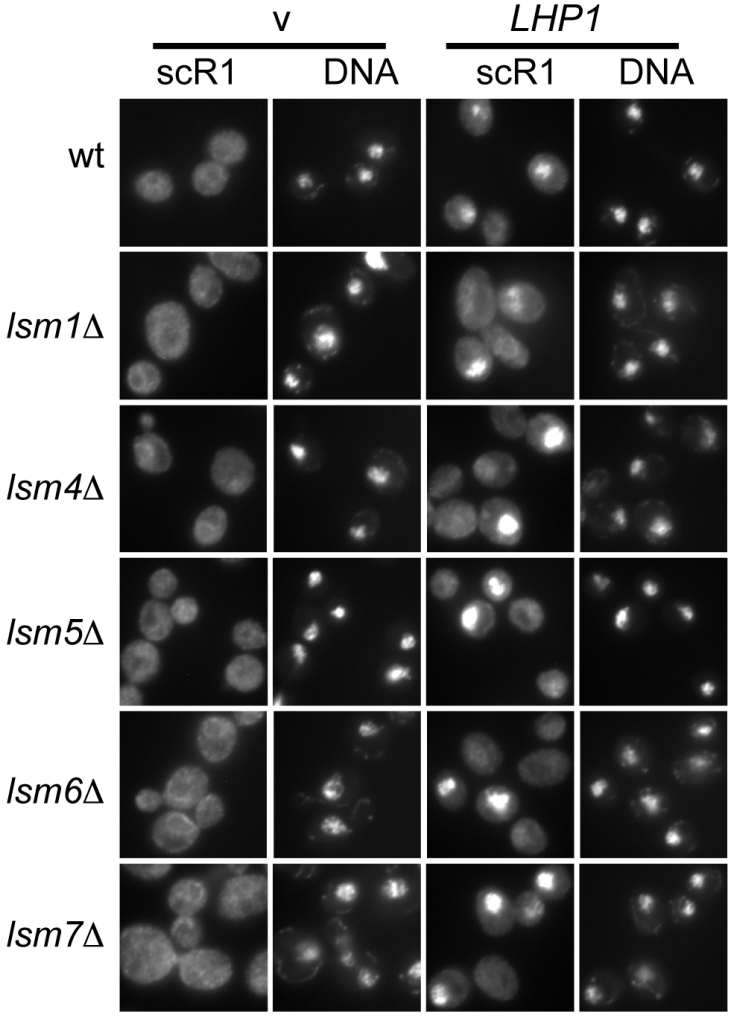

Figure S1 The nuclear LSM complex is not required for correct localisation of scR1, or for its nuclear accumulation on over-expression of Lhp1.
Fluorescence *in situ* hybridisation (FISH) was carried out on the cells indicated, which contained high copy (2μ) plasmids that were either empty (v) or contained *LHP1*, using fluorescently labelled probe scR1A (scR1). DNA was stained with DAPI (DNA). Lsm1 is exclusively part of the cytoplasmic Lsm complex, and provided a control, whereas Lsm4-7 are components of both the cytoplasmic and

nuclear Lsm complexes. Individual channels are shown. Fluorescence images of cells were captured as described (Materials and Methods).

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