The WASp homologue Las17p functions with the WIP homologue End5p/verprolin and is essential for endocytosis in yeast

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Several end mutations that block the internalisation step of endocytosis in Saccharomyces cerevisiae also affect the cortical actin cytoskeleton [1]. END5 encodes a proline-rich protein (End5p or verprolin) required for a polarised cortical actin cytoskeleton and endocytosis [2,3]. End5p interacts with actin [4], but its exact function is not yet known. To help elucidate End5p function, we sought other End5p-interacting proteins and identified the LAS17/BEE1 gene (encoding the yeast homologue of the human Wiskott-Aldrich Syndrome protein, WASp) as a high-copy-number suppressor of the temperature-sensitive growth and endocytic defects of end5-1 cells (carrying a frameshift mutation affecting the last 213 residues of End5p). LAS17 is unable to suppress a full deletion of END5 (end5^Δ), however, suggesting that the defective End5-1p in end5-1 mutants may be stabilised by Las17p. The amino terminus of Las17p interacts with the carboxyl terminus of End5p in the yeast two-hybrid system and similar interactions have been shown between WASp and a mammalian End5p homologue, WASp-interacting protein (WIP) [5]. As las174 deletion mutants are blocked in endocytosis, we conclude that Las17p and End5p interact and are essential for endocytosis.

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Received: **15 April 1998** Revised: **18 June 1998** Accepted: **13 July 1998**

Published: 17 August 1998

Current Biology 1998, 8:959–962 http://biomednet.com/elecref/0960982200800959

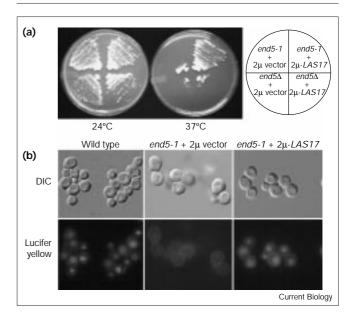
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Results and discussion

To identify genes that can, in high copy number, suppress the temperature-sensitivity of *end5-1* cells, we transformed these cells (AMY66) with a high copy number (2μ) yeast genomic library and selected for loss of temperature-sensitivity. All of the suppressor plasmids contained either *END5* or *LAS17/BEE1* (Figure 1a). The smallest *LAS17* insert to have suppressor activity contained no other open reading frame. *LAS17* encodes the yeast homologue of a human protein defective in patients with Wiskott–Aldrich Syndrome [6]. In these patients, haematopoietic cells have a defective cortical actin cytoskeleton [7]. WASp is a proline-rich protein that interacts with Cdc42p, a low molecular weight GTPase important in regulating the cortical actin cytoskeleton [8–10].

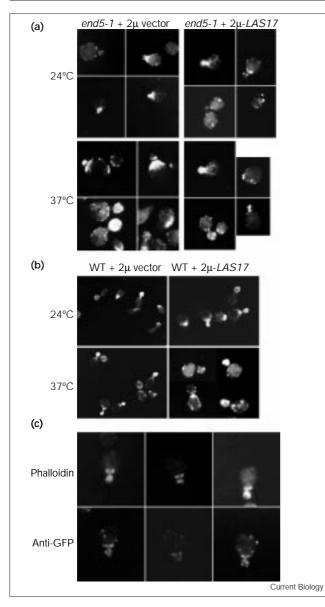
The 2μ -LAS17 plasmid (pAM155) suppressed the temperature-sensitivity of *end5-1* cells (RH2075), but a centromeric plasmid containing LAS17 (cen-LAS17, pAM161) did not have this ability. We tested the ability of 2μ -LAS17 to suppress the temperature-sensitivity of mutants defective in actin (*act1-1*, RH2150), fimbrin

Figure 1



(a) The 2μ -*LAS17* plasmid suppresses the temperature-sensitivity of *end5-1*, but not *end5∆*, cells. Ability to form colonies at 37°C was tested for *end5-1* cells (RH2075) or *end5∆* cells (RH2892) transformed with the 2μ vector (YEplac181) or with the same plasmid containing *LAS17* (2μ -*LAS17*, pAM155). (b) The 2μ -*LAS17* plasmid suppresses the fluid-phase endocytosis defect of *end5-1* cells. Accumulation of the endocytic marker dye lucifer yellow in the vacuole at 37°C was assayed in *end5-1* cells transformed with the 2μ vector or with 2μ -*LAS17*. The same field of cells is shown with differential interference contrast (DIC) optics to highlight the vacuole (appears as an indentation) and with fluorescein isothiocyanate (FITC) fluorescence optics to visualise lucifer yellow.

Figure 2



(a) The 2µ-LAS17 plasmid does not restore a polarised distribution of cortical actin patches to end5-1 cells. The distribution of F actin in end5-1 cells transformed with the 2µ vector or with 2µ-LAS17 was visualised by staining fixed cells with rhodamine-labelled phalloidin. Cells were kept at 24°C or shifted to 37°C for 2 h before fixation. Note that the abnormal cell size seen for end5-1 cells after shift to 37°C is corrected by 2µ-LAS17, even though a polarised distribution of cortical actin patches is not restored. (b) The 2µ-LAS17 plasmid disrupts the polarised distribution of cortical actin patches in wild-type (WT) cells. The distribution of F actin in wild-type cells (RH1800) carrying the 2µ vector or carrying 2µ-LAS17 was examined as in (a). (c) End5p–GFP localises to some, but not all, cortical actin patches. Shown are end5-1 cells expressing a partially functional End5p-GFP fusion protein from a centromeric plasmid (pAM162) double-stained with rhodamineconjugated phalloidin and with rabbit anti-GFP antibodies and FITC conjugated goat anti-rabbit IgG secondary antibodies. Cells were visualised using rhodamine-specific (phalloidin, upper panels) or FITCspecific (anti-GFP, lower panels) light filters, respectively. A few of the End5p-GFP patches do not colocalise with cortical actin patches.

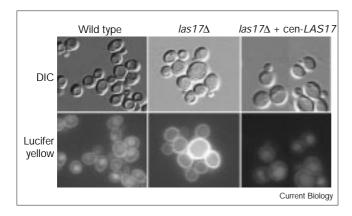
(sac6A, RH2651), and the products of the SLA1 (sla1A, RH2546), END3 (end3-1, RH1623; end3A, RH1995), and END4/SLA2 (end4-1, RH1597; end4Δ, RH1965) genes, all of which are required for endocytosis ([11–14]; A. Wesp, H. Riezman, unpublished data). In addition, we tested for suppression of the temperature-sensitivity of cdc42-1 (WAY299) [15], because mammalian WASp binds mammalian Cdc42p. Suppression of temperature-sensitivity was complete for end5-1, weak for end3-1, and absent for the other mutants tested; 2µ-END5 (pAM160) was also found to be unable to suppress temperature-sensitivity for any of the above mutants except *end5-1* (and *end5* Δ , see below). Using the endocytic marker dye lucifer yellow, 2µ-LAS17 was shown to be able to restore endocytosis to end5-1 cells at 37°C (Figure 1b), but not at 24°C (data not shown).

To test whether the cytoskeletal defect of *end5-1* cells could be corrected by *LAS17*, *end5-1* cells bearing 2μ -*LAS17* were grown at 24°C and then either left at 24°C or shifted to 37°C. F actin was visualised by staining with rhodamine-labelled phalloidin (Figure 2a). Although the abnormal size of *end5-1* cells at 37°C was corrected by 2μ -*LAS17*, there was no obvious change in cortical actin patch distribution at 24°C or 37°C. Some abnormalities within cortical actin patches in *end5-1* mutants may have been corrected without a restoration of normal localisation. When the same experiment was carried out on wild-type cells carrying 2μ -*LAS17* (Figure 2b), the distribution of cortical actin patches was found to be perturbed in a temperature-dependent manner, and this effect of *LAS17* may explain the lack of suppression seen in Figure 2a.

As End5p and Las17p are both unusually proline-rich, we tested whether overexpression of Las17p can functionally replace End5p. Neither temperature-sensitivity nor endocytosis were corrected in $end5\Delta$ cells transformed with 2μ -LAS17 (Figure 1a and data not shown), suggesting that the correction of defects in end5-1 cells relies on residual activity of mutant End5-1p. Characterisation of the end5-1 gene showed that it has a frameshift mutation after codon 604 (of 818), leading to mistranslation for 146 codons before termination.

Las17p has been shown to localise to cortical actin patches [6]. To determine the localisation of End5p, we used the gene for green fluorescent protein (GFP) fused to the last codon of intact *END5*. When carried on a centromeric plasmid this *END5–GFP* construct is partially functional (see Materials and methods; data not shown). End5p–GFP can be seen in live cells in patches that are concentrated in small buds and putative bud sites like cortical actin patches (data not shown). In double-labelling immunofluorescence experiments, colocalisation of End5p–GFP and F actin to some, but not all, cortical patches was observed (Figure 2c).

Figure 3



LAS17 is essential for fluid-phase endocytosis in yeast. Lucifer yellow accumulation assays were performed at 24°C on wild-type cells (IDY19) and on an isogenic *las17* strain (IDY166) transformed with a centromeric vector (YCplac111) or with the same plasmid containing *LAS17* (cen-*LAS17*, pAM161). The same fields of cells are shown with DIC optics to visualise the vacuoles (upper panels) and with FITC fluorescence optics to visualise lucifer yellow (lower panels).

Deletion of the LAS17 gene was shown to block fluidphase endocytosis (Figure 3). Like end5 cells, las17 Δ cells are temperature-sensitive (data not shown) and the 2μ -END5 construct did not suppress their temperaturesensitivity. To determine the phenotype of end5 Δ las17 Δ cells, we crossed a las17 Δ strain to an end5 Δ strain and isolated recombinant haploid spores. Whereas las17 Δ and end5 Δ spores formed colonies at 24°C, the las17 Δ end5 Δ spores germinated but formed only microcolonies (see Supplementary material published with this article on the internet), showing that some functions of End5p and Las17p in growth are redundant.

Recently, a human gene encoding a proline-rich WASpinteracting protein (WIP) was isolated using a yeast twohybrid screen [5]. WIP and End5p share a short stretch of high homology in their amino-terminal domains (in the putative actin-binding motif) and some homology in the remainder of the proteins [5] (see Supplementary material). Testing WIP deletions for interaction with WASp revealed that the carboxy-terminal 126 residues of WIP are required for binding to WASp [5]. WIP could be a human homologue of End5p. If so, it is interesting that the region missing in end5-1 shows some homology to that region in WIP which is required for interaction with WASp. It is possible that the mutant protein encoded by end5-1 interacts poorly with Las17p and overexpression of Las17p is necessary to produce sufficient interaction. We tested whether full-length Las17p and End5p interact in the yeast two-hybrid system [16] and found that they interact strongly. We then tested interactions between different parts of Las17p and End5p and showed that, in an analogous manner to WIP and WASp, the amino terminus

Table 1

The carboxyl terminus of End5p interacts with the amino terminus of Las17p.

Activation domain fusion	Binding domain fusion	β-gal activity in Miller units
End5p 1-816	_	0.13
Las17p 2–266	-	0.079
-	End5p 480-816	0.11
-	Las17p 2–633	0.15
End5p 1-816	Las17p 2–633	80.08
Las17p 2–266	End5p 480-816	146.05

Interaction between End5p and Las17p was tested using the yeast two-hybrid system. β -galactosidase (β -gal) activity was assayed to assess the strength of the interaction. Data shown here represent an average of three independent assays.

of Las17p interacts with the carboxyl terminus of End5p (Table 1).

We have identified *LAS17* as a gene which, in high copy number, can suppress the growth defects and endocytosis defect of *end5-1* mutants. We suggest that End5p and Las17p form a complex that plays a crucial role in endocytosis based on the following observations: Las17p and End5p both localise to cortical actin patches; Las17p and End5p are each required for endocytosis; suppression by 2μ -*LAS17* relies on residual End5-1p function; and Las17p interacts with End5p in the yeast two-hybrid system. By analogy to the interaction of human WASp with WIP, interaction of Las17p and End5p may normally involve interaction of the amino-terminal domain of Las17p with the carboxy-terminal domain of End5p.

Materials and methods

Strains, growth conditions, genetic methods, and manipulation of DNA

Standard methods and media for yeast growth, sporulation and tetrad analysis were used [17]. All DNA manipulations were as described [18]. AMY66 is a haploid derived from a cross of RH2075 to the wild-type *ade2* strain RH2878. The high-copy-number suppressor screen involved transformation of a yeast genomic DNA library (a gift of M.I. Geli, A. Wesp and H. Riezman, University of Basel) carried in the *ADE2* 2µ vector pASZ12 (a gift of P. Linder, University of Geneva) into AMY66 and selection for growth at 37°C on SD selective medium. Plasmids present in the resulting colonies were isolated, amplified in *Escherichia coli* and retransformed into AMY66 to confirm that suppression is conferred by the plasmid.

Plasmid construction

A 3 kb *Bam*HI–*Sph*I fragment (derived from the smallest library clone, pAM150) which contains the promoter and coding region of *LAS17* was subcloned into the centromeric vector YCplac111 [19] and the 2µ-based vector YEplac181 [19] to create plasmids pAM161 and pAM155, respectively. The *las17*Δ::*LEU2* and *las17*Δ::*URA3* alleles have the DNA sequence between base pairs 42 and 1863 of the *LAS17* open reading frame replaced by *LEU2* or *URA3*, respectively. The *end5*Δ::*URA3* allele has the entire open reading frame of *END5* from the upstream *Not*I site to the downstream *Nco*I site replaced by *URA3*.

We constructed an *END5–GFP* gene fusion as follows: the S65T mutant *GFP* gene [20] (provided by R. Tsien, HHMI, UC San Diego) was cloned into YCplac111 to yield pAM158. The *END5* gene (lacking its termination codon) was then ligated in-frame and upstream of the *GFP* gene in pAM158 to obtain pAM162, which complements the temperature-sensitivity of *end5-1* (RH2075) but not *end5* Δ (RH2892), while pAM158 complements neither.

 2μ -*END5* (pAM160) was made by subcloning a 3.4 kb *Hin*dIII–*Bam*HI fragment containing the promoter and entire coding region of *END5* from pEND5.1 into YEplac181.

Microscopy

Fluorescence microscopy was performed using a Leica DMLB fluorescence microscope and images were captured either digitally, using an Optronix DEI-470T cooled charge-coupled device camera (Leica Pte. Ltd, Singapore), or on Kodak TMAX-400 film, using a 35 mm film camera. Cells were fixed with formaldehyde for 30 min at the temperature of growth before staining. F actin was visualised by staining with rhodamine–phalloidin (Sigma) as described [21].

For immunofluorescence, *end5-1* cells (RH2075) transformed with pAM162 were grown in SD medium at 24°C, fixed, and stained with rabbit polyclonal anti-GFP antibodies (a gift from J. Kahana and P. Silver, Dana Farber Cancer Institute, Boston, MA) followed by FITC-conjugated donkey anti-rabbit IgG antibodies (Jackson Immunore-search Laboratories) and rhodamine–phalloidin, using standard procedures. Stained cells were visualised using FITC- and rhodamine-specific light filters.

Lucifer yellow uptake assay

Assays for measuring fluid-phase endocytosis of Lucifer yellow were performed at 24°C or 37°C as described [22].

Yeast two-hybrid interaction test

Yeast two-hybrid interactions [16] were measured using the method and kit supplied by Clontech Laboratories.

Supplementary material

Additional materials and methods, the tables of yeast strains and plasmids used in this study, the genetic data showing synthetic lethality of the $end5\Delta$ and $las17\Delta$ mutations, and the amino-acid sequence comparison of End5p and WIP are published with this article on the internet.

Acknowledgements

We thank H. Riezman and A. Wesp for permission to cite unpublished data and J. Lee and M. Balasubramanian for critically reading the manuscript. We thank N. Naqvi and J. Liu for help with the figures and sequence comparisons, and members of the Balasubramanian laboratory and M. Cai for stimulating discussions. S.N.N., R.Z., and A.L.M. were funded by the National Science and Technology Board of Singapore. D.A.M. was funded by NIH Postdoctoral Fellowship 5F32GM18002-03 and NIH grant GM30027 to G.F. Sprague. B.J.S. was funded by a grant to H. Riezman from the Swiss National Science Foundation and by the Kanton Baselstadt.

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Supplementary material

The WASp homologue Las17p functions with the WIP homologue End5p/verprolin and is essential for endocytosis in yeast

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Current Biology 17 August 1998, 8:959–962

Materials and methods

Construction of the END5-GFP fusion

The primers used for amplifying the GFP gene were 5'GFPC-BamHI (5'-GATAGGATCCATGAGTAAAGGAG-3') and 3'GFP-Smal (5'-GCGCGCCCCGGGTCATTTGTATAGTTCATCCAT-3'). Amplification with these primers creates a BamHI site immediately before the GFP start codon. The BamHI-Smal fragment was ligated into YCplac111 to make pAM158. A HindIII-Sall fragment derived from pEND5.1 provided the 5' upstream regulatory sequences and amino-terminus-encoding half of the END5 open reading frame. The primers used for amplifying the carboxyl-terminus-encoding half of the END5 open reading frame were E5F2 (5'-GCTCCGCCTCCACCACCAC-3') and E5C BamHI (5'-ATGGAGGGATCCTCGCGTAAAT-3'). Amplification using these primers removes the termination codon of END5 and adds a BamHI site at this position. The fragment encoding the carboxyl terminus of END5 was digested with Sall and BamHI and ligated with a HindIII-Sall fragment (derived from pEND5.1) encoding the amino terminus of END5 to reconstruct a complete END5 gene lacking only the termination codon. This was then ligated with pAM158 cut with HindIII and BamHI to place END5 upstream of, and in frame with, the GFP gene.

Sequence of end5-1

The *END5* and *end5-1* genes were amplified from wild-type (RH1800) and *end5-1* (RH2075) cells, respectively, using *Pfu* polymerase (Stratagene). Primers used to amplify the genes were END5 N (5'-AAC-CGTTTGTTGAAGAAGCCTACC-3') and END5 C (5'-TCACAGCGAAAAGGACGGGAAGCT-3'). The PCR products were cloned into the pCR-script SK+ cloning vector (Stratagene). Several different clones of *END5* and *end5-1* were sequenced using an Omni base Sequencing Kit (Promega).

Yeast two-hybrid interaction test

Activation domain fusion constructs pAM173 (End5p 1–816 in pB42AD) and pAM174 (Las17p 2–266 in pB42AD) and LexA DNAbinding domain fusion constructs pAM175 (End5p 480–816 in pLexA) and pAM178 (Las17p 2–633 in pLexA) were used to transform EGY48 individually and in combinations. The DNA fragments contained in the two-hybrid fusion constructs were obtained by PCR amplification of the fragments using primers containing appropriate restriction sites.

Figure S1

	END5	1	MAGAËAPËPËPËPËALGGSAËKPAGSVMQGËDATEGTRKGMGLKGA
	WIP	1	.MPVËPËAPËPËPTALGGSAËKPAGSVMQGËDATEGTRKGMGLKGA
	END5	48	ENDRSAPTVGGVVSSASGSSGTVSSKGPSMSAPPIPGMGAPO
	WIP	51	VNDRSAPTLDKPKGAGAGGGGGGSGGGFGGGGGGGGGGGGGGGGGGGGGGGG
	END5	92	IGDILAGGIPKUKHINNNASTKPSPSASAPPIPGAVFSVAMPPIPNAPLS
	WIP	101	IGGLFQAGMPKURSTANRDNDSGGSRPPLLPPGGRSTSAKOFS
	END5	142	PAPAVP SIPS SSAPPIPDIPS SAAP TPIVPS SPAP PLPL SGASAP KVPQ
	WIP	144	PPSGPGRFPVPS PGHRSGP BEDORNRMP.PPRPD VGSK PD SIPP
	END5	192	NRDHMDSVR PAHRSHORKSSNISLPSVSAP PLPSASLPTHVSNPPOAPPP
	WIP	187	PVPSTPRPIQSSLHNRGSPPVPGGPROPSP
	END5	242	PPTPIGLDSKNIKPTDNAVSPSSEVPÄGGLPFLAEINARSERGAVEG
	WIP	217	GPTPNRGTALG
	END5	292	VSSTKIQTENHKSPSOPPIPSSAPPIPTSHAPPIPTAPPFSLPNVTSA
	WIP	233	GGSIROSPISSSPFSNRPPLPPTP
	END5	342	PKKATSAPAPPPPLPAAMSSASTNSVKATPVPPTLAPPLPNTTSVPPNK
	WIP	257	.SRALDDKPPPPPPPVGNRPSIHREAVPP
	END5 WIP		ASSMPAPPPPPPPPPPPPSVATSVDSALSASSIPLAPLPPPPPSVATSVDSAP PPPQNNKPPVPSTP.RPSAPHRPHLRPPPPSRPSPP
	END5	442	PPETLTTNK PSASSKOSKISSSSSSSSSSSS
	WIP	321	PLPESSGNDETPRLFORNLSLSSSTP.PLE
	END5 WIP		VGGDTGYTTQDKQEDVIGSSKDDNVRPSPI <mark>SE</mark> SINP <mark>2</mark> KQSSQNGMSFLDE
	END5	542	IESKLHKQTSSNAFNA <mark>PPP</mark> HTDAMAPPIPPSA <mark>PPPT</mark> TSLPTPTASGDDH
	WIP	357	PPPPSERPPPPVR
	END5	592	TNDKSETVLGMKKAKADALPGHVPPPVVLSDDSKNNVPAASLLHDVL
	WIP	371	DPBGRSGPLPPPPVSRNGSTSRAL
	END5	642	PSSNLEKPPSPPVAABPLPTFSAPSLEQQSVSTSIDSPPVAPT/SVRT
	WIP	397	P
	END5 WIP	692 422	
	END5	742	NTHINOPDVDVGRYTIGG <mark>S</mark> NSIVGAKSCNERIVIDDSRFKWINVSOMEKP
	WIP	467	EPYVQIIKSYPSKLARNESRSGSNRERGGPPLPEIP
	END5	792	PFQNKTKLYPSGKGSSVPLDLTLFT
	WIP	504	Current Biology
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End5p shows amino-acid sequence homology to WIP, a human WASp-interacting protein. An alignment is shown between the aminoacid sequences encoded by *S. cerevisiae END5/VRP1* (Genbank accession number X87806) and human *WIP* (AF031588). Identical residues are shaded in black and conservative substitutions in grey.

Table S1

The end5 Δ and las17 Δ mutations exhibit synthetic lethality.

Tetrad class	Parental ditype	Tetratype	Non-parental ditype	Total
Phenotype of spores	2 Leu+ Ura- 2 Leu- Ura+	1 Leu+ Ura- 1 Leu- Ura+ 1 Leu- Ura- 1 inviable	2 Leu- Ura- 2 inviable	
Genotype of spores	2 las17∆ END5 2 LAS17 end5∆	1 las17Δ END5 1 LAS17 end5Δ 1 LAS17 END5 1 las17Δ end5Δ (inviable)	2 LAS17 END5 2 las17∆ end5∆ (inviable)	
Number of tetrads	9	20	9	38

An *end5*₂::*URA3* strain (RH2893) was crossed with a *las17*₂::*LEU2* strain (IDY223) and the resulting diploid (AMY25) was sporulated. A total of 38 tetrads were dissected and the genotypes of the spores scored.

Table S2

Name	Genotype	Source
AMY25	MATα /MATa his3/HIS3 his4/HIS4 leu2/leu2 ura3/ura3 lys2/LYS2	This study
	trp1/TRP1 las17∆::LEU2/LAS17 end5∆::URA3/END5 bar1/BAR1	
AMY66	MAT α his3 his4 leu2 ura3 ade2 end5-1 bar1	This study
RH1800	MATa his4 leu2 ura3 bar1	H. Riezman
RH1597	MATa his4 leu2 ura3 end4-1 bar1	H. Riezman
RH1623	MATa his4 leu2 ura3 end3-1 bar1	H. Riezman
RH1965	MATa his4 leu2 ura3 lys2 end4∆::LEU2 bar1	H. Riezman
RH1995	MATa his4 leu2 ura3 end3∆::URA3 bar1	H. Riezman
RH2075	MATα his4 leu2 ura3 end5-1 bar1	H. Riezman
RH2076	MATa his4 leu2 ura3 trp1∆::URA3 end5-1 bar1	H. Riezman
RH2150	MATa his4 leu2 lys2 act1-1 bar1	H. Riezman
RH2546	MATa ura3 lys2 sla1∆::URA3 bar1	H. Riezman
RH2651	MATα his3 leu2 ura3 trp1 sac6Δ::URA3 (bar1?)	H. Riezman
RH2878	MATa his3 leu2 ura3 lys2 ade2 bar1	H. Riezman
RH2892	MATa his4 leu2 ura3 lys2 end5∆::URA3 bar1	H. Riezman
RH2893	MATα his4 leu2 ura3 lys2 end5∆::URA3 bar1	H. Riezman
VAY299	MATα his3 leu2 ura3 lys2 trp1 cdc42-1 bar1Δ::LYS2	A. Wesp
DY19	MATa his3 leu2 ura3 trp1 mfa2∆:: FUS1:lacZ	G. Sprague
DY166	MATa his3 leu2 ura3 trp1 las17∆::URA3	This study
DY223	MATa his3 leu2 ura3 trp1 las17∆::LEU2	This study
GY48	MATα his3 ura3 trp1 LexA _{op(x6)} -LEU2	Clontech

Table S3

Plasmids used in this study.

Name	Description	Source
pAM150	Library clone: pASZ12 containing LAS17	This study
pASZ12	2µ-containing ADE2 vector	P. Linder
YEplac181	2µ-containing LEU2 vector	[19]
YCplac111	ARS-CEN containing LEU2 vector	[19]
pEND5.1	END5 in YCplac111	[3]
pCR-script SK+	Ap ^R cloning vector	Stratagene
pEND5	END5 carried in pCR-Script SK+	This study
pend5-1	end5-1 carried in pCR-Script SK+	This study
pAM155	LAS17 under its own promoter in YEplac181	This study
pAM158	GFP in YCplac111	This study
pAM160	END5 under its own promoter in YEplac181	This study
pAM161	LAS17 under its own promoter in YCplac111	This study
pAM162	END5 fused with GFP in pAM158	This study
pLexA	Cloning vector for DNA-binding domain fusion constructs	Clontech
pB42AD	Cloning vector for activation domain fusion constructs	Clontech
pAM173	pB42AD expressing End5p ₁₋₈₁₆	This study
pAM174	pB42AD expressing Las17p ₂₋₂₆₆	This study
pAM175	pLexA expressing End5p ₄₈₀₋₈₁₆	This study
pAM178	pLexA expressing Las17p ₂₋₆₃₃	This study