Supporting Information

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SI Materials and Methods

Reagents, Antibodies, and Plasmids. Yeast nitrogen base was purchased from Difco and cerulenin from Fermentek. Rabbit anti-FAS antibodies were a kind gift from Michael Thumm (Stuttgart, Germany). Mouse anti-Pgk1 was from Molecular Probes, mouse anti-GFP was from Covance, and rabbit anti-GFP was from Invitrogen. Anti-ApeI polyclonal antibodies were prepared by using two synthetic peptides that were conjugated to keyhole limpet hemocyanin and then injected into rabbits to produce anti-ApeI antiserum that recognizes both precursors. The pRS316-GFP-Atg8 plasmid under the promoter of Atg8 and the Pyes-GFP-Atg8 plasmid under the galactose promoter were previously described (1). All mutations in the Atg8 ORF were created with the Quik-Change Site-Directed Mutagenesis Kit (Stratagene). pEW410 Atg24-GFP under the promoter of Atg24 was a kind gift from Hugh Pelham (Cambridge, UK).

Microscopy. Fluorescence microscopy was performed using Delta-Vision microscope (Applied Precision). DeltaVision images were deconvoluted using the SoftWoRx software (Applied Precision). For FM4-64 staining, 40 μ M FM4-64 (Invitrogen) was added to the cells at room temperature for 15–30 min. The cells were then collected (1,500 × g, 5 min) and resuspended in fresh medium (YPD or SD-N) for 15–30 min, and the chase was repeated once. Cells were washed (1,500 × g, 5 min) and visualized in a fluorescence microscope.

Coimmunoprecipitation. For immunoprecipitation experiments, cells (50 OD_{600} units) were harvested during log-phase or under nitrogen starvation, washed with double distilled water (DDW), and resuspended in breaking buffer (PBS + 0.5% Nonidet P-40) with glass beads and a mixture of protease inhibitors. Cells were lysed by vortexing for 1 min and then incubated for 1 min on ice. This process was repeated seven times. Extracts were centrifuged at 1,000 × g for 5 min at 4 °C to remove intact cells and cell-wall debris. The total yeast lysate was then centrifuged at 245,000 × g for 30 min and supernatant was taken for immunoprecipitation experiments using rabbit polyclonal anti-GFP antibody. Proteins (2 mg) were immunoprecipitated from total cellular material and subjected to SDS/PAGE followed by Western blot analysis.

Silver Staining. After samples were separated on SDS gel, proteins were fixed for 30 min in 50:5:45 (vol/vol) methanol:acetone: water. Gels were washed twice with DDW and incubated for 1 h on a shaker with DDW. Gel sensitization was performed for 1–2 min in sensitizing solution (0.02% sodium thiosulfate) and washed twice with water. Gels were then incubated for 30 min at 4 °C with chilled 0.1% AgNO₃. The silver nitrate was discarded and the gel was washed twice with DDW and developed in 0.04% formaldehyde, 2% sodium carbonate (wt/vol). Staining was quenched with 1% acetic acid.

Mass Spectrometry. Mass spectrometry (MS) analysis was performed at the Biological Mass Spectrometry Unit in the Department of Biological Services at the Weizmann Institute of Science. Samples were analyzed in LTQ-Orbitrap (Thermo Fisher Scientific) operated in the positive-ion mode nano-LC-ESI-MS/ MS. Peptide mixtures were separated by online reversed-phase nanoscale capillary LC and analyzed by ESI-MS/MS. For LC-MS/ MS, samples were injected into an in-house-made 15-cm reversed phase spraying fused-silica capillary column (ID 75 µm) packed with 3 µm ReproSil-Pur C18 A18 media (Dr. Maisch), using an UltiMate 3000 Capillary/Nano LC System, consisting of FamosTMMicro Autosampler, SwitchosTM Micro Column Switching Module (LC Dionex/Packings). The LC setup was connected to the LTQ Orbitrap mass spectrometer (Thermo Fisher Scientific) equipped with a nanoelectrospray ion source (Thermo Fisher Scientific). The flow rate through the column was 250 nL/min. An acetonitrile gradient was used with a mobile phase containing 0.1% and 0.2% formic acid in Milli-Q water in buffers A and B, respectively. The injection volume was 5 µL. Peptides were separated with 50 min gradients from 5 to 65% CH3CN (vol/vol). In the nano-electrospray ionization source, the end of the capillary from the nano-LC column was connected to the emitter with picotip silica tubing, ID 20 µm (New Objective) by stainless steel union, with a PEEK sleeve for coupling the nanospray with the on-line nano-LC. The voltage applied to the union to produce an electrospray was 2.4 kV. Helium was introduced as a collision gas at a pressure of 3 psi. The mass spectrometer was operated in the data-dependent mode. Survey MS scans were acquired in the Orbitrap with the resolution set to 60,000. Up to the seven most intense ions per scan were fragmented and analyzed in the linear trap. For analysis of tryptic peptides, survey scans were recorded in the FT-mode followed by data-dependent collision-induced dissociation of the seven most intense ions in the linear ion trap (LTQ). Raw spectra were processed using open-source software DTA SuperCharge (msquant.sourceforge.net). The data were searched with MASCOT (Matrix Science) against a Swissprot or National Center for Biotechnology Information database. Search parameters included variable modifications of 57.02146 Da (carboxyamidomethylation) on Cys, 15.99491 Da (oxidation) on Met, and 0.984016 Da (deamidation) on Asn and Gln. The search parameters were as follows: maximum two missed cleavages, initial precursor ion mass tolerance 6 ppm, fragment ion mass tolerance 0.6 Da. The peptides were identified from the detected collisioninduced dissociation products by Mascot, Protein Discoverer (Thermo Fisher) and were confirmed by Scaffold Software (Proteome Software) and by manual inspection of the fragmentation series.

^{1.} Amar N, Lustig G, Ichimura Y, Ohsumi Y, Elazar Z (2006) Two newly identified sites in the ubiquitin-like protein Atg8 are essential for autophagy. *EMBO Rep* 7(6):635–642.



Fig. S1. FAS is rapidly degraded under nitrogen starvation. $atg8\Delta$ (TOS006) *Saccharomyces cerevisiae* strain-expressing GFP-Atg8 from the promoter of Atg8, *FAS1-GFP* (TOS016) and *FAS2-GFP* (TOS017) strains were grown to midlog phase and shifted to SD-N medium for 4 h in the presence of ethanol or 1 mM PMSF. Cell lysates were subjected to SDS/PAGE, followed by Western blot analysis using anti-GFP antibodies.



Fig. 52. FAS degradation depends on the core autophagy genes. WT (BY4741) and the indicated autophagy mutants (TOS001–TOS004 and TOOS6–TOS014) were grown to midlog phase and shifted to SD-N medium for 8 h. Cell lysates were subjected to SDS/PAGE, followed by Western blot analysis using anti-Fas1 and anti-Pgk1 antibodies.



Fig. S3. Vac8 and Atg24 are essential for efficient degradation of FAS. (A) *FAS1-GFP* (TOS016) and *FAS1-GFP vac8* Δ (TOS019) S. *cerevisiae* cells were grown to midlog phase and shifted to SD-N medium for the indicated time periods. Cell lysates were subjected to SDS/PAGE, followed by Western blot analysis using anti-GFP, anti-Pgk1, and anti-Ape1 antibodies. (*B*) Quantification of Apel maturation in WT (BY4741) and *vac8* Δ (TOS028). Error bars represent the SDs of three independent experiments (*Right*) n.s., not significant; ***P* < 0.01 (Student's *t* test). (*C*) WT (BY4741), *atg24* Δ (TOS012), and *atg24* Δ (TOS012) cells expressing Atg24-GFP from the promoter of Atg24 were grown as in *A*. Cell lysates were subjected to SDS–PAGE electrophoresis, followed by Western blot analysis using anti-Fas1 and anti-GFP antibodies. (*D*) *pho8* Δ :: *pho8* Δ 60 *pho13* Δ (TN124) S. *cerevisiae* cells were grown to midlog phase and shifted to SD-N medium for the indicated time periods. Cell lysates were subjected to SDS–PAGE electrophoresis, followed by Western blot analysis using anti-Fas1 and anti-GFP antibodies. (*D*) *pho8* Δ :: *pho8* Δ 60 *pho13* Δ (TN124) S. *cerevisiae* cells were grown to midlog phase and shifted to SD-N medium for the indicated time periods. Cell lysates were subjected to SDS–PAGE electrophoresis, followed by Western blot analysis using anti-Fas1 and anti-GFP antibodies. (*D*) *pho8* Δ :: *pho8* Δ 60 *pho13* Δ (TN124) S. *cerevisiae* cells were grown to midlog phase and shifted to SD-N medium for the indicated time periods. Cell lysates were subjected to SDS–PAGE electrophoresis, followed by Western blot analysis using anti-Pho8 and anti-Pgk1 antibodies. Error bars represent the SDs of three independent experiments (down), ***P* < 0.01, ****P* < 0.001 (Student's *t* test).

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FAS1 Matched peptides shown in Bold Red

1	MDAYSTRPLT	LSHGSLEHVL	LVPTASFFIA	SQLQEQFNKI	LPEPTEGFAA	
51	DDEPTTPAEL	VGKFLGYVSS	LVEPSKVGQF	DQVLNLCLTE	FENCYLEGND	
101	IHALAAKLLQ	ENDTTLVKTK	ELIKNYITAR	IMAKRPFDKK	SNSALFRAVG	
151	EGNAQLVAIF	GGQGNTDDYF	EELRDLYQTY	HVLVGDLIKF	SAETLSELIR	
201	TTLDAEKVFT	QGLNILEWLE	NPSNTPDKDY	LLSIPISCPL	IGVIQLAHYV	
251	VTAKLLGFTP	GELRSYLKGA	TGHSQGLVTA	VAIAETDSWE	SFFVSVRKAI	
301	TVLFFIGVRC	YEAYPNTSLP	PSILEDSLEN	NEGVPSPMLS	ISNLTQEQVQ	
351	DYVNKTNSHL	PAGKQVEISL	VNGAKNLVVS	GPPQSLYGLN	LTLRKAKAPS	
401	GLDQSRIPFS	ERKLKFSNRF	LPVASPFHSH	LLVPASDLIN	KDLVKNNVSF	
451	NAKDIQIPVY	DTFDGSDLRV	LSGSISERIV	DCIIRLPVKW	ETTTQFKATH	
501	ILDFGPGGAS	GLGVLTHRNK	DGTGVRVIVA	GTLDINPDDD	YGFKQEIFDV	
551	TSNGLKKNPN	WLEEYHPKLI	KNKSGKIFVE	TKFSKLIGRP	PLLVPGMTPC	
601	TVSPDFVAAT	TNAGYTIELA	GGGYFSAAGM	TAAIDSVVSQ	IEKGSTFGIN	
651	LIYVNPFMLQ	WGIPLIKELR	SKGYPIQFLT	IGAGVPSLEV	ASEYIETLGL	
701	KYLGLKPGSI	DAISQVINIA	KAHPNFPIAL	QWTGGRGGGH	HSFEDAHTPM	
751	LOMYSKIRRH	PNIMLIFGSG	FGSADDTYPY	LTGEWSTKFD	YPPMPFDGFL	
801	FGSRVMIAKE	VKTSPDAKKC	IAACTGVPDD	KWEQTYKKPT	GGIVTVRSEM	
851	GEPIHKIATR	GVMLWKEFDE	TIFNLPKNKL	VPTLEAKRDY	IISRLNADFQ	
901	KPWFATVNGQ	ARDLATMTYE	EVAKRLVELM	FIRSTNSWFD	VTWRTFTGDF	
951	LRRVEERFTK	SKTLSLIQSY	SLLDKPDEAI	EKVFNAYPAA	REQFLNAQDI	
1001	DHFLSMCQNP	MQKPVPFVPV	LDRRFEIFFK	KDSLWQSEHL	EAVVDQDVQR	
1051	TCILHGPVAA	QFTK VIDEPI	KSIMDGIHDG	HIKKLLHQYY	GDDESKIPAV	
1101	EYFGGESPVD	VQSQVDSSSV	SEDSAVFKAT	SSTDEESWFK	ALAGSEINWR	
1151	HASFLCSFIT	QDKMFVSNPI	RKVFKPSQGM	VVEISNGNTS	SKTVVTLSEP	
1201	VQGELKPTVI	LKLLKENIIQ	MEMIENRTMD	GKPVSLPLLY	NFNPDNGFAP	
1251	ISEVMEDRNQ	RIKEMYWKLW	IDEPFNLDFD	PRDVIKGKDF	EITAKEVYDF	
1301	THAVGNNCED	FVSRPDRTML	APMDFAIVVG	WRAIIKAIFP	NTVDGDLLKL	
1351	VHLSNGYKMI	PGAKPLQVGD	VVSTTAVIES	VVNQPTGKIV	DVVGTLSRNG	
1401	KPVMEVTSSF	FYRGNYTDFE	NTFQKTVEPV	YOMHIKTSKD	IAVLRSKEWF	
1451	QLDDEDFDLL	NKTLTFETET	EVTFKNANIF	SSVKCFGPIK	VELPTKETVE	
1501	IGIVDYEAGA	SHGNPVVDFL	KRNGSTLEQK	VNLENPIPIA	VLDSYTPSTN	
1551	EPYARVSGDL	NPIHVSRHFA	SYANLPGTIT	HGMFSSASVR	ALIENWAADS	
1601	VSSRVRGYTC	QFVDMVLPNT	ALKTSIQHVG	MINGRKLIKF	ETRNEDDVVV	
1651	LTGEAEIEQP	VTTFVFTGQG	SQEQGMGMDL	YKTSKAAQDV	WNRADNHFKD	
1701	TYGFSILDIV	INNPVNLTIH	FGGEKGKRIR	ENYSAMIFET	IVDGKLKTEK	
1751	IFKEINEHST	SYTFRSEKGL	LSATQFTQPA	LTLMEKAAFE	DLKSKGLIPA	
1801	DATFAGHSLG	EYAALASLAD	VMSIESLVEV	VFYRGMTMQV	AVPRDELGRS	
1851	NYGMIAINPG	RVAASFSQEA	LQYVVERVGK	RTGWLVEIVN	YNVENQQYVA	
1901	AGDLRALDTV	TNVLNFIKLQ	KIDIIELQKS	LSLEEVEGHL	FEIIDEASKK	
1951	SAVKPRPLKL	ERGFACIPLV	GISVPFHSTY	LMNGVKPFKS	FLKKNIIKEN	
2001	VKVARLAGKY	IPNLTAKPFQ	VTKEYFQDVY	DLTGSEPIKE	IIDNWEKYEQ	
2051	S					

FAS1 Matched peptides shown in Bold Red

1	MDAYSTRPLT	LSHGSLEHVI.	LUPTASEFTA	SOLOFORNET	LPEPTEGEAA
51	DDEDTTDAEL	VCKFLCVVSS	LVEPSKUGOF	DOVINICITE	FENCYLECND
101	THATAAKILO	ENDTTLVKTK	ELIKNVITAR	TMAKRPFDKK	SNSALFRAVG
151	EGNAOLVATE	GGOGNTDDYF	FELRDLYOTY	HVLVGDLTKF	SAETLSELTR
201	TTLDAEKVET	OGLNTLEWLE	NPSNTPDKDV	LISTPISCEL	TOUTOLAHYV
251	WTAKLIGETP	GELRSVIKGA	TCHSOCLUTA	VATAETDSWE	SFFUSURKAT
301	TVLEFIGVRC	VEAVENTSLP	PSTLEDSLEN	NEGUPSPMLS	ISNL TOFOVO
351	DYVNKTNSHL	PAGKOVETSI.	VNGAKNLVVS	GPPOSLYGLN	LTLRKAKAPS
401	GLOOSPIPES	FRELKESNRE	L.DVASDEHSH	LLUPASDLIN	KDLUKNNUSE
451	NAKDTOTPVY	DTEDGSDLRV	LSGSTSERTV	DCTTRLPVKW	ETTTOFKATH
501	TLDECRCCAS	GL CUL THRNK	DCTCURUTUA	GTLDINPDDD	VGEKOETEDV
551	TSNGLKKNPN	WI.EEVHPKI.T	KNKSCKTEVE	TKESKLIGPP	PLLVPGMTPC
601	TUSPDEVAAT	TNAGYTTELA	GGGYFSAAGM	TAATDSVVSO	TEKGSTEGIN
651	LTYVNPFMLO	WGIPLIKELR	SKGYPIOFLT	TGAGVPSLEV	ASEVIETLGL
701	KYLGLKPGST	DATSOVINIA	KAHPNFPIAL	OWTGGRGGGH	HSFEDAHTPM
751	LONVERTORH	DNTML TECSC	FCSADDTVDV	LTCEWSTKED	VPPMPEDCET.
801	FCSPUMTAKE	VKTSDDAKKC	TAACTCUPDD	KMEOTAKKDA	CCTUTURSEM
851	GEDTHKIATR	GUMLWKEFDE	TTENLPKNKI.	VPTLEAKRDY	TISPLNADEO
901	KPWFATUNCO	APDLATMTVE	FUNKPLUETM	FIRSTNEWED	VTWRTFTCDF
951	LERVEERETK	SKTLSLIOSY	SLLDKPDFAT	FEVENAVDAA	REOFLNAODT
1001	DHFLSMCONP	MOKPUPFUPU	LORREETEEK	KDSLWOSEHL.	FAVVDODVOR
1051	TCILHGPVAA	OFTKVIDEPI	KSTMDGTHDG	HIKKLTHOAA	GDDESKTPAV
1101	EVECCESPUD	VOSOVDSSSV	SEDSAVEKAT	SSTDEESWEK	ALAGSETNWR
1151	HASFLCSFIT	ODEMEVSNPT	REVERPSOGM	VVETSNONTS	SKTUUTI.SEP
1201	VOGELKPTVI	LELLKENTTO	MEMTENRTMD	GKPVSLPLLV	NENPDNGEAP
1251	TSEVMEDRNO	RIKEMVWKLW	TDEPENLDED	PROVINGENDE	FITAKEVVDE
1301	THAVGNNCED	FUSEPDETMI.	APMDFATVVG	WRATTKATEP	NTVDGDLLKT.
1351	VHLSNGYKMT	PGAKPLOVGD	VUSTTAVIES	VVNOPTCKTV	DVVGTLSRNG
1401	KPVMEVTSSF	FYRGNYTDFE	NTFORTVEPV	YOMHIKTSKD	TAVLESKEWE
1451	OLDDEDEDLT.	NETLTPETET	EVTERNANTE	SSVKCEGPTK	VELPTKETVE
1501	TGTVDYEAGA	SHGNPVVDFL.	KRNGSTLEOK	VNLENPTPTA	VIDSYTPSTN
1551	EPYARVSGDL	NPTHVSRHFA	SYANLPGTIT	HGMESSASVR	ALTENWAADS
1601	VSSRVRGYTC	OFVDMVL.PNT	ALKTSTOHVG	MINGRKLIKE	ETRNEDDVVV
1651	LTGEAETEOP	VTTEVETGOG	SOEOGMGMDL	YKTSKAAODV	WNRADNHFKD
1701	TYGESILDIV	INNPVNLTIH	FGGEKGKRIR	ENVSAMIFET	IVDGKLKTEK
1751	IFKEINEHST	SYTFRSEKGL	LSATOFTOPA	LTLMEKAAFE	DLKSKGLTPA
1801	DATFAGHSLG	EVAALASLAD	VMSTESLVEV	VEYRGMTMOV	AVPRDELGRS
1851	NYGMTAINPG	RVAASESOEA	LOYVVERVGK	RTGWLVETVN	YNVENOOYVA
1901	AGDLRALDTV	TNVLNFIKLO	KIDITELOKS	LSLEEVEGHL	FEIIDEASKK
1951	SAVKPRPLKL	ERGFACIPLV	GISVPFHSTY	LMNGVKPFKS	FLKKNIIKEN
2001	VKVARLAGKY	IPNLTAKPFO	VTKEYFODVY	DLTGSEPIKE	IIDNWEKYEO
2051	S				
	Tel	hal	10		D
3	10	al	IF	Anti-GF	Ρ
	055				
	GFP	GFP-Atg	3 GF	-P GFP-	Atg8
Fas1	Bernard	Sector Sector		- Berlin	
		The second se			
GFP-Ata8					
				_	

Fig. 54. FAS coimmunoprecipitates with Atg8 in an N-terminal-dependent manner. (A) Mass spectrometric analysis of the high molecular-weight band that specifically coimmunoprecipitated with the full-length GFP-Atg8. Peptides identified by mass spectrometry (bold red) are presented on the sequence of Fas1 and Fas2. (*B*) $atg8\Delta$ (TOS006) cells expressing pYES-GFP-Atg8 or pYES-GFP were grown to midlog. Cell lysates were immunoprecipitated using anti-GFP antibodies. Immunoprecipitates were subjected to SDS/PAGE, followed by Western blot analysis using anti-Fas1 and anti-GFP antibodies. Total is 5% of the lysate.

В

GFP



Fig. S5. FAS degradation is important for cell survival under nitrogen starvation. (*A*) WT (BY4741) *S. cerevisiae* cells were grown to midlog phase and incubated with DMSO, 50 μ M cerulenin (cer), 50 μ M cerulenin + 0.1 mM palmitic/stearic/myristic acids (cer + FA), or 50 μ M cerulenin + 200 nM rapamycin. Cell viability was determined after 16 h using phloxine B. (Scale bar, 10 μ m.) (*B*) WT (BY4741), *atg24* Δ (TOS012), and *vac8* Δ (TOS028) *S. cerevisiae* cells were grown to midlog phase and shifted to SD-N medium for the indicated time periods. Cell viability was determined using phloxine B at the indicated time periods. Error bars represent the SDs of three independent experiments. n.s., not significant; **P* < 0.05, ****P* < 0.001 (Student's *t* test).

Table S1.	List of S.	cerevisiae strains	used in	this	study
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Strain	Genotype	Source
BY4741 (WT)	MATa, his3∆1, leu2∆0, met15∆0, ura3∆0	(1)
TOS001	BY4741 MATa atg1∆::KAN	(2)
TOS002	BY4741 MATa atg2∆::KAN	(2)
TOS003	BY4741 MATa atg3∆::KAN	(2)
TOS004	BY4741 MATa atg4Δ::KAN	(2)
TOS005	BY4741 MATa atg7∆::KAN	(2)
TOS006	BY4741 MATa atg84::KAN	(2)
TOS007	BY4741 MATa atg11∆::KAN	(2)
TOS008	BY4741 MATa atg154::KAN	(2)
TOS09	BY4741 MATa atg19Δ::KAN	(2)
TOS010	BY4741 MATa atg20∆::KAN	(2)
TOS011	BY4741 MATa atg23∆::KAN	(2)
TOS012	BY4741 MATa atg244::KAN	(2)
TOS013	BY4741 MATa atg27∆::KAN	(2)
TOS014	BY4741 MATa atg34∆::KAN	(2)
TOS015	BY4741 MATa pep44::KAN	(2)
TOS016	BY4741 MATa FAS1-GFP::HIS	(2)
TOS017	BY4741 MATa FAS2-GFP::HIS	(2)
TOS018	BY4741 MATa PGK1-GFP::HIS	(2)
TOS019	BY4741 MATa <i>FAS1-GFP</i> ::HIS vac8∆::HYGRO	Present study
TOS020	BY4741 MATa FAS1-GFP::HIS pep4∆::HYGRO	Present study
TOS021	BY4741 MATa FAS2-GFP::HIS vac8∆::HYGRO	Present study
TOS022	BY4741 MATa <i>FAS2-GF</i> P::HIS <i>pep4</i> ∆::Hygro	Present study
TOS023	BY4741 MATa <i>FAS2-GFP</i> ::HIS atg8∆::HYGRO	Present study
TOS024	S288C MATa his3∆1 leu2∆0 met15∆0 ura3∆0 FAS1-proteinA::HIS3	TAP fusion library (Open
		Biosystems) (3)
TOS025	S288C MATa his3∆1 leu2∆0 met15∆0 ura3∆0 <i>FAS2-proteinA</i> ::HIS3	TAP fusion library (Open
		Biosystems) (3)
TN124	MATa leu2–3,112 trp1 ura3-52 pho8::pho8∆60 pho13∆::LEU2	(4)
TOS026	MATa leu2–3,112 trp1 ura3-52 pho8::pho8∆60 pho13∆::LEU2 atg24∆::HYGRO	Present study
TOS027	MATa leu2–3,112 trp1 ura3-52 pho8::pho8∆60 pho13∆::LEU2 vac8∆::HYGRO	Present study
TOS028	BY4741 MATa vac8∆::KAN	(2)
TOS029	BY4741 MATa <i>fas1∆</i> ::TRP1	Present study
TOS030	BY4741 MATa <i>fas2∆</i> ::TRP1	Present study
TOS031	BY4741 DaMP-fas1::KAN	(5)
TO\$032	BY4741 <i>DaMP-fas1</i> ::KAN <i>atg7</i> ∆::NAT	Present study

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