

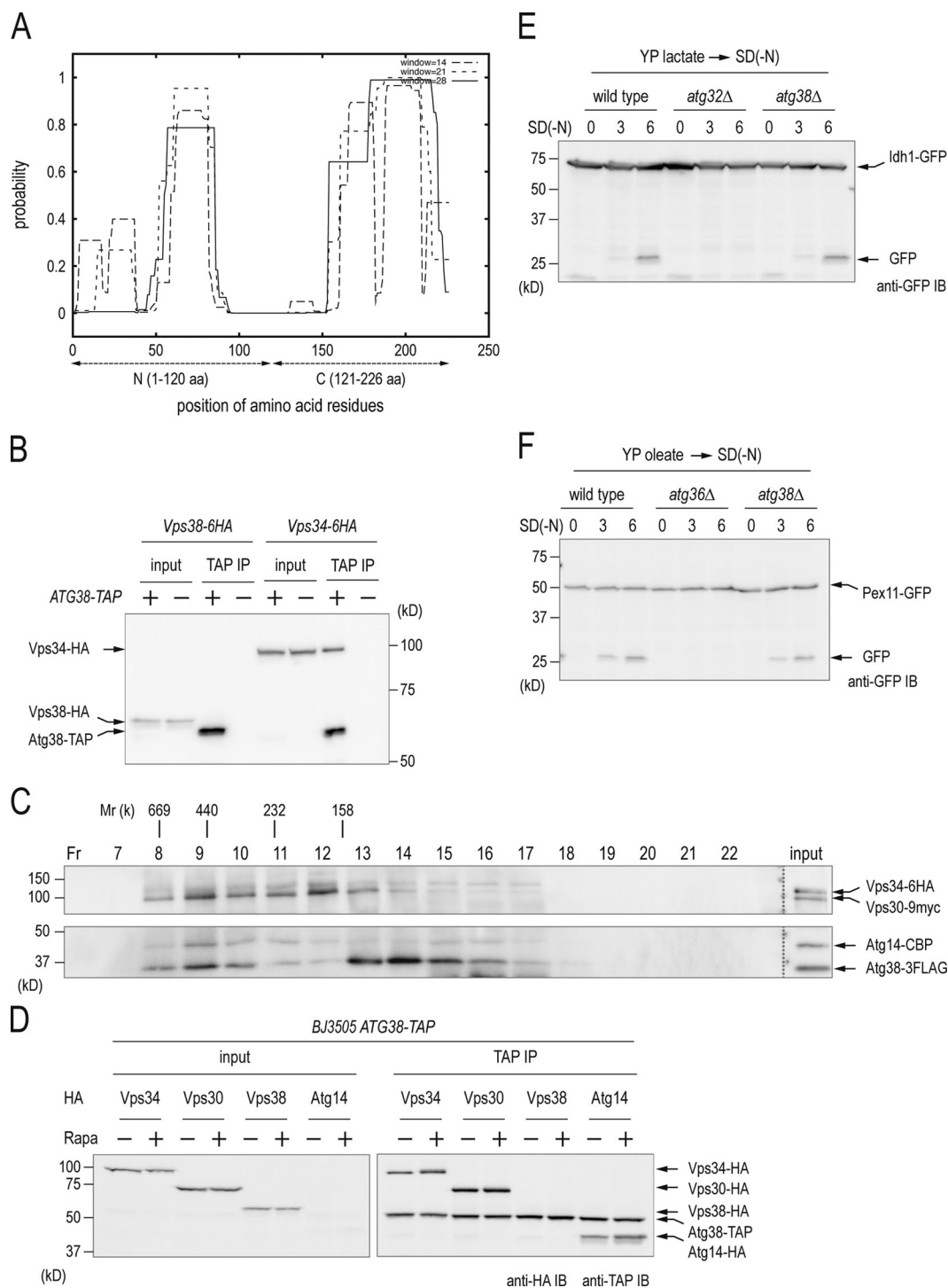
Araki et al., <http://www.jcb.org/cgi/content/full/jcb.201304123/DC1>

Figure S1. **Atg38 is a component of complex I.** (A) The presence of two coiled-coil domains is predicted within Atg38. (B) Cell extracts were prepared from yeast strains expressing TAP-tagged Atg38 and the indicated HA-tagged Vps38 and Vps34 proteins. The extracts were immunoprecipitated by IgG-Dynabeads. The whole-cell extract (input) and the precipitated proteins (TAP IP) were analyzed by immunoblotting with the indicated antibodies. (C) Complex I comprising Atg14-TAP was purified with IgG-Dynabeads and then eluted with TEV protease. The eluate was fractionated over a gel filtration column. Each fraction was analyzed by immunoblotting with the indicated antibodies. (D) *ATG38-TAP* cells with the indicated genotypes were grown in YPD and treated with rapamycin for 3 h at 30°C. Lysates from each group of cells were analyzed as in Fig. 1 B. (E) Cells expressing Ldh1-GFP were grown in YPL medium, then shifted to SD(-N) medium. The whole-cell extracts were analyzed by immunoblotting with anti-GFP antibody. (F) Cells expressing Pex11-GFP were grown in YM2 oleate medium, then shifted to SD(-N) medium. The whole-cell extracts were analyzed by immunoblotting with anti-GFP antibody.



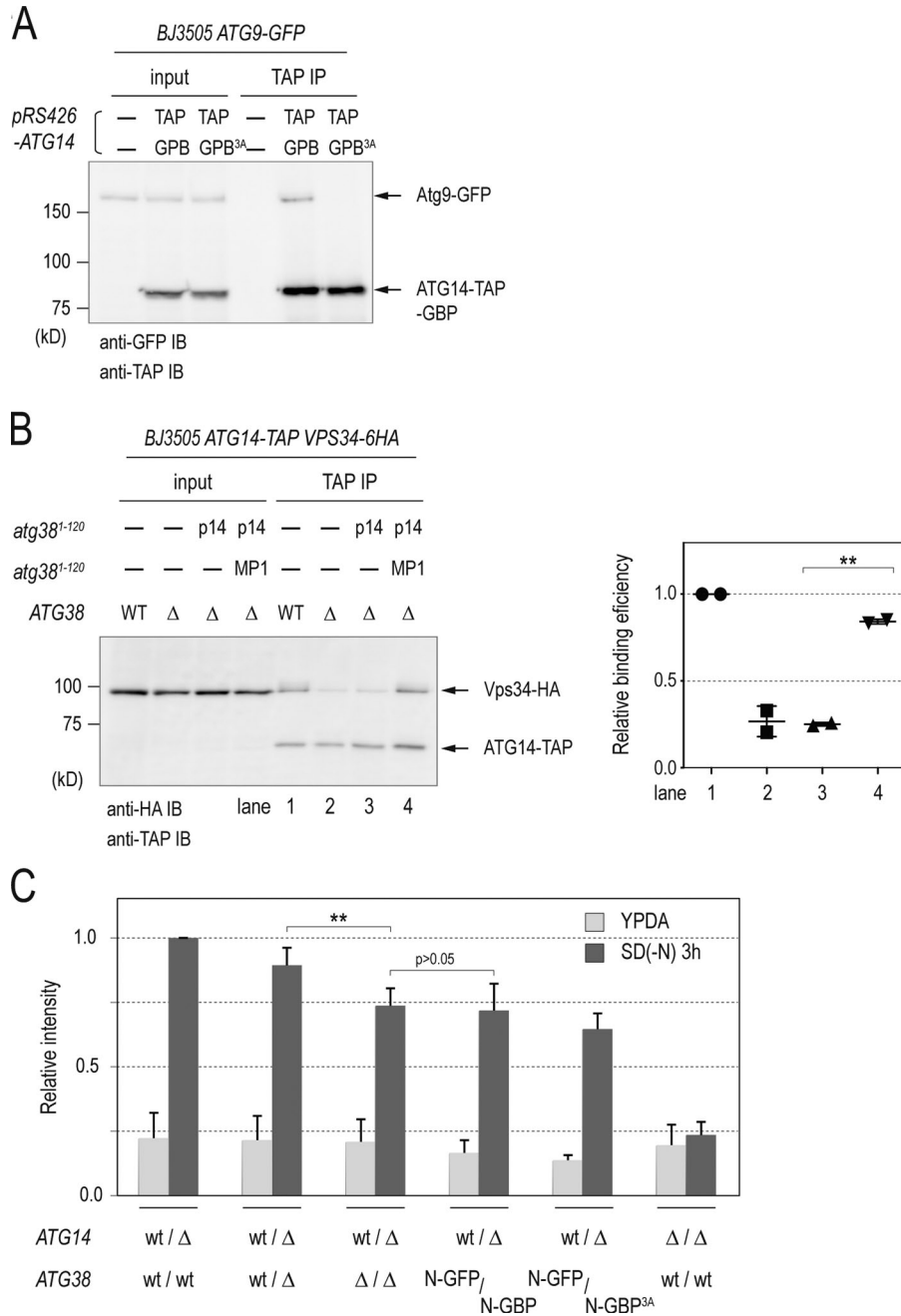


Figure S3. **An artificial tether facilitates the formation of PI3K complex I, but does not restore the defect in autophagy in *atg38Δ* cells.** (A) Introduction of three mutations (S33A R35A Y37A) to GBP compromises its interaction with GFP. Cell extracts were prepared from *ATG9-GFP atg14Δ* strains carrying the indicated *ATG14* constructs. The cell extracts were immunoprecipitated with IgG-Dynabeads. The precipitated proteins (TAP IP), together with the whole-cell extracts (input), were immunoblotted with the indicated antibodies. (B) Cell extracts were prepared from *ATG14-TAP* and either *VPS34-6HA* or *VPS15-6HA* strains expressing *Atg38<sup>1-120</sup>* fused with p14 and MP1. Interactions between the indicated proteins were analyzed as in A (left). Relative binding efficiency was determined as described in Fig. 3 A. Relative binding efficiency is shown as mean  $\pm$  SD of two independent experiments (right). (C) Cells expressing *Pho8Δ60* were grown in YPD and shifted to SD(-N) medium for 3 h at 30°C. Lysates from each group of cells were tested for ALP activity. ALP activity is shown as mean  $\pm$  SD of three independent experiments with the activity of wild-type cells normalized to 1.

Table S1. Yeast strains

Name	Genotype	Figure used
BJ3505	<i>MATa pep4::HIS3 prb1-D1.6R HIS3 lys2-208 trp1-D101 ura3-52 gal2 can1</i>	S2 A; Jones et al., 1982
BY4741	<i>MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0</i>	Brachmann et al., 1998
BY4743	<i>MATa/alpha his3Δ1/his3Δ1 leu2Δ0/leu2Δ0 LYS2/lys2Δ0 met15Δ0/MET15 ura3Δ0/ura3Δ0</i>	Brachmann et al., 1998
YAY1187	BJ3505 <i>VPS34-TAP-hphNT1</i>	1 A
YAY1298	BJ3505 <i>VPS34-6HA-natNT2</i>	1 B, 1 D, S1 B
YAY1299	BJ3505 <i>VPS15-6HA-natNT2</i>	1 B, 1 D
YAY1300	BJ3505 <i>VPS30-6HA-natNT2</i>	1 B, 1 D
YAY1301	BJ3505 <i>VPS38-6HA-natNT2</i>	1 B, S1 B
YAY1302	BJ3505 <i>ATG14-6HA-natNT2</i>	1 B
YAY1318	BJ3505 <i>ATG38-TAP-hphNT1 VPS34-6HA-natNT2</i>	1 B, 1 D, S1 B, S1 D
YAY1319	BJ3505 <i>ATG38-TAP-hphNT1 VPS15-6HA-natNT2</i>	1 B, 1 D
YAY1320	BJ3505 <i>ATG38-TAP-hphNT1 VPS30-6HA-natNT2</i>	1 B, 1 D, S1 D
YAY1321	BJ3505 <i>ATG38-TAP-hphNT1 VPS38-6HA-natNT2</i>	1 B, S1 B, S1 D
YAY1322	BJ3505 <i>ATG38-TAP-hphNT1 ATG14-6HA-natNT2</i>	1 B, S1 D
YAY1303	BJ3505 <i>ATG38-TAP-hphNT1</i>	1 C
YAY1358	BJ3505 <i>VPS34-6HA-natNT2 ATG14-TAP-hphNT1</i>	1 C, 4 A, 4 B, 7 A, S3 B
YAY1355	BJ3505 <i>ATG38-TAP-hphNT1 VPS34-6HA-natNT2 atg14Δ::kanMX4</i>	1 D
YAY1356	BJ3505 <i>ATG38-TAP-hphNT1 VPS15-6HA-natNT2 atg14Δ::kanMX4</i>	1 D, S2 A
YAY1357	BJ3505 <i>ATG38-TAP-hphNT1 VPS30-6HA-natNT2 atg14Δ::kanMX4</i>	1 D
YAY1394	BY4741 <i>ATG17-2mcherry-hphNT1 ATG38-2GFP-kanMX6</i>	1 E
YAY1427	BY4741 <i>ATG17-2mcherry-hphNT1 ATG38-2GFP-kanMX6 atg14Δ::natNT2</i>	1 E
TK1050	BY4741 <i>kanMX4-GPD promoter-pho8Δ60</i>	2 A, 2 B, 2 C
YAY1332	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 atg38Δ::natNT2</i>	2 A, 2 B, 2 C, 4 C
YAY1334	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 atg14Δ::natNT2</i>	2 A, 2 B, 2 C
YAY1640	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 ATG14-yeGFP-hphNT1</i>	2 A, 2 B
YAY1641	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 atg38Δ::CgURA3 ATG14-yeGFP-hphNT1</i>	2 A, 2 B
YAY1414	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 vps30Δ::natNT2</i>	2 C
YAY1778	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 VPS34-3myeGFP-KanMX6</i>	3A, 3B
YAY1781	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 VPS34-3myeGFP-KanMX6 atg38Δ::natNT2</i>	3A, 3B
YAY1780	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 VPS30-3myeGFP-KanMX6</i>	3A
YAY1783	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 VPS30-3myeGFP-KanMX6 atg38Δ::natNT2</i>	3A
YAY1776	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 ATG14-3myeGFP-KanMX6</i>	3A, 3B
YAY1777	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 ATG14-3myeGFP-KanMX6 atg38Δ::natNT2</i>	3A, 3B
YAY1774	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 ATG2-3myeGFP-KanMX6</i>	3A
YAY1786	BY4741 <i>ATG17-2mcherry-hphNT1 mRFP-APE1-URA3 ATG2-3myeGFP-KanMX6 atg38Δ::natNT2</i>	3A
YAY1359	BJ3505 <i>VPS15-6HA-natNT2 ATG14-TAP-hphNT1</i>	4 A, 7 A, S3 B
YAY1360	BJ3505 <i>VPS30-6HA-natNT2 ATG14-TAP-hphNT1</i>	4 A
YAY1368	BJ3505 <i>VPS34-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4</i>	4 A, 4 B, 7 A, S3 B
YAY1369	BJ3505 <i>VPS30-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4</i>	4 A, 7 A, S3 B
YAY1370	BJ3505 <i>VPS15-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4</i>	4 A
YAY1390	BJ3505 <i>VPS34-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4 ATG38<sup>1-120</sup>-yEGFP-URA3 ATG38<sup>1-120</sup>-GBP6His-TRP</i>	4 B, 7 A
YAY1814	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 ATG14-TAP-hphNT1</i>	4 C
YAY1815	BY4741 <i>kanMX4-GPD promoter-pho8Δ60 atg38Δ::CgURA3 ATG14-TAP-hphNT1</i>	4 C
YAY1536	BJ3505 <i>VPS34-6HA-natNT2 ATG14-TAP-hphNT1 VPS30-9myc-klTRP1 ATG38-3FLAG-10His-kanMX4</i>	4 D, S1 C
AH109	<i>MATa, trp1-901, leu2-3, 112, ura3-52, his3-200, gal4Δ, gal80Δ, LYS2::GAL1<sub>UAS</sub> GAL1<sub>TATA</sub>-HIS3, MEL1, GAL2<sub>UAS</sub>-GAL2<sub>TATA</sub>-ADE2, URA3::MEL1<sub>UAS</sub>-MEL1<sub>TATA</sub>-lacZ</i>	5 A, 5 B, 6 A, S2 B, S2 D (Takara Bio Inc.)
YAY1531	BJ3505 <i>VPS34-TAP-hphNT1 atg14Δ::natNT2 vps38Δ::kanMX4 vps30Δ::CgTRP1</i>	5 C
YAY1391	BJ3505 <i>VPS34-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4 ATG38<sup>1-120</sup>-yEGFP-URA3 ATG38<sup>1-120</sup>-GBP<sup>3A</sup>6His-TRP</i>	7 A
YAY1392	BJ3505 <i>VPS15-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4 ATG38<sup>1-120</sup>-yEGFP-URA3 ATG38<sup>1-120</sup>-GBP6His-TRP</i>	7 A

Table S1. Yeast strains (Continued)

Name	Genotype	Figure used
YAY1393	BJ3505 VPS15-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4 ATG38 <sup>1-120</sup> -yEGFP-URA3 ATG38 <sup>1-120</sup> -GBP <sup>3A</sup> 6His-TRP	7 A
YKM65	BY4741 ADHp-OsTIR1-9myc-URA3 IDH1-GFP-kanMX6	S1 E
YKM90	BY4741 ADHp-OsTIR1-9myc-URA3 IDH1-GFP-kanMX6 atg32Δ::hphNT1	S1 E
YAY1733	BY4741 ADHp-OsTIR1-9myc-URA3 IDH1-GFP-kanMX6 atg38Δ::hphNT1	S1 E
YNH798	BY4741 ADHp-OsTIR1-9myc-URA3 PEX11-eGFP-kanMX4	S1 F
YNH799	BY4741 ADHp-OsTIR1-9myc-URA3 PEX11-eGFP-kanMX4 atg36Δ::natNT2	S1 F
YAY1747	BY4741 ADHp-OsTIR1-9myc-URA3 PEX11-eGFP-kanMX4 atg38Δ::natNT2	S1 F
YAY1541	BJ3505 ATG9-yEGFP-kanMX4	S3 A
YAY1436	BJ3505 VPS34-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4 ATG38 <sup>1-120</sup> -p14-TRP1	S3 B
YAY1459	BJ3505 VPS34-6HA-natNT2 ATG14-TAP-hphNT1 atg38Δ::kanMX4 ATG38 <sup>1-120</sup> -p14-TRP1 ATG38 <sup>1-120</sup> -MPI-URA3.	S3 B
YAY1583	BY4743 kanMX4-GPD promoter-pho8Δ60/pho8Δ ATG14/atg14ΔATG38/atg38Δ	S3 C
YAY1584	BY4743 kanMX4-GPD promoter-pho8Δ60/pho8Δ ATG14/atg14Δ atg38Δ/atg38Δ	S3 C
YAY1585	BY4743 kanMX4-GPD promoter-pho8Δ60/pho8Δ ATG14/atg14ΔATG38/ATG38	S3 C
YAY1586	BY4743 kanMX4-GPD promoter-pho8Δ60/pho8Δ atg14Δ/atg14ΔATG38/ATG38	S3 C
YAY1587	BY4743 kanMX4-GPD promoter-pho8Δ60/pho8Δ ATG14/atg14Δ atg38Δ/atg38Δ ATG38 <sup>1-120</sup> -yEGFP-URA3 ATG38 <sup>1-120</sup> -GBP6His-HIS3	S3 C
YAY1588	BY4743 kanMX4-GPD promoter-pho8Δ60/pho8Δ ATG14/atg14Δatg38Δ/atg38Δ ATG38 <sup>1-120</sup> -yEGFP-URA3 ATG38 <sup>1-120</sup> -GBP <sup>3A</sup> 6His-HIS3	S3 C

Table S2. Plasmids

Name	Description	Figure used
pGBKT7-p53	pGBKT7-p53	5 A (Takara Bio Inc.)
pGADT7-large T	pGADT7-large T	5 A (Takara Bio Inc.)
pYA259	pGADT7-VPS30	5 A
pYA260	pGADT7-ATG14	5 A, 5 B, S2 D
pYA261	pGADT7-VPS34	5 A, S2 D
pYA633	pGADT7-ATG38	5 A, 5 B, 6 A, S2 B
pYA643	pGBKT7-ATG38	5 A, 5 B, 6 A, S2 B
pYA656	pGADT7-ATG38 <sup>1-120</sup>	5 B, 6 A
pYA657	pGADT7-ATG38 <sup>121-226</sup>	5 B, 6 A
pYA638	pGEX6P-ATG38	5 C, 6 B, 6 C
pYA658	pGEX6P-ATG38 <sup>1-120</sup>	5 C
pYA659	pGEX6P-ATG38 <sup>121-226</sup>	5 C
pYA662	pGBKT7-ATG38 <sup>1-120</sup>	5 A
pYA664	pGBKT7-ATG38 <sup>c121-226</sup>	5 A
pOK15	pRS426-ATG14-3HA-yEGFP	S2 A
pOK16	pRS426-ATG14 <sup>61-344</sup> -3HA-yEGFP	S2 A
pOK17	pRS426-ATG14 <sup>123-344</sup> -3HA-yEGFP	S2 A
pOK18	pRS426-ATG14 <sup>157-344</sup> -3HA-yEGFP	S2 A
pOK19	pRS426-ATG14 <sup>1-167</sup> -3HA-yEGFP	S2 A
pOK20	pRS426-ATG14 <sup>1-73+123-344</sup> -3HA-yEGFP	S2 A
pOK21	pRS426-ATG14 <sup>1-128+157-344</sup> -3HA-yEGFP	S2 A
pOK22	pRS426-ATG14 <sup>1-128</sup> -3HA-yEGFP	S2 A
pOK26	pRS426-ATG146 <sup>1-73</sup> -3HA-yEGFP	S2 A
pOK27	pRS426-ATG146 <sup>61-128</sup> -3HA-yEGFP	S2 A
pOK31	pRS426-ATG146 <sup>61-167</sup> -3HA-yEGFP	S2 A
pOK32	pRS426-ATG146 <sup>123-167</sup> -3HA-yEGFP	S2 A
pOK33	pRS426-ATG146 <sup>1-73+123-167</sup> -3HA-yEGFP	S2 A
pYA874	pGADT7-ATG38 <sup>1-80</sup>	S2 D
pYA875	pGADT7-ATG38 <sup>81-226</sup>	S2 D
pYA775	pPS306-ATG14-TAP-GBP <sup>3A</sup>	S3 A
pYA777	pPS306-ATG14-TAP-GBP	S3 A

Table S3 is available as a Microsoft Excel file.

## References

- Brachmann, C.B., A. Davies, G.J. Cost, E. Caputo, J. Li, P. Hieter, and J.D. Boeke. 1998. Designer deletion strains derived from *Saccharomyces cerevisiae* S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications. *Yeast*. 14:115–132. [http://dx.doi.org/10.1002/\(SICI\)1097-0061\(19980130\)14:2<115::AID-YEA204>3.0.CO;2-2](http://dx.doi.org/10.1002/(SICI)1097-0061(19980130)14:2<115::AID-YEA204>3.0.CO;2-2)
- Jones, E.W., G.S. Zubenko, and R.R. Parker. 1982. *PEP4* gene function is required for expression of several vacuolar hydrolases in *Saccharomyces cerevisiae*. *Genetics*. 102:665–677.