**SUPPLEMENTARY FIGURE LEGENDS**

**Figure S1.** Interaction between *S. pombe* Atg13CTD and Atg1CTD. (**A**) Sequence alignment of *S. cerevisiae* Atg13 (GenBank: AJW27260.1) and *S. pombe* Atg13 (GenBank: CAB11710.1) using Clustal Omega at EMBL-EBI. (**B**)Schematic of Atg1 and Atg13 constructs. (**C**)Coprecipitation experiments co-expressing His-Atg1CTD with GST or various constructs of GST-tagged Atg13. The Commassie Brilliant Blue-stained gel (*top panel*) shows the GST construct inputs (cell lysate) as well as the samples precipitated by glutathione beads (affinity isolate [pull down]). The asterisks to the right of each band indicate the GST-tagged protein. Glutathione resin was used for precipitation; 25% of each affinity isolate was loaded. The western blot (*bottom panels*) was probed using anti-His antibody where 25% of the affinity isolate was loaded. S.E., short exposure; L.E., long exposure.

**Figure S2**. Interaction between *S. pombe* Atg17 and *S. cerevisiae* Atg31. (**A**) Top 15 most populated class averages obtained from the 2D classification of 4,313 negatively-stained SpAtg17-ScAtg31-29 particles using Relion. Side length of each panel is 672 nm. Class averages with SpAtg17 showing characteristic bending were outlined in red. (**B**) The *S. cerevisiae* *atg17∆* (XLY134)or *atg17∆ ATG31-PA* (XLY159)strains were transformed with either pCu(416)-GFP-ScAtg17 or pCu(416)-GFP-SpAtg17. These cells were cultured to mid-log phase in SMD-Ura before they were shifted to nitrogen starvation medium (SD-N) for 3 h. Cell lysates were prepared and incubated with IgG-Sepharose for affinity isolation. The total lysates and eluted proteins were analyzed using SDS-PAGE and detected with monoclonal anti-YFP antibody and an antibody that binds to PA. S.E., short exposure; L.E., long exposure.

**Figure S3.** Interaction between Atg101 and Atg13HORMA. (**A**) Atg13HORMA, His-Atg101 and the His-Atg101-Atg13HORMA complex were purified from *E. coli* cells and subjected to the DSS crosslinker (0-640 µM). The double asterisk indicates a higher molecular weight complex indicative of a heterodimer. (**B**) CXMS analysis of the His-Atg101-Atg13HORMA complex. Inter-(*dashed lines*) and intramolecular (*solid lines*) interactions observed between the 2 proteins (*top panel*). Intermolecular cross-links observed mapped onto the *S. pombe* Atg101-Atg13HORMA crystal structure using PDB 4YK8 (*bottom panels*). (**C**) Differential scanning fluorimetry analyses of His-Atg101 (*green*), Atg13HORMA (*purple*) and the His-Atg101-Atg13HORMA complex (*orange*). The relative fluorescence signal is calculated and plotted as a function of the increase in temperature (*left*). The first derivative of the relative fluorescence is plotted as a function of the increase in temperature. The peak for each sample is used to estimate the melting temperature of the protein-protein complex (*right*).