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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

Sample size was not determined. From experience, six biological replicates provides a high statistical power for proteomics experiments.

2. Data exclusions

Describe any data exclusions.

Proteomics data: hits for contaminants and "reverse" hits were removed (pre-established, normal practice)

3. Replication

Describe whether the experimental findings were reliably reproduced.

Attempts at replication were successful.
All replicates in tables or figures containing quantitative data were independent biological replicates (except for one case of biological duplicates presented from each of three independent experiments and noted in the supplementary figure legend) or involved quantification of a substantial number of individual cells per condition. Replication of individual experiments, including microscopy analyses, is noted in the relevant methods sections and figure legends.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

In vitro experiments, none performed.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

In vitro experiments, none performed.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☒	☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

Proteomics: As described in the paper, MaxQuant (v1.4.1.2 and v1.5.1.7) and Perseus software were used. The difference in MaxQuant versions is due to the different times when the experiments were performed.
Microscopy images: OMERO suite and Fiji, as described and referenced.
GO analysis: Candida Genome Database, as described and referenced.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

n/a

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Anti-Hcp and anti-Ssp2 are custom polyclonal antisera that have been previously validated for use in western blotting in the same species (Serratia marcescens); published references within the manuscript.
Monoclonal anti-GFP (mouse IgG1K, mix of monoclonal clones 7.1 and 13.1, cat # 11814460001, lot # 10521400, Roche) is a standard reagent, validated for western blot in yeast in: Nair et. al. GFP-Atg8 protease protection as tool to monitor autophagosome biogenesis, Autophagy 7, 1546-1550 (2011).
Polyclonal anti-Pgk1 (rabbit IgG, Immunogen PA5-28612, a recombinant fragment corresponding to a region within amino acids 1 and 217 of human PGK1, target species yeast, western blot applications show reactivity with human, mouse rat and yeast samples as stated on suppliers webpage; cat # 13472727, lot # RC2177369, Invitrogen) has been used as control protein in yeast in: Mochida et. al. Receptor-mediated selective autophagy degrades the endoplasmic reticulum and the nucleus, Nature 522, 359-362 (2015).
Secondary antibodies were peroxidase-conjugated goat anti-mouse (cat# 170-6516) and goat anti-rabbit secondary (# 170-6515) antibodies (BioRad).

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used. n/a

b. Describe the method of cell line authentication used. n/a

c. Report whether the cell lines were tested for mycoplasma contamination. n/a

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use. n/a

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study. n/a

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants. n/a