# Supporting information

## Supplementary tables

Table S1: Yeast strains used in this paper.

| Strains          | Description                                      | Reference         |
|------------------|--------------------------------------------------|-------------------|
| WT               | BY4742 MATa hisΔI leu2Δ0 lys2Δ0 ura3Δ0           |                   |
| Δpex3            | BY4742 Δpex3::KanMX4                             | Euroscarf collection |
| Δpex5            | BY4742 Δpex5::KanMX4                             | Euroscarf collection |
| Δpex6            | BY4742 Δpex6::KanMX4                             | Euroscarf collection |
| Δ3’pex5          | BY4742 Δ3’pex5::KanMX4                           | this study         |
| Δpot1            | BY4742 Δpot1::KanMX4                             | Euroscarf collection |
| Δtgl3            | BY4742 Δtgl3::KanMX4                             | Euroscarf collection |
| Δpex3Δpot1       | BY4742 Δpex3::KanMX4 Δpot1::NatMX4               | this study         |
| Δpex7            | BY4742 Δpex7::KanMX4                             | Euroscarf collection |
| WT GFP.SKL       | BY4742 pMET25-GFP.SKL/Zeo^8                      | this study         |
| Δatg1            | BY4741 Δatg1::KanMX4                             | Euroscarf collection |
| Δatg1Δpex3       | BY4741 Δpex3::KanMX4 Δatg1::NatMX4               | this study         |
| Δpex5/PEX5       | BY4742 Δpex5::KanMX4 pRS316-PEX5                 | this study         |
| Primers  | Sequence 5’-3’                                                                                       |
|----------|------------------------------------------------------------------------------------------------------|
| Pex5UP   | TATGCAAAGGTTCATAAAACGGAGAACCACCTGATCGATGATAAAAGAAGA-                                             |
|          | A-CAGCTGAAGCTTTCGTACGC                                                                            |
| Pex5DN   | CTCTCTTCAAAGTCTCTTATAACAGTATCTTTGATACGTATTCAAGAGAGAT-GCATAGGCCACTAGTGGATCTG                        |
| Pex5.1   | GGCGTCTTTAATGAGAGTGCACT                                        |
| Pex5.2   | ATGGCCTGCTTCACTTCTTGG                                      |
| Pex5.5   | ATCCGCTCAGAGATATCTTGG                                     |
| Pex5.6   | TCCATGTCTTTCTCCCTGATAAAG                                  |
| Pex5.A   | GCTTGGCTTATTTTACCTGATGTAT                                 |
| Pex5.B   | GAGAGCTTTTTTCTCTCCCTGATAACA                                 |
| Pot1.1   | CTACAGCTGCTAAACGCTACACCGACCAA                           |
| Pot1.2   | CTTAGGATCCCTGTACTCAGAGCCACAAG                            |
| Pot1.3   | CTAAGTCTGCCGCGCCACATCTT                                   |
| Pot1.4   | CTACCGCGGCAGTACCTGATAGTATGGCTATCG                         |
| Pot1.5   | GAGGATGCACTTCCGATATA                                      |
| Pot1.6   | AATTCAACGCTGCTTGAGG                                       |
| Pot1.7   | GACATCATCTGCCCAGATGC                                      |
| Pot1.8   | TGGAGGGGAAGAAGGATGAGG                                     |
| GFP SKL-3| TATCCGCGCGCGCGCAATTAACCTCA                              |
| GFP SKL-4| TATGCGGCGCGCGGTAACGCACGGTGGTTTT                         |
| MET25.1  | GGCGTCAAGATTTAGGTGAT                                      |
| ATG1up   | TTCAATCTCTCTTTTACAACACCAGACGAGAAATTAAGAAAGAGACGGATCCCCGGGATTATTA                                  |
| ATG1down | GGTCAATTCTACTAATAAGAAACCATTATGTCATCGACGCGCTGTAACGAGAGCCGCTTAA                                     |
| Atg1.1   | CTGGGGGAACAGAGAAGACGT                                     |
Supplementary experimental procedures

Construction of Δatg1Δpex3 strains

ATG1 gene was deleted in Δpex3 cells by replacing the open reading frame with nourseothricin resistance gene [Goldstein, 1999 #32]. The atg1::NatMX4 DNA fragment was amplified with ATG1up and ATG1down primers (Table S2) using pAG25 [Goldstein, 1999 #32] as template and transformed into Δpex3 cells. Correct insertion by homologous recombination was confirmed by colony PCR using Atg1.1 and Pot1.6 primers (Table S2).

Chronological aging experiment on peroxisome induction medium for pex mutants

Overnight cultures were grown in MM medium containing 0.5% glucose and required amino acids. Those cultures were then diluted twice at OD$_{600\text{ nm}}$ = 0.1 in fresh MM containing 0.3% glucose and grown for 8 hours. After the last pre-cultivation step, cells were diluted in MM containing 0.25% ammonium sulfate, 0.05% yeast extract, 0.1% oleic acid and 0.05% Tween 80 and 0.1% glucose. Cultures were incubated at 30°C, 200 rpm. Survival was assayed by counting colony-forming units (CFUs) after 2 days of incubation at 30°C on YPD agar plates. 24 hours after the last dilution (D1) was considered as 100% of survival. The results shown are mean values and standard error of mean. Statistical analyses were determined using two-way ANOVA. A p value of less than 0.05 was considered as a significant difference.