**Figure EV1.** Pgc1 degradation is independent of the vacuolar protease Pep4 but requires Doa10 and the cytoplasmic ubiquitin ligase Ubr1.

A, B The degradation of 3HA-Pgc1 was analyzed in cells with the indicated genotype as described in Fig 1A. The graphs show the average of two independent experiments; error bars represent the standard deviation.
A The degradation of Dga1-GFP was analyzed in cells with the indicated genotype as described in Fig 1A. A plasmid-borne GFP-Dga1 expressed from the constitutive ADH1 promoter was used. The graph shows the average of two independent experiments; error bars represent the standard deviation.

B The degradation of Yeh1-3HA was analyzed in cells with the indicated genotype as described in Fig 1A. A plasmid-borne Yeh1-3HA expressed from the endogenous promoter was used. The graph shows the average of two independent experiments; error bars represent the standard deviation.

C, D The degradation of Dga1-GFP was analyzed in cells with the indicated genotype as described in Fig 1A. The graphs show the average of two independent experiments; error bars represent the standard deviation.
Figure EV3. Degradation of Pgc1 and Dga1 in cdc48 mutant cells.

A The degradation of Dga1-GFP in temperature-sensitive cdc48-6 mutant cells was analyzed as in Fig 1C. The graph shows the average of three independent experiments; error bars represent the standard deviation.

B, C The degradation of 3HA-Pgc1 and Dga1-GFP in temperature-sensitive cdc48-3 mutant cells was analyzed as described in Fig 1C. The graphs show the average of two independent experiments; error bars represent the standard deviation.
Figure EV4. Pgc1 and Dga1 are degraded by the proteasome.

A The degradation of 3HA-Pgc1 was analyzed in proteasome-deficient (pre2) and wt control (PRE2) cells as described in Fig 1A. Asterisk indicates degradation products accumulating in proteasome-deficient cells. The graph shows the average of two independent experiments; error bars represent the standard deviation.

B The degradation of Dga1-GFP was analyzed in proteasome-deficient (pre2) and wt control (PRE2) cells as in Fig 1A. The graph shows the average of two independent experiments; error bars represent the standard deviation.

Figure EV5. The chimeric protein 3HA-Pgc1-GPAT160–216 is a Doa10 substrate.

The degradation of 3HA-Pgc1-GPAT160–216 was analyzed in cells with the indicated genotype as in Fig 1A. The graph shows the average of three independent experiments; error bars represent the standard deviation.