Supplemental material

Cruz-Garcia et al., http://www.jcb.org/cgi/content/full/jcb.201407119/DC1

Α Marker Grh1-2xmCherry Merged r=0.852 M1=0.837 M2=0.827 Uso1-2xGFP r=0.677 M1=0.543 M2=0.642 GFP-Sed5 r=0.436 M1=0.054 M2=0.058 Mnn2-GFP r=0.422 M1=0.053 M2=0.185 Mnn5-GFP B Pearson M1 M2 N (cells) Uso1 / Grh1 0.834±0.005 0.771±0.016 0.807±0.017 73 Sed5 / Grh1 0.685±0.012 0.420±0.024 0.668±0.028 54 Mnn2 / Grh1 0.405±0.009 0.059±0.011 0.146±0.025 57 0.108±0.023 Mnn5 / Grh1 0.434±0.011 0.056±0.014 54

Figure S1. **Quantitative colocalization analysis of Grh1 and Golgi proteins.** (A) Cells coexpressing Grh1-2xmCherry and Uso1-2xGFP, GFP-Sed5, Mnn2-GFP, or Mnn5-GFP were grown in complete medium, then washed and incubated in 2% potassium acetate. After 2 h of starvation, z stacks were acquired by spinning-disk confocal fluorescence microscopy. The panels show representative single confocal sections of the GFP and mCherry signals and the corresponding merged images. The numbers next to the merged images indicate the values of the Pearson's (r) and Manders' (M1 and M2) coefficients of the corresponding cropped stack of confocal sections. M1 refers to the proportion of the GFP signal overlapping with a signal in the mCherry channel over its total intensity. M2 refers to the proportion of the mCherry signal overlapping with a signal in the GFP channel over its total intensity. Broken lines indicate of the different proteins in A, as measured by the Pearson's and Manders' coefficients between the GFP and mCherry signals. Values represent the mean ± SEM of the indicated number of cells (N).



Figure S2. **CUPS formed in COPII or COPI mutant cells do not contain the early Golgi marker Anp1.** Wild-type, *sec31-1*, and *sec21-1* cells coexpressing Grh1-2×GFP and Anp1-RFP were grown to mid-log phase at 25°C, then preincubated at 37°C for 45 min followed by starvation in 2% potassium acetate at 37°C for 2 h. Cells were imaged by fluorescence microscopy just before starvation (Growth) and within 2 h of starvation. Bar, 2 µm.



Figure S3. **Colocalization analysis of Golgi-, endosome-, and autophagosome-specific proteins and lipids in CUPS.** (A and B) Cells coexpressing Grh1-2xGFP and mCherry-Osh2-2xPH (A) or mRFP-EEA1-FYVE (B) were grown in complete medium, then washed and incubated in 2% potassium acetate for 2 h. Cells were observed by fluorescence microscopy just before starvation (Growth) and at the indicated time points after starvation. (C and D) Cells coexpressing Grh1-2xGFP and Anp1-RFP (C) or Sec7-2xmCherry (D) were grown in rich medium, washed and cultured in 2% potassium acetate or SC-D (-glucose) medium for 2 h, and visualized by fluorescence microscopy. (E) Grh1-2xGFP-expressing cells transformed with plasmids coding for mCherry-Atg8 or mRFP-Atg9 were grown in complete medium, starved for 4 h in 2% potassium acetate, and imaged by fluorescence microscopy. Bar, 2 µm.

Table S1. Yeast strains used in this study

Name	Genotype	Source
BY4741	MATa his3∆1 leu2∆0 met15∆0 ura3∆0	EUROSCARF
BY4742	MAT $lpha$ his3 Δ 1 leu2 Δ 0 lys2 Δ 0 ura3 Δ 0	EUROSCARF
DCY001	BY4741 GRH1-2×GFP-HIS3MX6	This study
DCY002	BY4741 GRH1-2×mCherry-CaURA3	This study
DCY003	BY4741 GRH1-2×mCherry-CaURA3 USO1-2xGFP-HIS3MX6	This study
Uso1-GFP	BY4741 USO1-GFP-HIS3MX6	Invitrogen
DCY004	BY4741 USO1-GFP-HIS3MX6 grh1Δ::KanMX4	This study
DCY005	BY4741 GRH1-2×GFP-HIS3 vps34∆::KanMX4	This study
uso 1-1ª	BY4741 uso1-1-KanMX	C. Boone
sec13-1 ^b	BY4741 sec13-1-KanMX	C. Boone
sec31-1 ^b	BY4741 sec31-1-KanMX	C. Boone
sec21-1°	BY4741 sec21-1-KanMX	C. Boone
sec7-1 ^b	BY4741 sec7-1-KanMX	C. Boone
pik1-104 ^b	BY4741 pik1-104-KanMX	C. Boone
sec20-1 ^b	BY4741 sec20-1-KanMX	C. Boone
sly 1-ts ^b	BY4741 sly1-ts-KanMX	C. Boone
DCY006	BY4741 GRH1-2×GFP-HIS3MX6 uso1-1-KanMX	This study
DCY007	BY4741 GRH1-2×GFP-HIS3MX6 sec13-1-KanMX	This study
DCY008	BY4741 GRH1-2×GFP-HIS3MX6 sec31-1-KanMX	This study
DCY009	BY4741 GRH1-2×GFP-HIS3MX6 sec21-1-KanMX	This study
DCY010	BY4741 GRH1-2×GFP-HIS3MX6 sec7-1-KanMX	This study
ACY040	BY4741 GRH1-2×GFP-HIS3MX6 pik1-104-KanM	This study
vam 7Δ	BY4741 vam7Δ::KanMX4	EUROSCARF
DCY011	BY4741 GRH1-2×GFP-HIS3MX6 vam7∆::KanMX4	This study
DCY012	BY4741 GRH1-2×GFP-HIS3MX6 sec20-1-KanMX	This study
DCY013	BY4741 GRH1-2×GFP-HIS3MX6 sly1-ts-KanMX	This study
ACY041	BY4742 GRH1-2×mCherry-CaURA3	This study
Mnn2-GFP	BY4741 MNN2-GFP-HIS3MX6	Invitrogen
Mnn5-GFP	BY4741 MNN5-GFP-HIS3MX6	Invitrogen
DCY014	MATa GRH1-2×mCherry-CaURA3 MNN2-GFP-HIS3MX6	This study
DCY015	MATa GRH1-2×mCherry-CaURA3 MNN5-GFP-HIS3MX6	This study
Anp1-RFP	BY4742 ANP1-RFP-KanMX	E. O'Shea ^d
DCY016	BY4742 ANP1-RFP-NatMX	This study
DCY017	MATa GRH1-2×GFP-HIS3MX6 ANP1-RFP-NatMX	This study
DCY018	MATa GRH1-2×GFP-HIS3MX6 ANP1-RFP-NatMX sec31-1-KanMX	This study
DCY019	MATa GRH1-2×GFP-HIS3MX6 ANP1-RFP-NatMX sec21-1-KanMX	This study
DCY020	BY4741 GRH1-2×GFP-HIS3MX6 SEC7-2×mCherry-CaURA3	This study

^aThe mutation in the *uso1-1* allele is a truncation of most of its C-terminal tail. ^bThe mutation in this temperature-sensitive allele is unknown. ^cThe mutation in the *sec21-1* allele is G482D. ^dHarvard University, Cambridge, MA.