Supplemental Figures and Legends

Α.		
	<i>ypt1</i> ∆ +Ypt1 (URA3 plasmid)
yEVenus-Ypt1	000 0	2 °0
mCherry-Ypt1	0° 00 00	°" •© •
P		
plasmid (<i>LEU2</i>)	<i>ypt1</i> ∆ +Ypt1	(URA3 plasmid)
Ø		Per
Ypt1		
yEVenus-Ypt1		
mCherry-Ypt1	283	
	SD-leu-ura	SD-leu+5FOA
c		
plasmid (<i>LEU2</i>)	ypt31∆ypt32∆ + Y	pt31 (<i>URA3</i> plasmid)
Ø		e
Ypt31		
yEGFP-Ypt31		
	SD-leu-ura	SD-leu+5FOA

D.

Puncta per cell	# of cells (n)	# of puncta average	std dev
yEVenus-Ypt1	10	10.3	2
yEGFP-YPT31 /ypt32∆	10	11.5	2

Figure S1. Functionality of fluorescently tagged Ypt1 and Ypt31 (Related to Figures 2-4). A. Both yEVenus-Ypt1 and mCherry-Ypt1 show punctate fluorescence signal. Cells expressing the fluorescently tagged Ypt1 proteins from a CEN plasmid were visualized by live-cell microscopy. Shown are: DIC (left) and yEVenus-Ypt1 or mCherry-Ypt1 (right). Bar 5 mm. **B.** yEVenus-Ypt1, but not mCherry-Ypt1, is functional as a sole copy. Cells carrying $ypt1\Delta$ on the chromosome and expressing YPT1 from a CEN URA3 plasmid were transformed with a CEN LEU2 plasmid expressing Ypt1 from it own promoter and terminator (from top to bottom): Ø (empty vector control), Ypt1, yEVenus-Ypt1 (Ypt1 tagged at its N-terminus with yeast-codon-optimized enhanced Venus), or mCherry-Ypt1. Growth of transformants is shown on SD-Ura-Leu (left), and the ability of cells to lose the URA3 plasmid is shown on SD-Leu+5FOA (right). Whereas Ypt1 and yEVenus-Ypt1 are functional, mCherry-Ypt1 is not. C. yEGFP-Ypt31 is functional as a sole copy. Cells carrying $ypt31\Delta ypt32\Delta$ on the chromosome and expressing YPT31 from a CEN URA3 plasmid were transformed with a CEN LEU2 plasmid expressing Ypt31 from its own promoter and terminator (from top to bottom): Ø (empty vector control), Ypt31, yEGFP-Ypt31 (Ypt31 tagged at its N-terminus with yeast-codon-optimized enhanced GFP). Growth of transformants is shown on SD-Ura-Leu (left), and the ability to lose the URA3 plasmid is shown on SD-Leu+5FOA (right). Both Ypt31 and yEGFP-Ypt31 can support cell growth. Results shown in this figure represent at least two independent experiments. D. Table shows quantifications from two independent expreiments of total number of puncta of Ypt1 and Ypt31 per cell by live-cell microscopy.



	DIC	Sec7- yEGFP	Chc1- mRFP	merge
plasmid:				
2u	8	0	्र	Č,
2u Ypt1	$\overline{\mathfrak{G}}$	$\overset{\circ}{\otimes}$		

B. Sec7 and Chc1 (mRFP/GFP)





C.

Strain	Plasmid	# of cells (n)	co-localization (%) of Green with Red	std dev	# Green puncta/slice	std dev	# co-localized puncta/slice	# not co-localized puncta/slice	std dev
	Ø CEN	20	18.5	1	4.3	0.1	0.9		
	Ypt1 CEN	20	31.2	1	3.8	0.6	1.1	1	
Cop1-mRFP	Ø 2µ	20	18.7	1	4.3	0.2	0.9		
Sec7-yEGFP	Ypt1 2µ URA3	20	42.6	1	3.6	0.2	1.4		
	Ypt1 2µ LEU2	30	40	0	4	0.2	1.5		
	Ypt1-GTP 2µ	30	55	6	4.7	0.2	2.5		
	Ø CEN	28	78.8	3	5.2		4	1.2	0.4
See7 mBED	Ypt1 CEN	28	75.1	4	5.6		4.1	1.5	0.3
Chc1-GEP	Ø 2µ	28	64.5	3	5.6		3.6	2.1	0.2
	Ypt1 2µ	28	78.8	3	5.4		4.1	1.3	0.1
	Ypt1-GTP 2µ	28	83.5	3	5.4		4.4	1	0.2
	Ø CEN	20	88.5	3	4.2		3.6	0.6	
Sec7-yEGFP	Ypt1 CEN	20	91	4	3.7		3.3	0.4	
Chc1-mRFP	Ø 2µ	20	88.9	0	3.6		3.1	0.5	
	Ypt1 2µ	20	89.5	5	3.9		3.5	0.4	

Figure S2. Ypt1 overexpression does not affect Sec7 and Chc1 co-localization (Related to Figures 6-7). A. Cells expressing Sec7-yEGFP and Chc1-mRFP from their endogenous loci were transformed with *CEN* (left) and 2m (right) plasmids, empty (top) and for overexpression of Ypt1 (bottom). Information from this experiment was used in Figure 7E. B. Cells expressing Sec7-mRFP and Chc1-yEGFP from their endogenous loci were transformed with *CEN* (left) and 2m (right) plasmids, empty (top) and for overexpression of Ypt1 (bottom). C. Table shows quantifications from two independent experiments for panels A and B of this figure and Figures 6 and 7. The co-localization level of the two markers was determined using live cell microscopy. Bar, 5µm.

A. Sec7 and Chc1 (yEGFP/mRFP)

A. Cop1 and Sec7



B. Sec7 and Chc1



plasmid:	DIC	Sec7- yEGFP	Chc1- mRFP	merge	
piasiniu.	0				
2u	0		2	2	
	0	- × -		- * 1	
2u Ypt31	9			-	

C.

Strain	Plasmid	# of cells (n)	co-localization (%) of Green with Red	std dev	# Green puncta/slice	std dev	# co-localized puncta/slice	# not co-localized puncta/slice	std dev
	Ø CEN	20	14.3	5	4.6	0.2	0.7		
Cop1-mRFP	Ypt31 CEN	20	20.1	3	4.5	0.6	0.9		
Sec7-yEGFP	Ø 2µ	20	18.7	1	4.3	0.2	0.9		
	Ypt31 2µ	20	19.5	3	4.2	0.1	0.8		
	Ø CEN	20	81.1	1	5.2		4.1	1.1	0
See7 mDFD	Ypt31 CEN	20	70.5	3	6.3		4.5	1.9	0
Chc1-GEP	Ø 2µ	28	64.5	3	5.6		3.6	2.1	0.2
	Ypt31 2µ	28	64.4	4	6.3		4	2.3	0.3
	Ypt31-GTP 2µ	28	45.1	3	8.4		3.6	4.9	0.4
	Ø CEN	20	90.9	1	4		3.6	0.4	
Sec7-yEGFP	Ypt31 CEN	20	90.3	3	4.5		4.1	0.4	
Chc1-mRFP	Ø 2µ	20	88.9	0	3.6		3.1	0.5	
	Ypt31 2µ	20	88	4	4.4		3.9	0.5	

Figure S3. Effects of Ypt31 overexpression on co-localization of Golgi markers. (Related to Figures 6-7). A. Overexpression of Ypt31 does not affect the level of co-localization of Cop1 and Sec7. Cells expressing Sec7yEGFP and Cop1-mRFP from their endogenous loci were transformed with *CEN* (left) and 2m (right) plasmids, empty (top) and for overexpression of Ypt31 (bottom). Information from this experiment was used in Figure 6E-F. **B.** Overexpression of Ypt31 does not affect the level of co-localization of Sec7 with Chc1. Cells expressing Sec7yEGFP and Chc1-mRFP from their endogenous loci were transformed with *CEN* (left) and 2m (right) plasmids, empty (top) and for overexpression of Ypt31 (bottom). **C.** Table shows quantifications from two independent experiments for panels A and B of this figure and Figures 6 and 7. The co-localization level of the two markers was determined using live cell microscopy. Bar, 5µm.



Figure S4. The effect of *ypt1* and *ypt31/32* loss-of-function mutations on the co-localization of Golgi markers. (Related to Figures 6-7). The effect of *ypt1ts* and *ypt31\Delta/32ts* mutations on the co-localization of Golgi markers was determined at the permissive temperature using live-cell fluorescence microscopy: A-B. Cop1-Sec7. C-D. Sec7-Chc1. Wild type and mutant cells expressing tagged Golgi markers from their endogenous promoters were analyzed as described for Figures 6-7. Panels A and C: Shown from top to bottom: WT (*YPT1*), *ypt1ts*, WT (*YPT31/YPT32*), *ypt31\Delta/32ts*. Arrows show co-localization; arrowheads show green-only puncta. Bar, 5µm. Bar graphs showing the number of Cop1 (B) or Chc1 (D) puncta: Total puncta (blue+purple bars), and puncta that co-localize with Sec7 (purple bars). Error bars and +/- represent STDEV; brackets with stars represent p-value from significant (***); p-values of all other pairs were not significant. Quantifications from two independent experiments are detailed in Table S2.



Figure S5. The effect of Ypt1 or Ypt31 activation on their co-localization at the Sec7-marked Golgi compartment (Related to Figure 6-7). A. Cells were transformed with a CEN plasmid: empty (top), expressing Ypt1-GTP (middle), or Ypt31-GTP (bottom). Three-color IF microscopy was done as described in the legend for Figure 5C. The brightness of the Ypt1 staining in cells overexpressing Ypt1-GTP was reduced to enable the co-localization analysis (two bottom panels show the cells before the adjustment). Bar, 5µm. **B.** Bar graph showing the number of puncta in transformants of the three plasmids (from left-to-right): empty (CEN), Ypt1-GTP and Ypt31-GTP. The effect of each plasmid on co-localization of two or three proteins is color-coded (see key on the right): Ypt1+Sec7 (pink), Ypt31+Sec7 (yellow), Ypt1+Ypt31 (blue), and all three proteins (grey). Error bars and +/- represent STDEV; brackets with stars represent p-value; p-values for all other pairs were not significant. Quantifications from two independent experiments are detailed in Table S3.

A. Sec7-mRFP Cop1-eGFP Merge



Figure S6. The effect of overexpression of activated Ypt1 and Ypt31 on Golgi cisternal progression. (Related to Figure 8) Three-channel kymographs of puncta used for graphs shown in Figure 8A-F. A-C: Cop1-GFP and Sec7-mRFP. D-F: Sec7-mRFP and Chc1-GFP. Cells expressing a Golgi marker pair were transformed with one of the indicated 2m plasmids: empty, YPT1-GTP or Ypt31-GTP. For each transformant, left panel shows a merged live-cell image with a white arrow pointing to the punctum selected for the kymograph, which is shown to its right. For each kymograph, shown from top-to-bottom: mRFP, GFP, merge, time (secs). Bar, 5µm.

Supplemental Tables

Cop1-mRFP	# of cells (n)	co-localization (%) of Sec7 with Ypt1	std dev	# Sec7 puncta/slice	# co-localized puncta/slice	co-localization (%) of Ypt1 with Sec7	std dev	# Ypt1 puncta/slice
Cop1-mRFP		33.1	3	5	1.5	23.4	2	6.6
α-Ypt1	24	co-localization (%) of Sec7 with Cop1	std dev	# co-localized puncta/slice		co-localization (%) of Ypt1 with Cop1	std dev	# co-localized puncta/slice
		14.7	0	0.7	0.7 54.2 # of cells (n) co-localization (%) of Cop1+Sec7 with Ypt1	6	3.4	
co-localization of three	# of cells (n)	co-localization (%) of Ypt1+Sec7 with Cop1	std dev		# of cells (n)	co-localization (%) of Cop1+Sec7 with Ypt1	std dev	
markers	20	46.7	7		14	93.8	9	
	# of cells (n)	co-localization (%) of Sec7 with Ypt1	std dev	# Sec7 puncta/slice	# co-localized puncta/slice	co-localization (%) of Ypt1 with Sec7	std dev	# Ypt1 puncta/slice
Chc1-mRFP	# of cells (n)	co-localization (%) of Sec7 with Ypt1 32.3	std dev 1	# Sec7 puncta/slice 4.5	# co-localized puncta/slice 1.4	co-localization (%) of Ypt1 with Sec7 23	std dev 2	# Ypt1 puncta/slice 6.3
Chc1-mRFP Sec7-yEGFP α-Ypt1	# of cells (n) 24	co-localization (%) of Sec7 with Ypt1 32.3 co-localization (%) of Sec7 with Chc1	std dev 1 std dev	# Sec7 puncta/slice 4.5 # co-localized puncta/slice	# co-localized puncta/slice 1.4	co-localization (%) of Ypt1 with Sec7 23 co-localization (%) of Ypt1 with Chc1	std dev 2 std dev	# Ypt1 puncta/slice 6.3 # co-localized puncta/slice
Chc1-mRFP Sec7-yEGFP α-Ypt1	# of cells (n) 24	co-localization (%) of Sec7 with Ypt1 32.3 co-localization (%) of Sec7 with Chc1 58.2	std dev 1 std dev 3	# Sec7 puncta/slice 4.5 # co-localized puncta/slice 2.6	# co-localized puncta/slice 1.4	co-localization (%) of Ypt1 with Sec7 23 co-localization (%) of Ypt1 with Chc1 11.9	std dev 2 std dev 4	# Ypt1 puncta/slice 6.3 # co-localized puncta/slice 0.66
Chc1-mRFP Sec7-yEGFP α-Ypt1 co-localization of three	# of cells (n) 24 # of cells (n)	co-localization (%) of Sec7 with Ypt1 32.3 co-localization (%) of Sec7 with Chc1 58.2 co-localization (%) of Ypt1+Chc1 with Sec7	std dev 1 std dev 3 std dev	# Sec7 puncta/slice 4.5 # co-localized puncta/slice 2.6	# co-localized puncta/slice 1.4 # of cells (n)	co-localization (%) of Ypt1 with Sec7 23 co-localization (%) of Ypt1 with Chc1 11.9 co-localization (%) of Ypt1+Sec7 with Chc1	std dev 2 std dev 4 std dev	# Ypt1 puncta/slice 6.3 # co-localized puncta/slice 0.66

Table S1	Distribution of V	nt1 on the Golg	i using three-color	· IF microsconv	(Related to Fig	ire 3).
Table ST	Distribution of 1	pui on the Goig	i using un ce-coloi	II meroscopy	(Related to Figu	пе э).

Table S2. The effect of *ypt1* and *ypt31/32* loss-of-function mutations on the co-localization of Golgi markers (Related to Figure S4).

	Strain	# of cells (n)	co-localization (%) of green with Sec7	std dev	# green puncta/slice	std dev	p-value	# co-localized puncta/slice	std dev	p-value
Sec7-	YPT1	20	11.1	2	7.7	0.4	n/a	0.8	0.1	
mRFP	ypt1ts	20	7.8	1	10.0	0.1	0.0007***	0.7	0	
Chc1-	YPT31/32	20	11.9	1	8.4	0.3	n/a	0.9	0.1	
GFP	ypt31∆/32ts	20	11.0	4	8.3	0.6	0.8297	0.9	0.3	
Sec7-	YPT1	20	54.9	1	6.5	0.4	n/a	3.4	0.1	
mRFP	ypt1ts	20	56.8	1	6.6	0.8	0.7318	3.7	0.1	0.0374*
Cop1-	YPT31/32	20	63.6	7	6.4	0.5	n/a	4.0	0.1	
GFP	ypt31∆/32ts	20	56.6	3	5.6	0.1	0.0395*	3.1	0.1	0.0042**

Bolded numbers were used for graphs in Figure S4B,D.

Table S3. The effect of Ypt1 or Ypt31 activation on their co-localization at the Sec7-marked Golgi compartment (Related to Figure S5)

<i>yEGFP-</i> <i>YPT31/ypt32Δ</i> Sec7-mRFP α-Ypt1		# of Ypt1+Ypt31 puncta	% coloc Ypt1 with Ypt31	% coloc Ypt31 with Ypt1	# of Ypt1+Sec7 puncta	% coloc Ypt1 with Sec7	% coloc Sec7 with Ypt1	# of Ypt31+Sec7 puncta	% coloc Ypt31 with Sec7	% coloc Sec7 with Ypt31
CEN	ave	1.17	0.20	0.20	1.57	0.28	0.35	3.43	0.57	0.77
n=30	±	0.14	0.02	0.04	0.05	0.02	0.00	0.33	0.05	0.09
CEN-Ypt1-GTP	ave	1.73	0.29	0.27	2.50	0.43	0.54	3.73	0.60	0.81
n=30	±	0.38	0.04	0.07	0.14	0.02	0.04	0.19	0.02	0.02
		p=0.0240			p=0.0006			p=0.3474		
CEN-Ypt31-GTP	ave	1.00	0.16	0.16	1.60	0.28	0.40	3.70	0.61	0.83
n=30	±	0.00	0.01	0.01	0.57	0.11	0.17	0.05	0.06	0.02
		p=0.4038			p=0.8926			p=0.3934		

yEGFP- YPT31/ypt32Δ Sec7-mRFP α-Ypt1		# of red Sec7	# of green Ypt31	# of blue Ypt1	# of puncta co-loc of all three	% of Ypt1+Ypt31 with Sec7
CEN	ave	4.43	6.03	5.67	1.07	0.92
n=30	±	0.05	0.24	0.38	0.09	0.03
CEN-Ypt1-GTP	ave	4.63	6.33	5.97	1.60	0.93
n=30	±	0.05	0.00	0.52	0.28	0.04
					p=0.0350	
CEN-Ypt31-GTP	ave	4.43	6.27	5.90	0.93	0.93
n=30	±	0.05	0.47	0.33	0.00	0.00
					p=0.5132	

Bolded numbers were used for graphs in Figure S5B.

Supplemental Experimental Procedures

Yeast Strains

NSY number	Alias	Genotype	Reference
NSY862	Cop1-mRFP	mat alpha his3 delta1 leu2 delta 0 lys2 delta 0 ura3 delta 0 COP1::mRFP-kanMX6	1
NSY1733	Cop1-mRFP Vrg4-yEGFP	NSY862 VRG4::yEGFP-nat	this study
NSY1734	Cop1-mRFP Sec7-yEGFP	NSY862 SEC7::yEGFP-nat	this study
NSY1735	Cop1-mRFP Chc1-GFP	NSY862 CHC1::GFP-hyg	this study
NSY863	Chc1-mRFP	mat alpha his3 delta1 leu2 delta 0 lys2 delta 0 ura3 delta 0 CHC1::mRFP-kanMX6	1
NSY1736	Chc1-mRFP Vrg4-yEGFP	NSY863 VRG4::yEGFP-nat	this study
NSY1737	Chc1-mRFP Cop1-GFP	NSY863 COP1::GFP-hyg	this study
NSY1738	Chc1-mRFP Sec7-yEGFP	NSY863 SEC7::yEGFP-nat	this study
NSY825	WT- BY4741	mat a leu2 delta 0 ura3 delta 0 his3 delta 1 met15 delta 0	2
NSY1739	Sec7-mCherry	BY4741 SEC7::mCherry-NatR	this study
NSY1740	Vrg4-yEGFP	BY4741 VRG4::yEGFP-NatR	this study
NSY1221	yEGFP-Ypt31/ypt31∆	mat alpha ade2 ura3-52 leu2-3,112 his3 delta 200 lys2 ypt32::kan yEGFP-Ypt31(LYS2) in Ypt31 locus	this study
NSY1741	yEGFP-Ypt31/ypt31∆ Sec7-mRFP	mat alpha ade2 ura3-52 leu2-3,112 his3 delta 200 lys2 ypt32::kan yEGFP-Ypt31(LYS2) in Ypt31 locus SEC7::mRFP-HygR	this study
NSY1742	Chc1-GFP	BY4741 CHC1::GFP-HygR	this study
NSY1743	Chc1-GFP Sec7-mRFP	BY4741 CHC1::GFP-HygR SEC7::mRFP-G418R	this study
NSY1744	Sec7-mRFP	BY4741 SEC7::mRFP-G418R	this study
NSY1745	Cop1-GFP Sec7-mRFP	BY4741 SEC7::mRFP-G418R COP1::GFP-HygR	this study
NSY128	WT- DBY4985	mat alpha ade2 his3 delta 200 leu2-3,112 lys2-801 ura3-52	David Botstein
NSY1746	Chc1-GFP	NSY128 CHC1::GFP-HygR	this study

NSY1747	Chc1-GFP Sec7-mRFP	NSY128 CHC1::GFP-HygR SEC7::mRFP-G418R	this study
NSY1748	Cop1-GFP	NSY128 COP1::GFP-HygR	this study
NSY1749	Cop1-GFP Sec7-mRFP	NSY128 COP1::GFP-HygR SEC7::mRFP-G418R	this study
NSY1541	<i>ypt1∆</i> + pRS316-Ypt1	NSY128 pRS316-YPT1 yptt1 delta::HygR	3
NSY302	<i>ypt31∆/ypt32∆</i> + pRS316-Ypt31	mat alpha ade2 his3 delta 200 leu2-3 lys2 ura3-52 deltaYPT31::HIS2 pRS316-Ypt31 deltaYPT32::KanR pRS316-Ypt31	4
NSY220	WT- YPT1	mat alpha ura3-52 lys2 his4	5
NSY222	ypt1ts	mat alpha ura3-52 his4 ypt1A136D	5
NSY125	WT- YPT31/32	mat a ura3-52 lys2 his4	6
NSY348	ypt31∆/ypt32ts	mat a ura3-52 lys2 his4-539 deltaYPT31::HIS3 ypt32- A141D	6
NSY1750	YPT1 Sec7-mRFP	NSY1081 SEC7::mRFP-G418R	this study
NSY1754	YPT1 Sec7-mRFP Cop1-GFP	NSY1081 SEC7::mRFP-G418R COP1::GFP-HygR	this study
NSY1756	YPT1 Sec7-mRFP Chc1-GFP	NSY1081 SEC7::mRFP-G418R CHC1::GFP-HygR	this study
NSY1751	<i>ypt1ts</i> Sec7-mRFP	NSY1082 SEC7::mRFP-G418R	this study
NSY1758	<i>ypt1ts</i> Sec7-mRFP Cop1-GFP	NSY1082 SEC7::mRFP-G418R COP1::GFP-HygR	this study
NSY1760	<i>ypt1ts</i> Sec7-mRFP Chc1-GFP	NSY1082 SEC7::mRFP-G418R CHC1::GFP-HygR	this study
NSY1752	YPT31/32 Sec7-mRFP	NSY125 SEC7::mRFP-G418R	this study
NSY1762	YPT31/32 Sec7-mRFP Cop1-GFP	NSY125 SEC7::mRFP-G418R COP1::GFP-HygR	this study
NSY1764	YPT31/32 Sec7-mRFP Chc1-GFP	NSY125 SEC7::mRFP-G418R CHC1::GFP-HygR	this study
NSY1753	ypt31∆/ypt32ts Sec7-mRFP	NSY348 SEC7::mRFP-G418R	this study
NSY1766	<i>ypt31∆/ypt32ts</i> Sec7-mRFP Cop1-GFP	NSY349 SEC7::mRFP-G418R COP1::GFP-HygR	this study
NSY1768	ypt31∆/ypt32ts Sec7-mRFP Chc1-GFP	NSY350 SEC7::mRFP-G418R CHC1::GFP-HygR	this study

Plasmids

PNS number	Alias	Genotype	Reference
pNS245	empty CEN	pRS315 CEN, LEU2, Amp ^r	7
pNS1430	yEVenus-Ypt1	pRS315-yEVenus-YPT1	8
pNS1431	mCherry-Ypt1	pRS315-mCherry-YPT1	This study
pNS1364	CEN Ypt1	pRS315-YPT1	9
pNS661	GFP-Ypt31	pRS315-GFP- <i>YPT31</i>	Ruth Collins
pNS221	CEN Ypt31	pRS315-YPT31	4
pNS246	empty CEN	pRS316 CEN, URA3, Amp ^r	7
pNS636	CEN Ypt1	pRS316- <i>YPT1</i>	Ruth Collins
pNS220	CEN Ypt31	pRS316-YPT31	4
pNS719	empty CEN	pRS317 CEN, LYS2, Amp ^r	10
pNS939	CEN Ypt31	pRS317- <i>YPT31</i>	This study
pNS994	yEGFP-Ypt31	pRS317-yEGFP-YPT31	This study
pNS180	empty 2µ	pRS425 2µ, <i>LEU2</i> , Amp ^r	7
pNS993	2µ Ypt1	YEp423-YPT1 LEU2	5
pNS1556	2µ Ypt1-GTP	YEp423-YPT1Q67L	This study
pNS781	2µ Ypt31	pRS425-Ypt31	Scott Emr
pNS782	2µ Ypt31-GTP	pRS425- <i>YPT31Q72L</i>	Scott Emr
pNS274	empty 2µ	YEp24 2µ, URA3, Amp ^r	New England Biolabs, MA
pNS489	2µ Ypt1	YEp24-YPT1	11
pNS229	2µ Ypt31	YEp24- <i>YPT31</i>	6

pNS1527	tagging plasmid	pFA6a-mRFP-G418 ^r	1
pNS1557	tagging plasmid	pFA6a-GFP-Hyg ^r	This study
pNS1506	tagging plasmid	pKT127-yEGFP replaced with mCherry-G418r replaced with Natr	12
pNS1533	tagging plasmid	pKT127-yEGFP-G418r replaced with Nat ^r	This study
pNS1558	CEN Ypt1-GTP	pRS315-YPT1Q67L	This study
pNS1559	CEN Ypt31-GTP	pRS315-YPT31Q72L	This study

Plasmid construction

Plasmid for expression of mCherry-Ypt1 was constructed by sub-cloning mCherry to replace yEVenus in pNS1430. pNS220 (pRS316-Ypt31) was described in (Jedd et al., 1997). pNS939 (pRS317-Ypt31) was made by subcloning the Ypt31 containing ClaI-XbaI fragment from pRS316-Ypt31 into pRS317. pNS939 (pRS317-yEGFP-Ypt31) was made as follows: first, PciI site was removed from the vector backbone and introduced upstream of Ypt31 by sitedirected mutagenesis, then yEGFP was cloned in frame with Ypt31 using PciI. pNS993 was previously described(Liang et al., 2007). pNS1556 (Ypt1Q67L in a 2μ LEU2) was made by site-directed mutagenesis of pNS993. pNS1557 (pFA6a-GFP-HygR) was made by replacing G418R cassette with HygR cassette using BgIII and SacI sites. pNS1533 (pKT-yEGFP-NatR) was made by replacing G418R cassette with NatR cassette using BgIII and SacI sites. The CEN plasmids pNS1558 and pNS1559 were constructed by sub-cloning Ypt1Q67L and Ypt31Q72L from the 2μ plasmids pNS1556 and pNS782, respectively, using the Sal1 and Xba1 sites of pNS245 (*CEN Leu2*).

Yeast strain construction and growth

Golgi proteins were tagged on the chromosome at their C-termini with mRFP, GFP, mCherry, or yEGFP using a standard technique (Wach et al., 1997) using appropriate plasmids listed in the plasmid table. All GFP-tagged strains were checked to ensure that the tagged product is stable by using immuno-blot analysis and mouse monoclonal anti-GFP antibodies (Roche Diagnostics).

Media preparation and yeast culture growth were done as previously described (Segev and Botstein, 1987).

Supplemental References

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