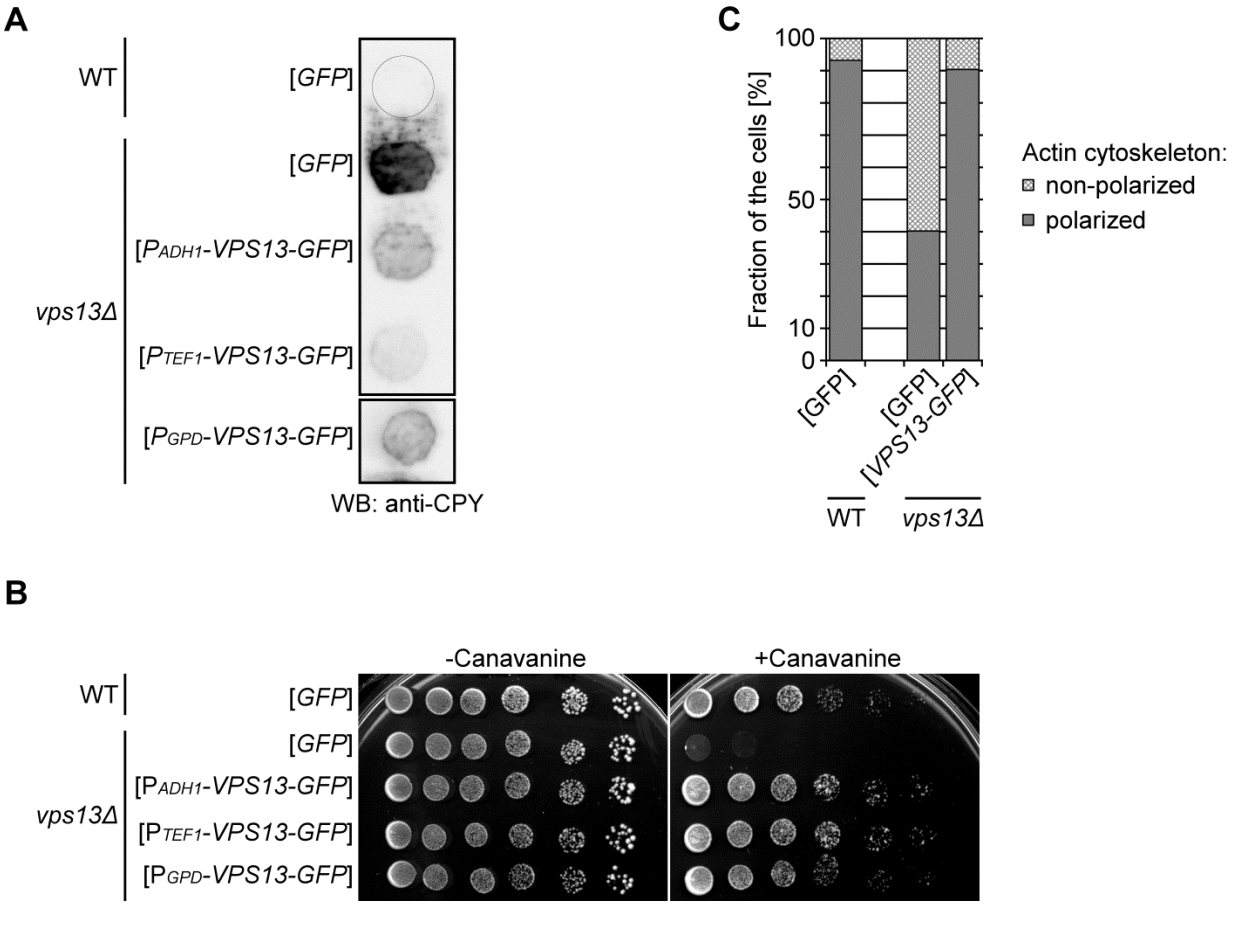
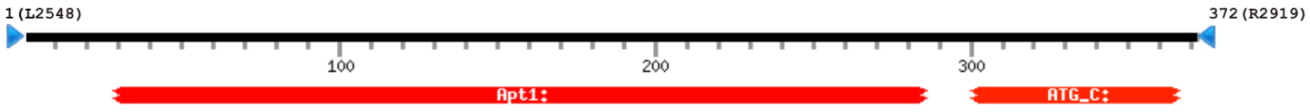


Figure S1. ***VPS13-GFP*** **under the transcriptional control of** ***ADH1*****,** ***TEF1*** **or** ***GPD*** **promoter complements transport defects and improves actin cytoskeleton organization in** ***vps13Δ*****. A**. Secretion of CPY. Yeast cultures were spotted on nitrocellulose membrane plated on SD-leu medium, incubated for 14-16 h and washed off. The level of secreted CPY was estimated using anti-CPY antibody. **B**. Sensitivity of yeast strains to canavanine. Serial dilutions of wild type and *vps13Δ* strains bearing indicated plasmids were spotted on synthetic minimal medium supplemented with (3 μg ml^{-1}) or without canavanine. **C**. Graphic representation of actin cytoskeleton organization in *vps13Δ* cells. The *vps13Δ* cells expressing P_{TEF1}-*VPS13-GFP* or bearing empty vector was grown to log-phase, fixed, stained using labeled phalloidine and observed by fluorescence microscopy. Wild-type cells bearing empty vector were used as a control. At least 100 cells were observed and the percentage of cells with well-polarized and non-polarized actin cytoskeleton is indicated.



Query Vps13 (seq=LYKLKTASAT...SVTQDLEFQR Len=372 Neff=9.4 Nseqs=141)
Parameters score SS:yes search:local realign with MAP:no

Hit		Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
PF10351	Apt1: Golgi-body loca	99.7	5.9E-15	3.8E-19	141.2	25.1	222	27-283	164-477 (478)
PF09333	ATG_C: Autophagy-rela	97.0	0.00077	4.9E-08	48.2	6.5	64	299-363	21-84 (96)

>PF10351 **Apt1 domain**: Golgi-body localisation protein domain. This domain is found in fungi, metazoans and plants. These include FMP27 and "maize" protein APT1 and *Arabidopsis* homologues SABRE and KIP. APT1 is required for pollen tube growth. It is a Golgi-localised protein and appears to regulate vesicular trafficking. SABRE and KIP are APT1 homologues and they are involved in the elongation of root cortex cells and pollen tubes respectively.

Probab=99.68 E-value=5.9e-15 Score=141.23 Aligned_cols=222 Identities=14% Similarity=0.176 Sum_probs=0.0

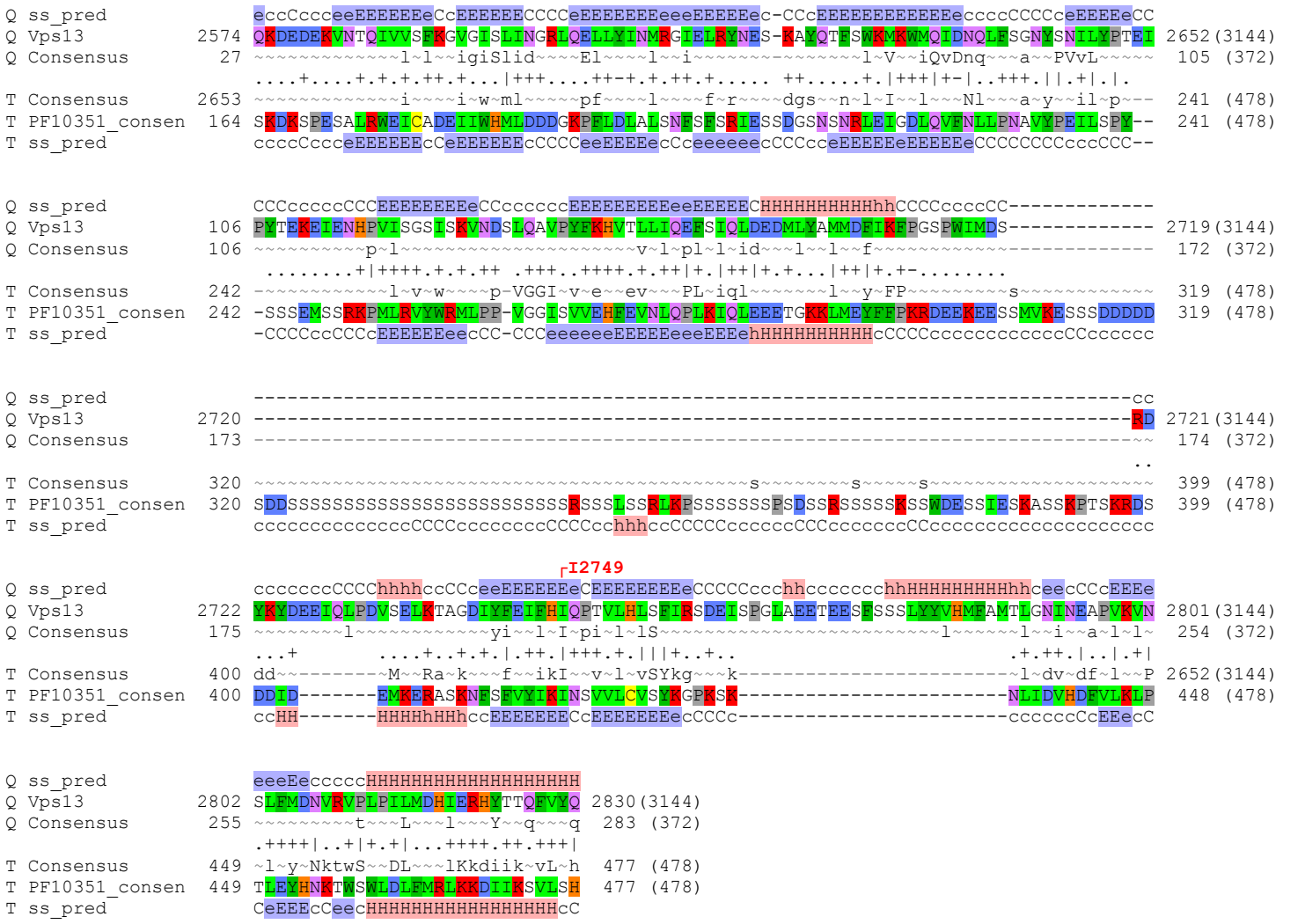


Figure S2. **Prediction of the presence of APT1 domain in yeast Vps13 protein**. Analysis was performed using HHpred package (Söding et al., 2005; https://toolkit.tuebingen.mpg.de/hhpred) with standard parameters and PfamA (ftp://ftp.ebi.ac.uk/pub/databases/Pfam/) ver. 04-Jul-16 as a template HMM database. ***Upper panel***, graphical representation of predicted domain structure**.** ***Lower panel***, an alignment with secondary structure prediction of Vps13 region L2548-R2919 to a consensus sequence for the APT1 domain (PF10351). Additionaly, the position of isoleucine 2749 in Vps13 is indicated. Abbreviations: Q, query sequence; T, template sequence; ss_pred, secondary structure as predicted by PSIPRED (upper case letters: high probability, lower case letters: low probability; C, coil; E, β-sheet; H, helix). Symbols used in consensus line: "=", very bad match (column score below -1.5); "-", bad match (score between -1.5 and -0.5); ".", neutral match (score between -0.5 and +0.5); "+",good match (score between +0.5 and +1.5); "|", very good match (score above +1.5).

Söding J, Biegert A, Lupas AN (2005) The HHpred interactive server for protein homology detection and structure prediction. *Nucleic Acids Res* 33 (suppl 2), W244-W248.

Table S1. Mutant *vps13-I2749R* is defective in sporulation					
Genotype	**Independent diploid**	**Transformant**	**Cells**	**Tetrads**	**% of tetrads**
vps13Δ/vps13Δ [—]	I	1	259	0	0
		2	306	0	0
		3	156	0	0
	II	1	321	0	0
		2	546	0	0
		3	384	0	0
vps13Δ/vps13Δ [*VPS13*]	I	1	320	144	45
		2	256	70	27
		3	166	43	26
	II	1	347	147	42
		2	359	151	42
		3	335	129	39
vps13Δ/vps13Δ [*vps13-I2749R*]	I	1	281	0	0
		2	198	0	0
		3	215	0	0
	II	1	373	0	0
		2	576	0	0
		3	457	0	0

Diploid strain from the cross of JK197-7B (*MAT***a** *vps13Δ::URA3 ura3-52 his3Δ200 met15Δ0 leu2,3-112*) with JK197-8C (*MATα vps13Δ::URA3 ura3-52 lys2-801 trp1-1 leu2,3-112*) was obtained twice. Each diploid was transformed with empty vector [—] or plasmids bearing *VPS13* or *vps13-I2749R* allele. Three independent transformants were sporulated for one week at 28ºC. Full tetrads were counted twice for each culture.

Table S2. Mutation *vps13-I2749R* is synthetically lethal with mutation *mmm1Δ*		
Strain	**Transformant**	**Full tetrads**
vps13Δ/VPS13 mmm1Δ/MMM1 [─]	1	3 PD
	2	1 PD
	3	3 PD
vps13Δ/VPS13 mmm1Δ/MMM1 [*VPS13*]	1	4 PD + 3 TT
	2	3 PD + 2 TT
	3	3 PD
vps13Δ/VPS13 mmm1Δ/MMM1 [*vps13-I2749R*]	1	1 PD
	2	6 PD
	3	5 PD

Diploid strain was obtained by crossing WR11 (*MAT*α *LAS17-7Ala-mRFP::HIS3 ura3-52 leu2,3-112 lys2-801 his3Δ200 trp1-1 vps13Δ::URA3*) with BY4741 *mmm1Δ* (*MAT***a** *ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 mmm1Δ::KanMX*). The diploid was transformed with empty vector [─] or plasmid bearing wild-type *VPS13* or mutated *vps13-I2749R* allele. Three independent transformants of each type were sporulated. Full tetrads were dissected and growth of spore clones was analyzed on SC-ura and YPD+G418 media to follow *vps13Δ::URA3* and *mmm1Δ::KanMX* presence. PD, parental ditype; TT, tetratype.