## Supplementary figure legends

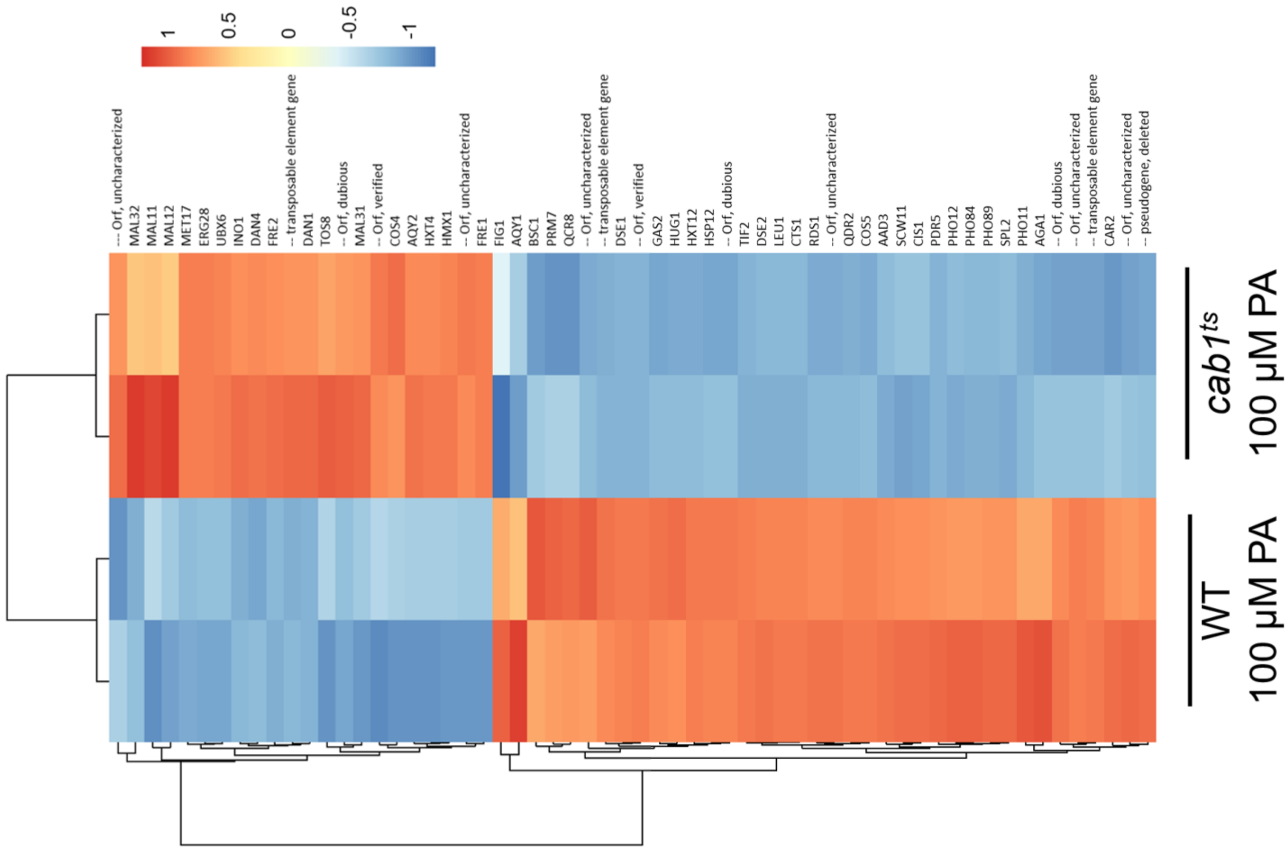

**Fig. S1. Changes in global yeast gene transcription between WT and cab1$^{ts}$ cells.** Both strains were grown in minimal media supplemented with 100 µM PA. The two independent replicates of WT cell mRNA are represented by the left two columns, and the two replicates of *cab1*$^{ts}$ cell mRNA are represented by the right two columns. Genes were selected as significantly upregulated or downregulated between the WT and *cab1*$^{ts}$ strains if q-values were less than 0.05 for the $\log_2$ change between the two samples. 22

genes were found to be significantly upregulated and 38 genes significantly downregulated in *cab1*$^{ts}$ cells compared to wild type cells. It was found that globally, maltose fermentation (*MAL11*, *MAL12*, *MAL31*, *MAL32*) was upregulated in the *cab1*$^{ts}$ mutant. Additionally, there was downregulation of phosphate import into the *cab1*$^{ts}$ cell (*PHO11*, *PHO12*, *PHO84*, *PHO89*), modulation of amino acid anabolic and catabolic pathways (*MET17*, *LEU1*, *CAR2*), and systematic downregulation of genes of genes transcriptionally regulated by factors involved in pleiotropic drug resistance (*CIS1*, *PDR5*, regulated by transcription factors Pdr1p, Yrr1p).

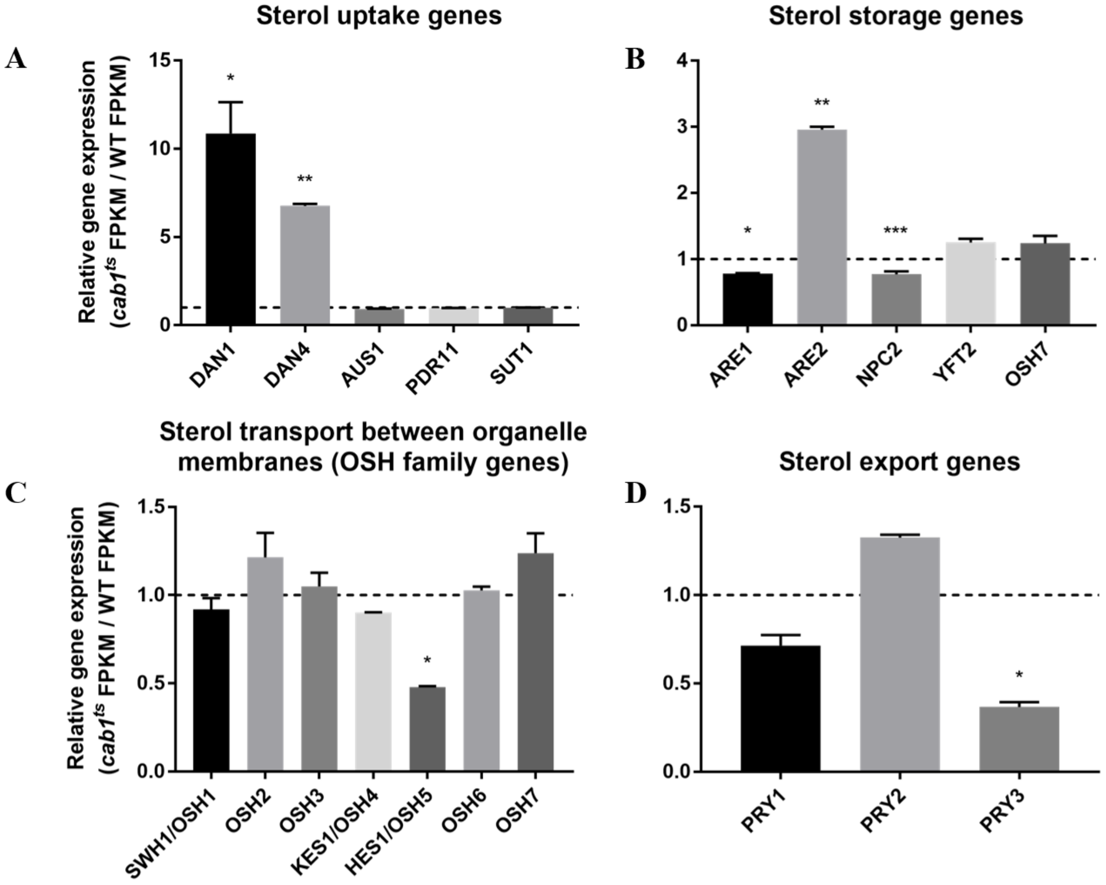

**Fig. S2. Effect of altered pantothenate phosphorylation on genes regulating sterol trafficking.** Fold change of gene expression levels (FPKM) between wild type and $cab1^{ts}$ strains (n=2) grown in minimal medium supplemented with 100 µM PA. For each gene, the level in the wild type was set to 1 to normalize the data. The bars show relative fold change of $cab1^{ts}$ cells to wild type for each gene. A) Genes regulating sterol uptake. *p-value 0.0198, **p-value 0.0052. B) Genes regulating sterol storage. *p-value 0.0266, **p-value 0.0189, ***p-value 0.0482. C) Genes regulating sterol transport between organelle membranes. *p-value 0.0195. D) Genes regulating exogenous sterol uptake. *p-value 0.0085.