

Supplementary figures

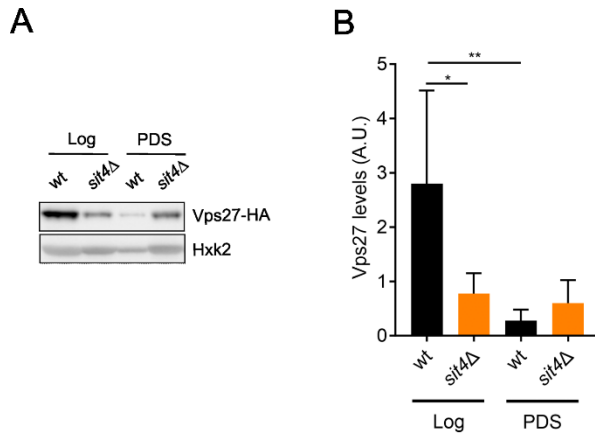


Figure S1 – *SIT4* deletion decreases Vps27 levels at the Log phase. **(A)** Cells harbouring the plasmid YCpHAC33-*Prom-Vps27-3xHA* were grown to late exponential (Log) and post-diauxic shift (PDS) phases and Vps27 levels on total protein extracts were assessed by immunodetection. Hxk2 was used as a loading control. A representative blot of at least three independent experiments is shown. **(B)** Quantification of Vps27 (normalized to Hxk2). Values are the mean \pm SD; * $p \leq 0.05$; ** $p \leq 0.01$; one-way ANOVA.

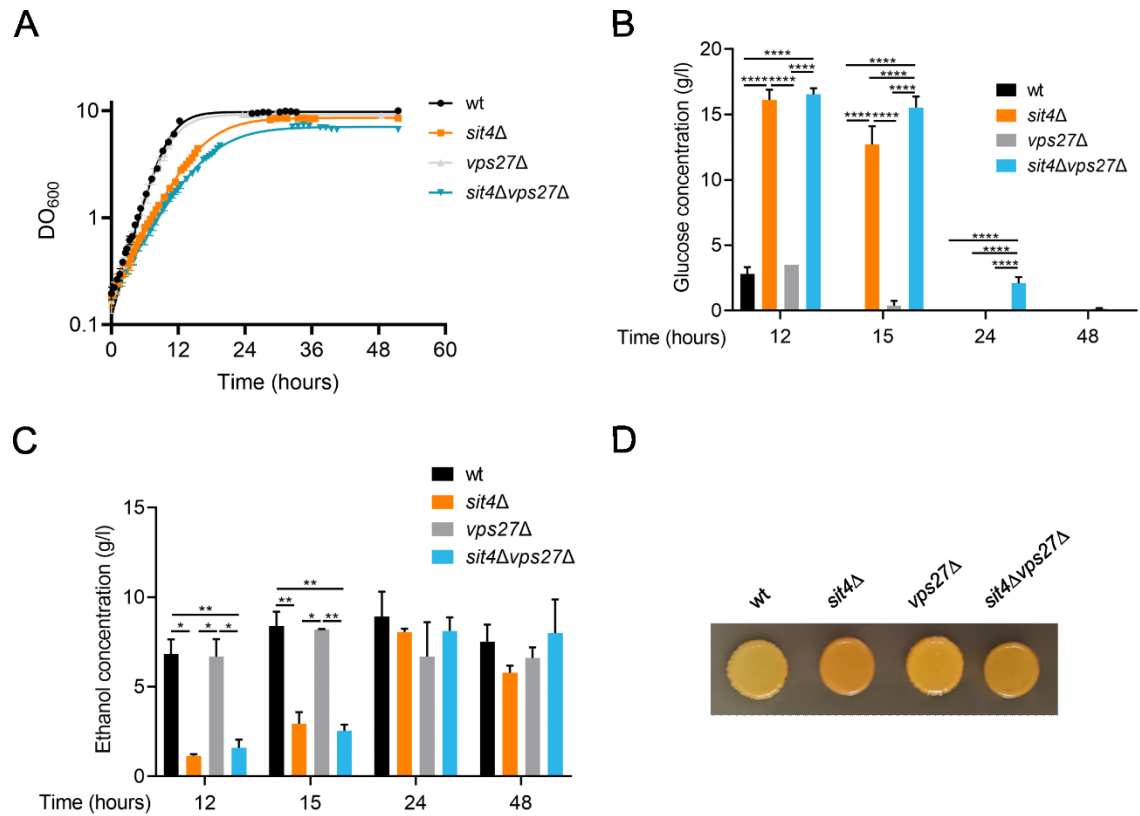


Figure S2 – Growth and metabolic profile of indicated strains. **(A)** Cells were grown until OD_{600nm}=0.2 (time 0) in SC media and the OD_{600nm} was monitored over time. Data are the mean ± SD ($n = 2$). **(B)** glucose and **(C)** ethanol levels were quantified at 12, 15, 24, and 48 h. Data are the mean ± SD ($n \geq 3$); * $p \leq 0.05$; ** $p \leq 0.01$; **** $p \leq 0.0001$; one-way ANOVA. **(D)** Yeast colonies were exposed to iodine vapor to qualitatively evaluate the glycogen content. A representative figure is shown ($n = 2$).

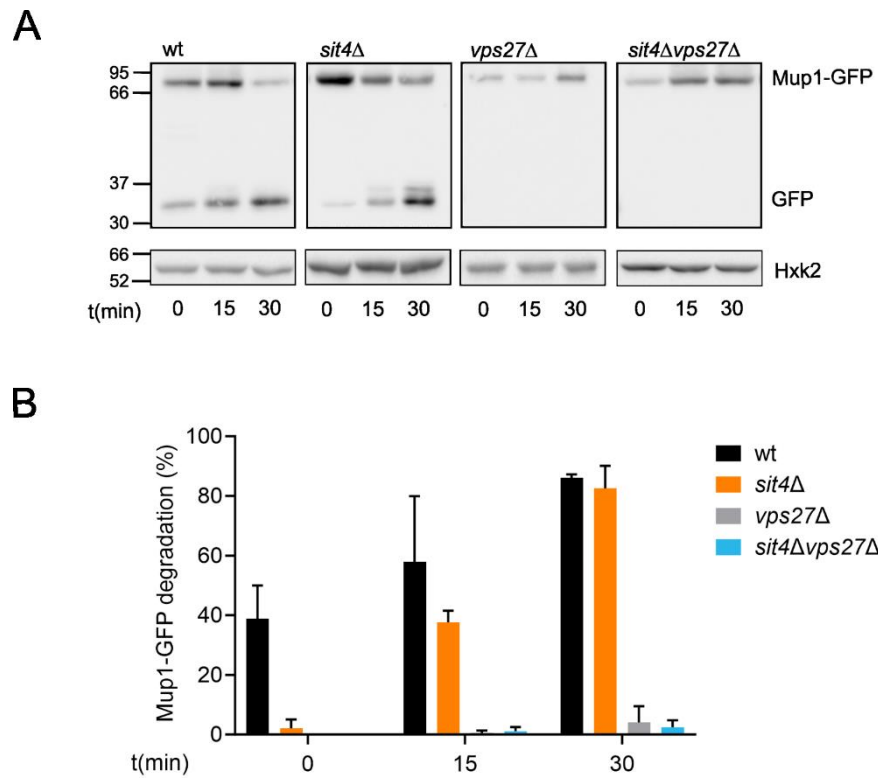


Figure S3 – Methionine increases Mup1-GFP degradation in *sit4Δ* cells. **(A)** Cells expressing pRS416-*MUP1-GFP* were grown in MM medium to the Log phase (0 min) and 38 mg L⁻¹ of methionine was added as indicated. Mup1-GFP and GFP were detected by immunoblotting. Hxk2 was used as a loading control. **(B)** The induction of the MVB pathway (ratio between free GFP and the sum of GFP and Mup1-GFP) in response to methionine was evaluated. Values are the mean ± SD (*n* = 2).

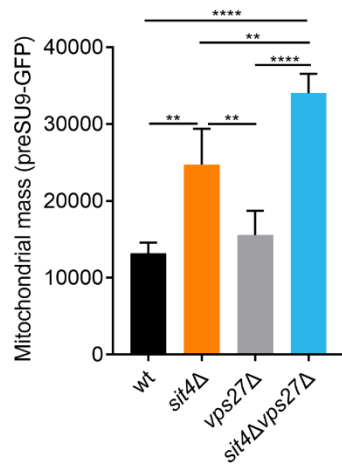


Figure S4 – Mitochondrial mass increases in *sit4Δ* and *sit4Δvps27Δ* cells. Cells expressing a fusion protein containing GFP with a mitochondrial presequence (pVT100U-*preSU9-GFP*), were grown in SC medium to Log phase. GFP intensity was quantified by flow cytometry and used as an indicator of mitochondrial mass. Values are the mean \pm SD ($n = 4$); ** $p \leq 0.01$; **** $p \leq 0.0001$; one-way ANOVA.

Original images

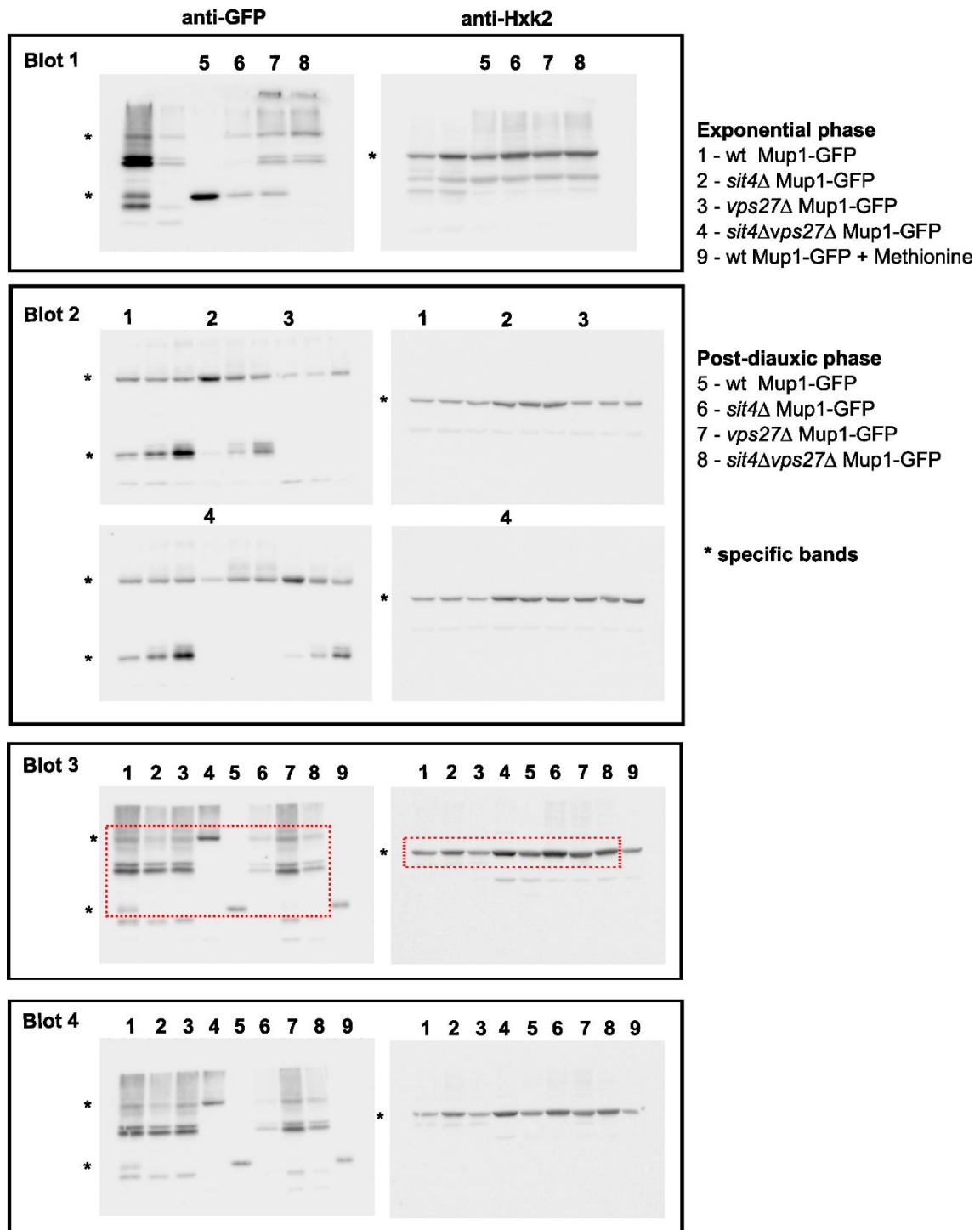


Figure S5 - Original images of Western blots used for data quantification displayed in Figures 3A and 3B. Red rectangles are used to highlight the images displayed in Figure 3A.

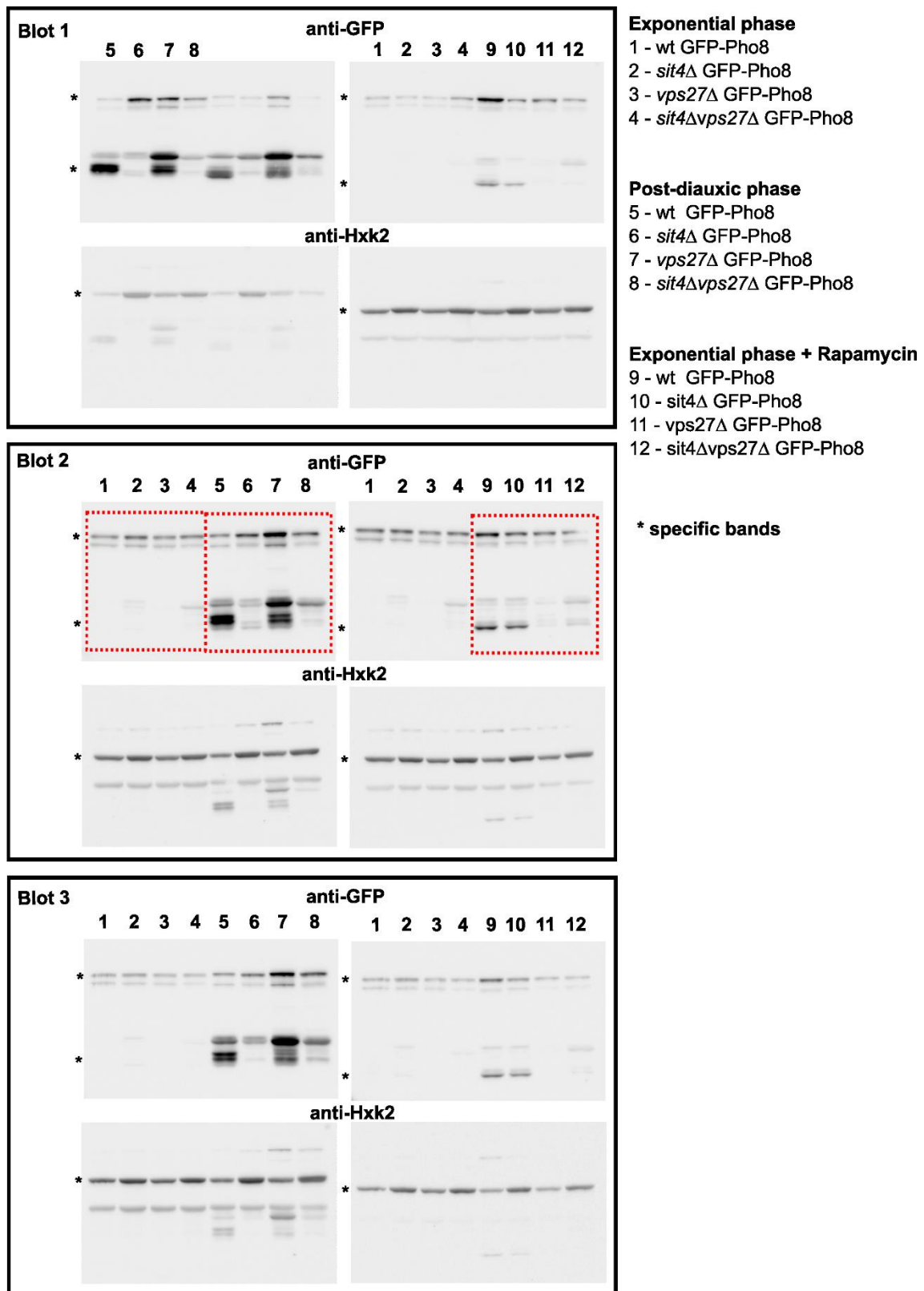


Figure S6 - Original images of Western blots used for data quantification displayed in Figures 3C and 3D. Red rectangles are used to highlight the images displayed in Figure 3C.

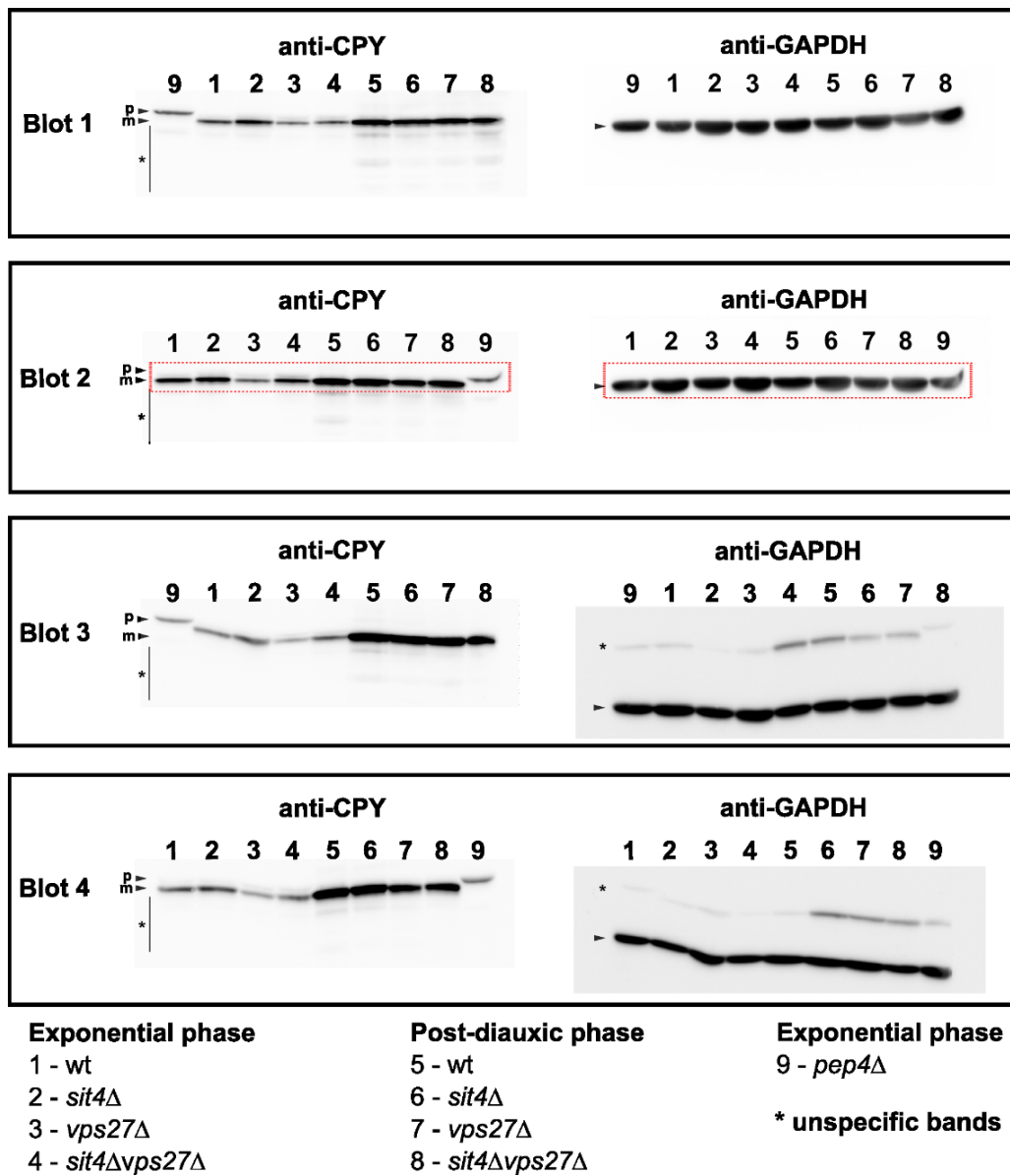


Figure S7 - Original images of Western blots used for data quantification displayed in Figures 4A and 4B. Red rectangles highlight the images displayed in Figure 4A.

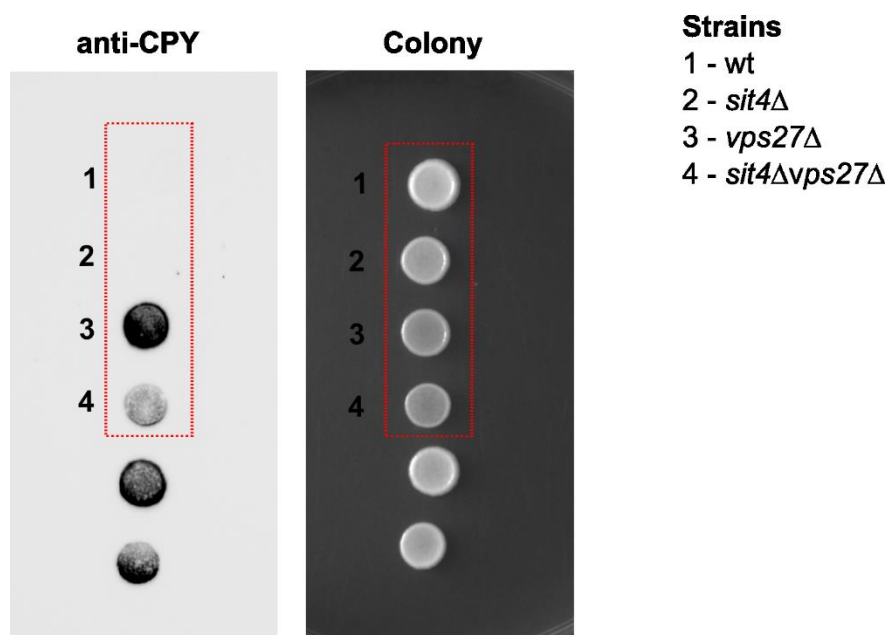


Figure S8 – Uncropped and unadjusted original image of the colony immunoblot displayed in Figure 4C (highlighted by the red rectangles).

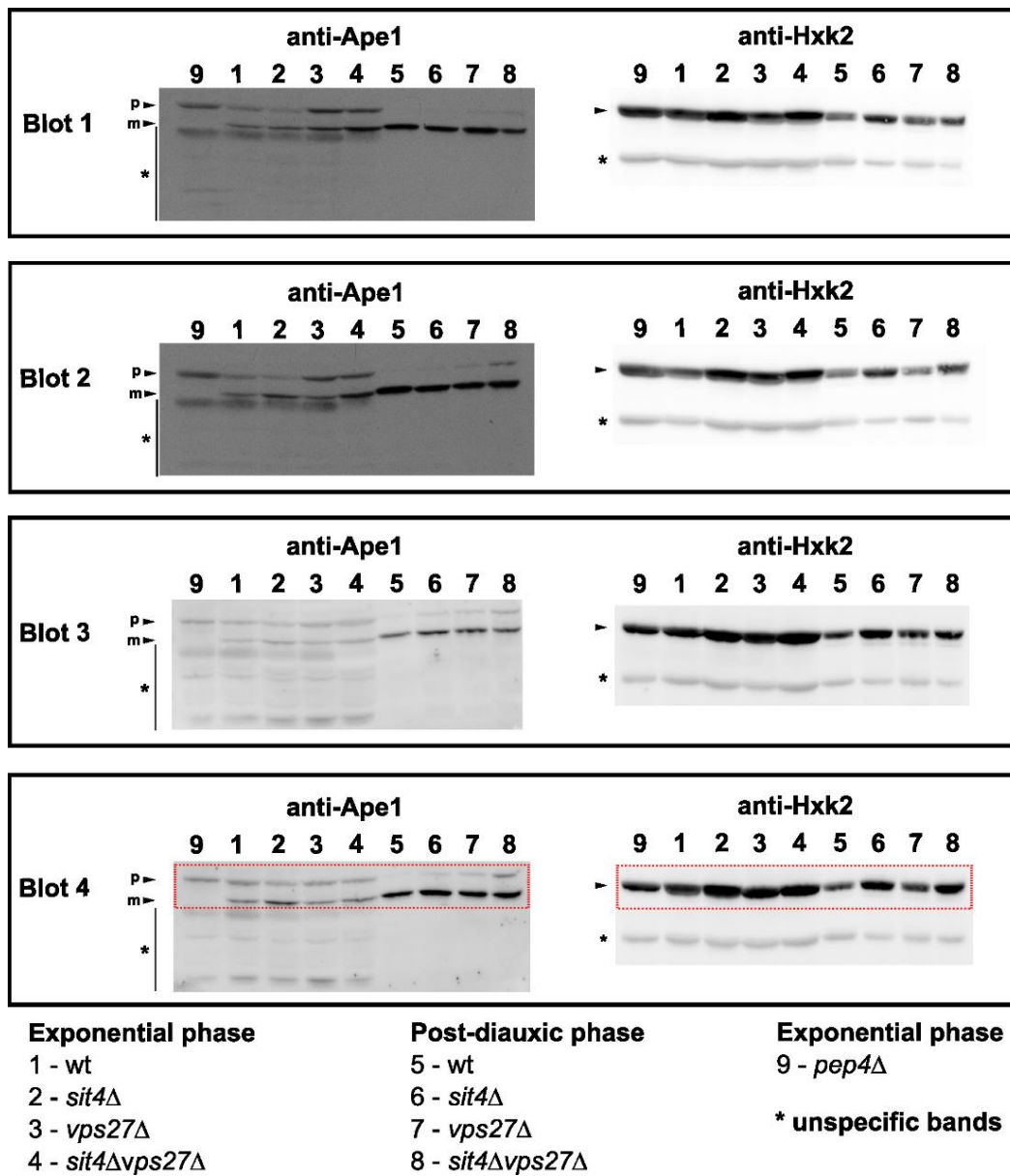


Figure S9 - Original images of the Western blots used for the data quantification displayed in Figures 5A and 5B. Red rectangles highlight the images displayed in Figure 5A.

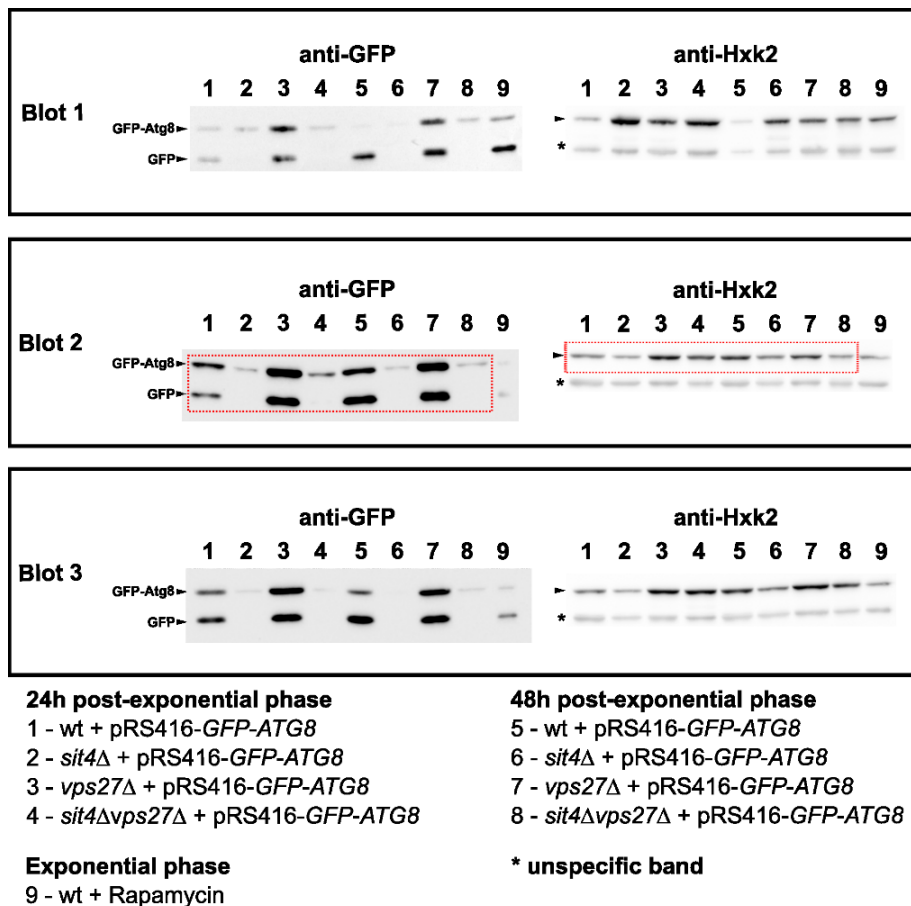


Figure S10 - Original images of Western blots used for the data quantification displayed in Figures 5C and 5D. Red rectangles are used to highlight the images displayed in Figure 5C.

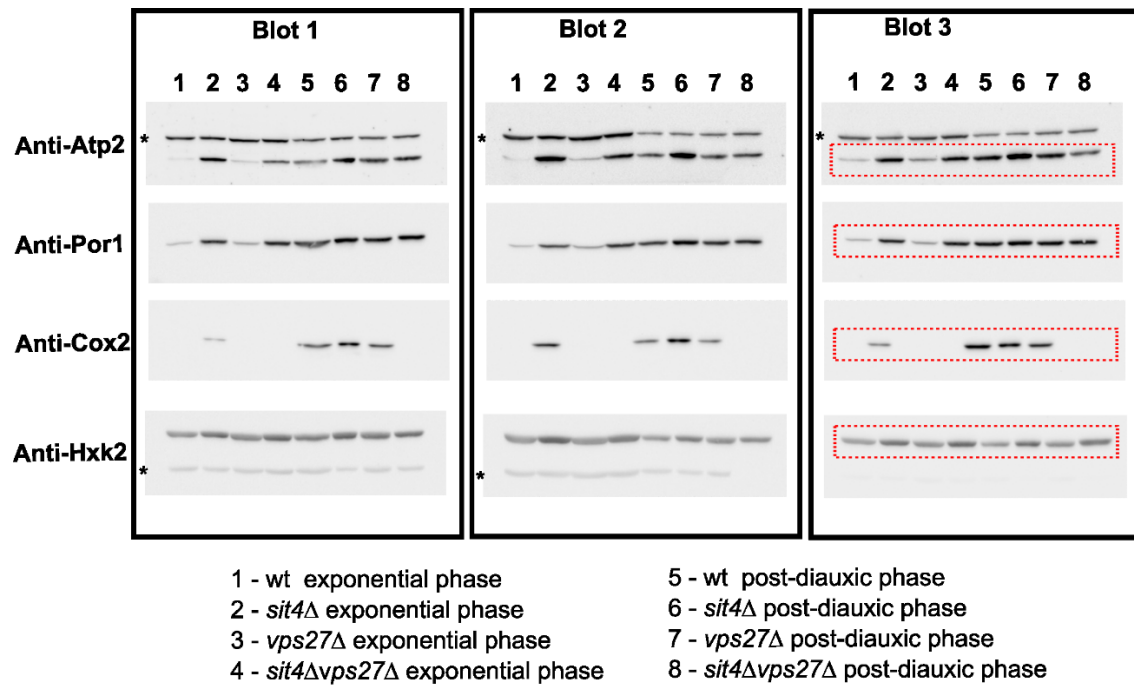


Figure S11- Original images of Western blots used for the data quantification displayed in Figures 8B-8E. Red rectangles are used to highlight the images displayed in Figures 8C-8E.

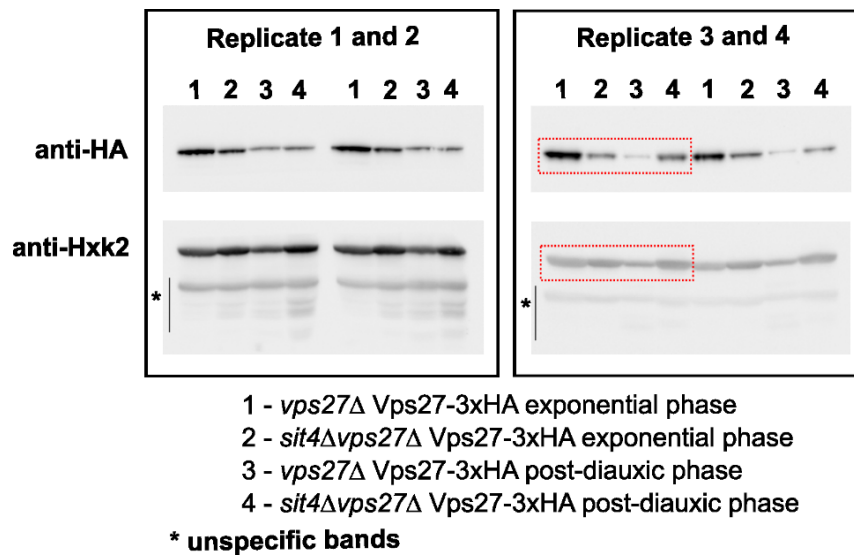


Figure S12 - Original images of Western blots used for the data quantification displayed in Figures S1A and S1B. Red rectangles are used to highlight the images displayed in Figure S1A.

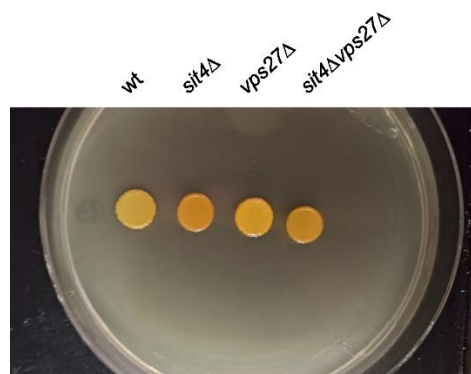


Figure S13 - Uncropped and unadjusted original image of the yeast colonies exposed to iodine vapor to qualitatively evaluate the glycogen content displayed in Figure S2D.