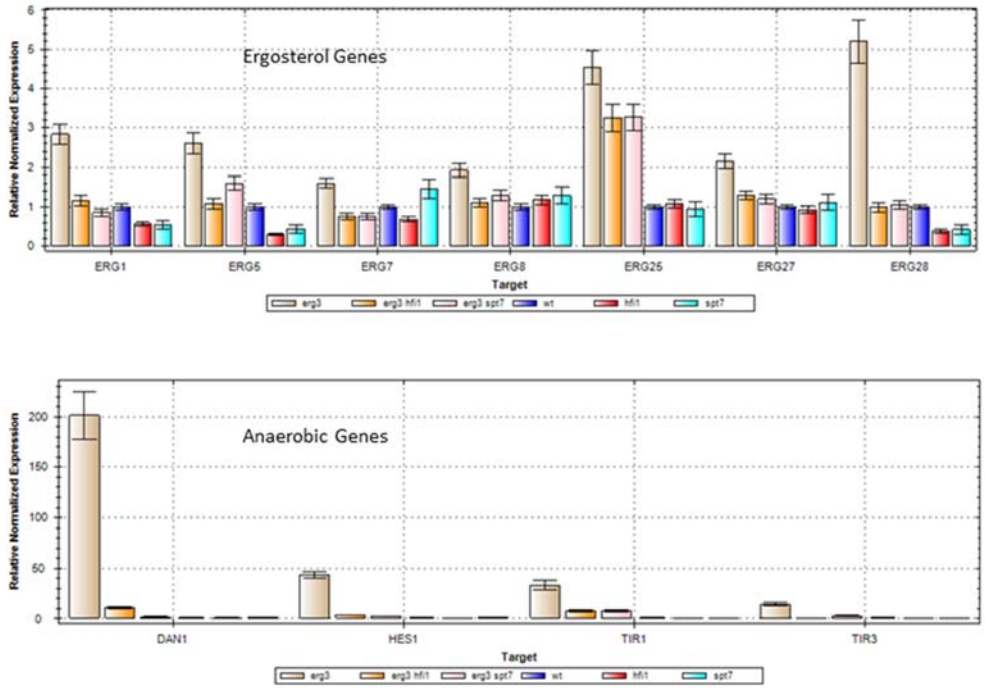
Supplemental Materials

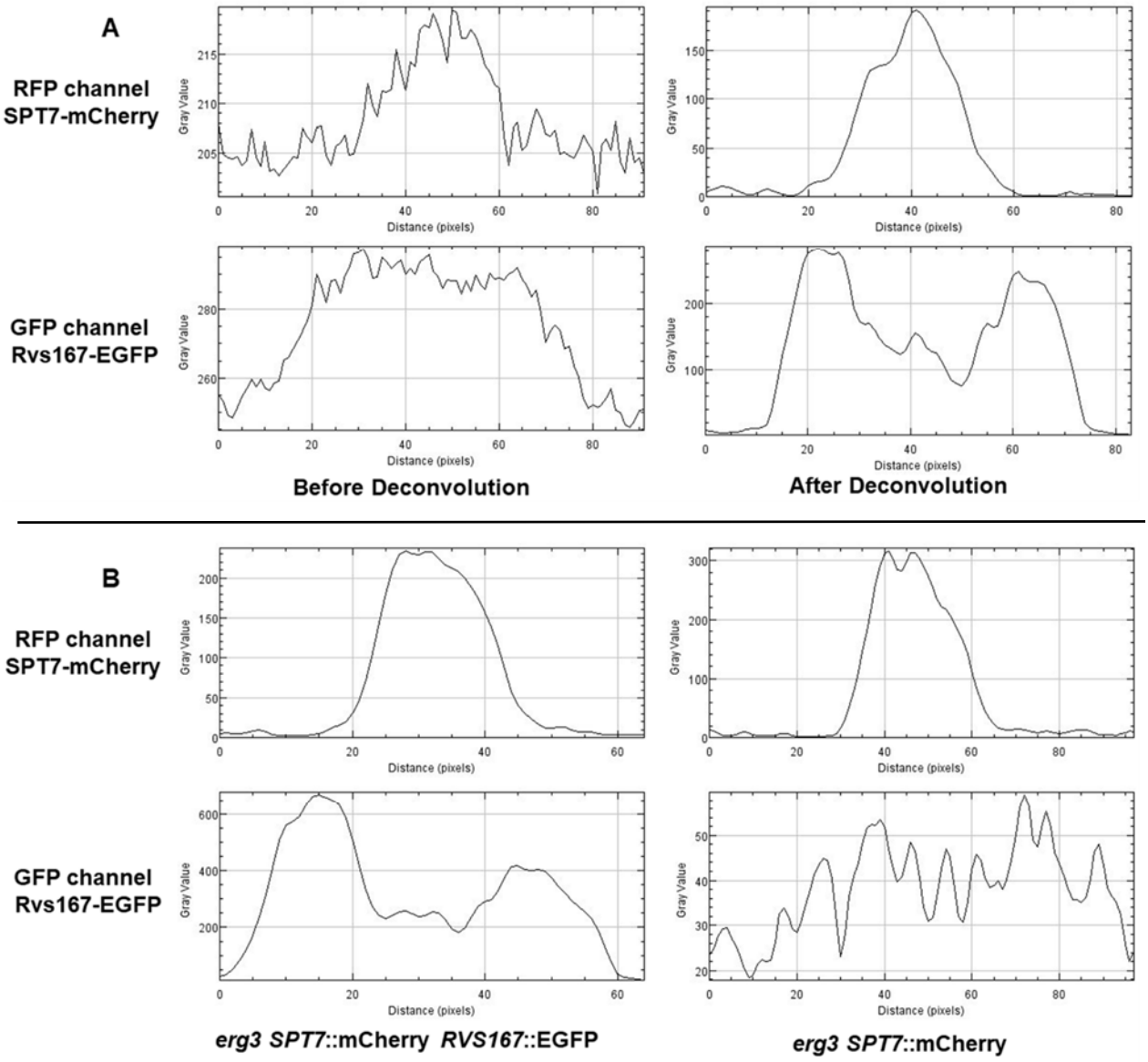
Molecular Biology of the Cell

Dewhurst-Maridor et al.

Supplementary



Supplementary Figure 1. qPCR results of mRNAS from ergosterol biosynthesis and anaerobic genes in wild type, *erg3* and double mutants with *spt7*Δ and *hfi1*Δ. The effect of the SAGA complex mutations on the *erg3*-dependent gene induction is prevalent, but slightly less important for the *ERG25* mRNA. In some cases the SAGA mutations affect mRNA levels in wild type cells, but in other cases not. The error bars represent standard error on the mean.



Supplementary Figure 2. Examples for deconvolution and determination of background in the GFP channel. A. Images of the *erg3 SPT7*::mCherry *RVS167*::EGFP strain focused on the mCherry signal were analyzed using Cell profiler and the intensity of the signal along a line going through the cell and nucleus was plotted before and after deconvolution for the mCherry and EGFP signals. Deconvolution clearly removed noise from the signal and improved the possibilities for quantitation. B. Deconvoluted images focused on the mCherry signal were obtained from *erg3 SPT7*::mCherry *RVS167*::EGFP and *erg3 SPT7*::mCherry strains and analyzed as in A. The background signal due to autofluorescence or other technical issues was at approximately 40 on the gray value scale. The EGFP signal in the nucleus was over 200 on the gray value scale, approximately 5 times above background.

Supplementary Table 1. Fold enrichment of transcripts in *erg3* compared to wild type

Gene	qPCR	Microarray	Expression/Function
HES1	43.9	24.9	Anaerobic gene/Sterol binding
DAN1	176.3	190.5	Anaerobic gene
ERG28	5.8	4.5	Ergosterol biosynthesis
ERG25	3.5	1.6	Ergosterol biosynthesis
HSP42	2.0	2.6	Stress response
ARG3	4.3	8	Arginine biosynthesis
LYS20	2.3	0.8	Lysine biosynthesis
YSR3	3.2	4.5	Sphingolipid degradation

Supplementary Table 2. Excel table containing the ChIP seq recoveries from all yeast promotors from untagged wild type and *erg3* strains, as well as HFI1-TAP and SPT7-TAP tagged strains. The data is sorted (highest to lowest) on the ratio of promotor recovery using the SPT7-TAP in the *erg3*/wild type strains.

Supplementary Table 3. Excel table containing the results from the semi-quantitative proteomics experiments including the ratio of proteins recoveries with the SPT7-TAP tagged SAGA complex from *erg3* over wild type. Sheet 1 shows the intensities of proteins recoveries and calculations. Sheet 2 summarizes experiment 1. Sheet 3 summarizes experiment 2 and sheet 4 combines the enrichments from the two experiments. The genes investigated further are highlighted in red (sheet 4).

Supplementary Table 4. Excel table with different sheets containing the strains, plasmids, qPCR oligos and cloning oligos used in this study.