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Supplementary figures

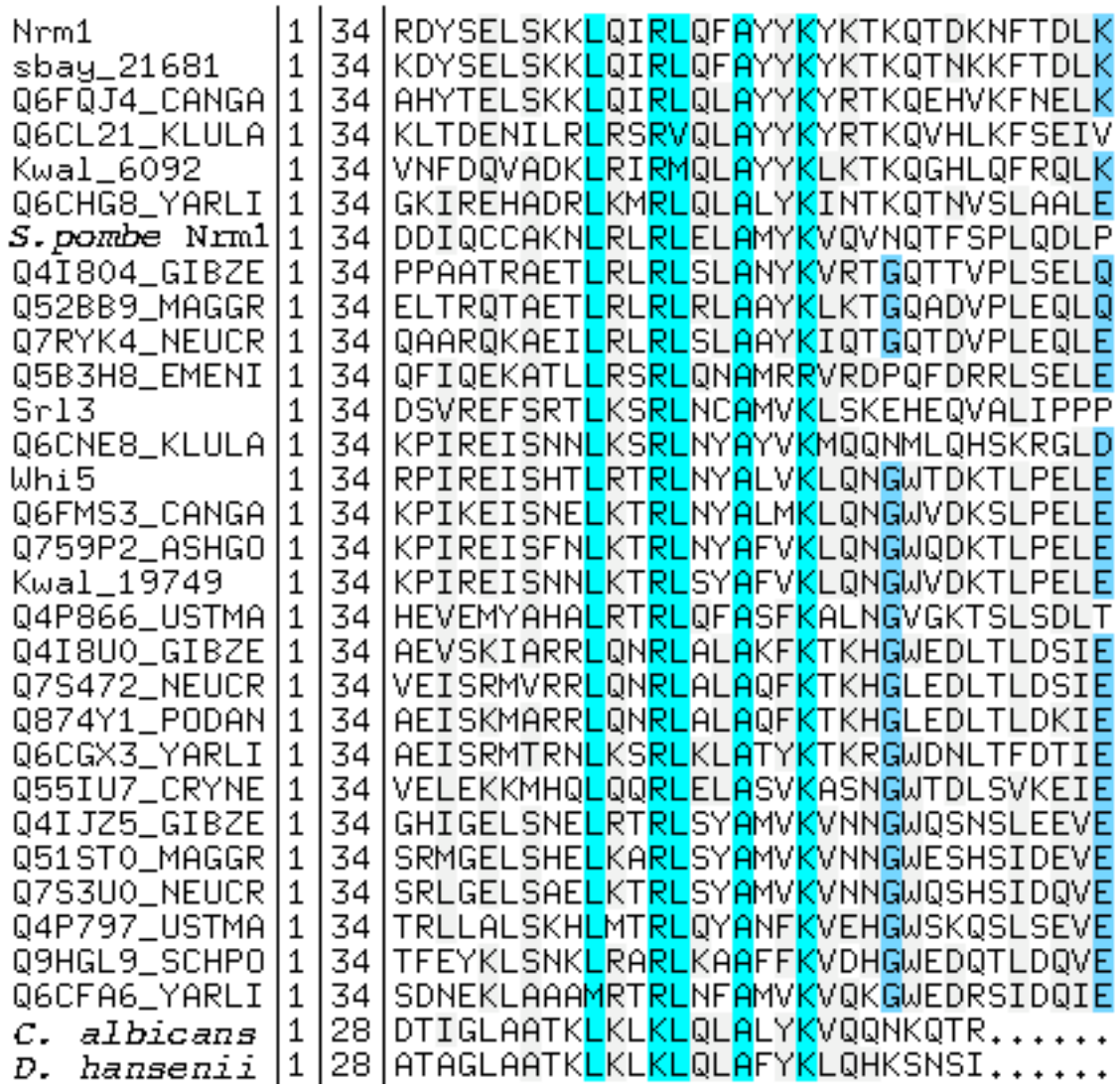

Fig. S1. Identification of Whi5 / Nrm1 homologs. In order to identify potential Whi5 homologs in the *C. albicans* genome, we used the generalized profile method (Bucher *et al.*, 1996), starting from a multiple alignment of *S. cerevisiae* Whi5 and its obvious homologs from other yeast species, including *S. pombe* Nrm1. After five cycles of iterative profile refinement, a conserved sub-region of the Whi5 family was identified to be present in several fungal proteins without overt sequence similarity to Whi5. The full sequences of the proteins aligned in this figure, together with additional *Candida spp.* homologous sequences, can be found in Table S4.

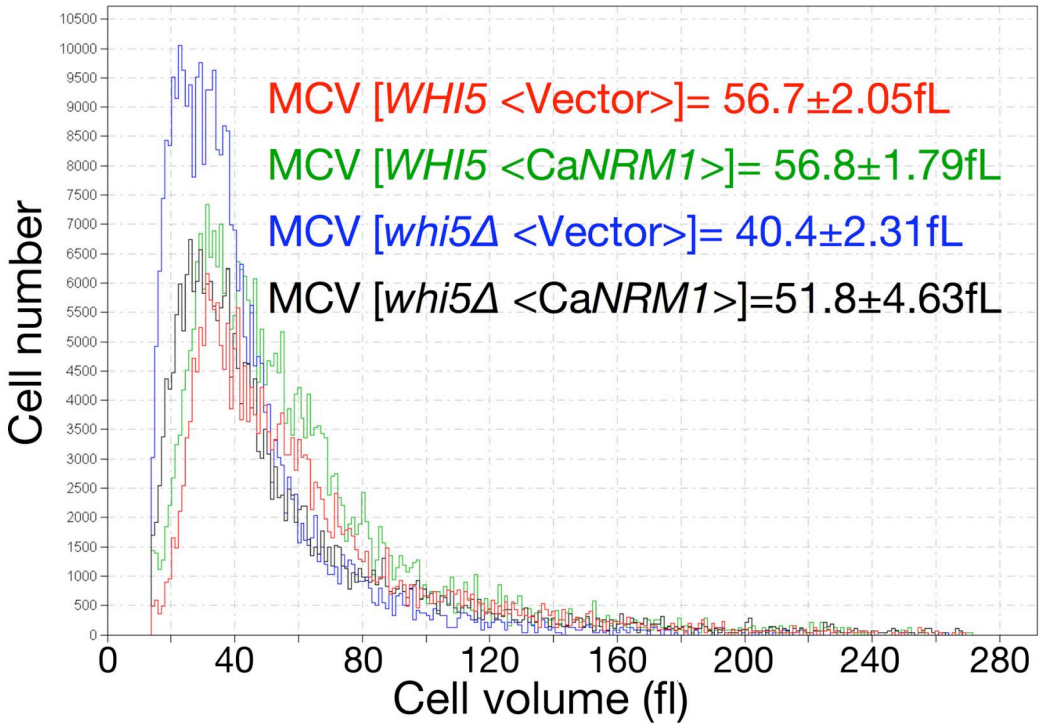

Fig. S2. CaNrm1 can complement the reduced cell size phenotype of *S. cerevisiae whi5Δ*. The *S. cerevisiae whi5Δ* strain (Y01859) and its isogenic wild-type (BY4741) were transformed with either the Ca*NRM1*-carrying plasmid KB1879 or the B2201 vector plasmid. Cells were grown to log phase, and tested as described in *Methods*. Representative curves of a single experiment are shown; the Mean Cell Volume (MCV) data represent the average +/- SD of 6 experiments.

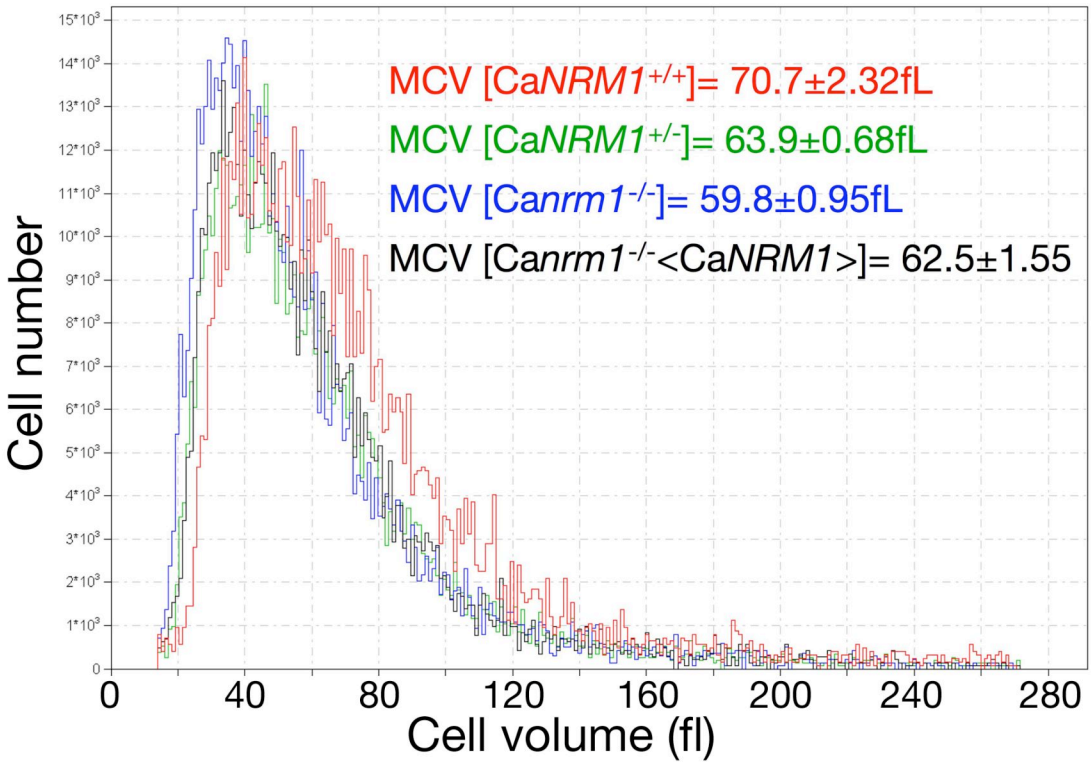

Fig. S3. CaNrm1 affects cell size in *C. albicans*. Cell size analysis of the Ca*nrm1*$^{-/-}$ mutant (KC356) vs. heterozygote (KY352), wild-type (CAI4 <Ca*URA3*>) and reintegrant (KC436). Cells were grown to log phase, and tested as described in *Methods*. Representative curves of a single experiment are shown; the Mean Cell Volume (MCV) data represent the average +/- SD of 6 experiments.

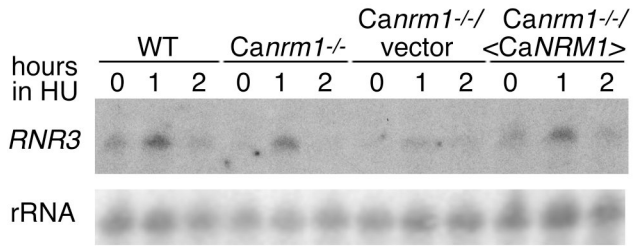

Fig. S4. Effect of Ca*NRM1* deletion and HU (200 mM) on *RNR3* expression (orf19.5845). Cells were exposed to 200 mM HU for the indicated amounts of time. Northern blotting was performed to assess the induction of *RNR3*. rRNA hybridization served as loading control.The low signal level precluded quantitation by phosphorimager. The strains are indicated as follows: + = CAI4 (wild-type); Δ = KC392 (Ca*nrm1*$^{-/-}$); Δ/**v** is KC392 transformed with vector plasmid pBES116; and Δ/+ is KC392 transformed with the Ca*NRM1* plasmid KB1993.

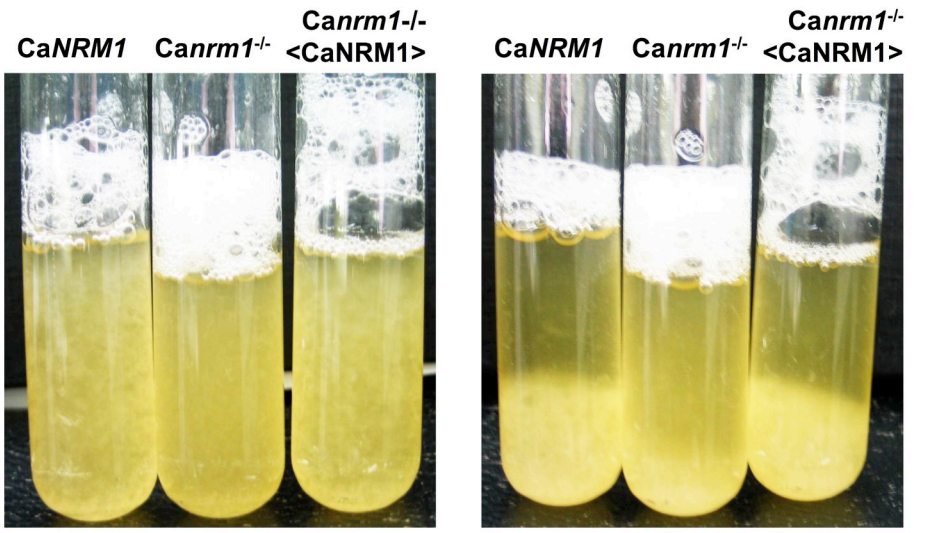

Fig. S5. Sedimentation. The indicated strains were grown overnight in YPD, then diluted 1:10 in YPD + 10% serum and grown for 2 h at 30°C. The test tubes were photographed right after retrieval from the roller drum and vigorous vortexing, or after having been left standing 5 min on the bench. The strains used are KC403, KC435, KC436 (all Ura+).

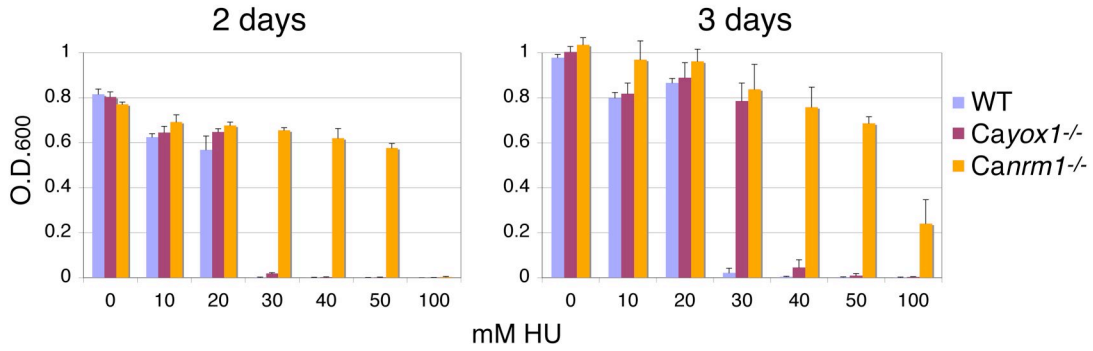

Fig. S6. Effect of Ca*YOX1* deletion on HU resistance. The Ca*YOX1* deletion mutant and its isogenic wild-type strain, as well as the Ca*NRM1* deletion strains for comparison, were grown in quadruplicate at the indicated concentrations of HU at 30°C. O. D. was measured after 2 and 3 days, as indicated.