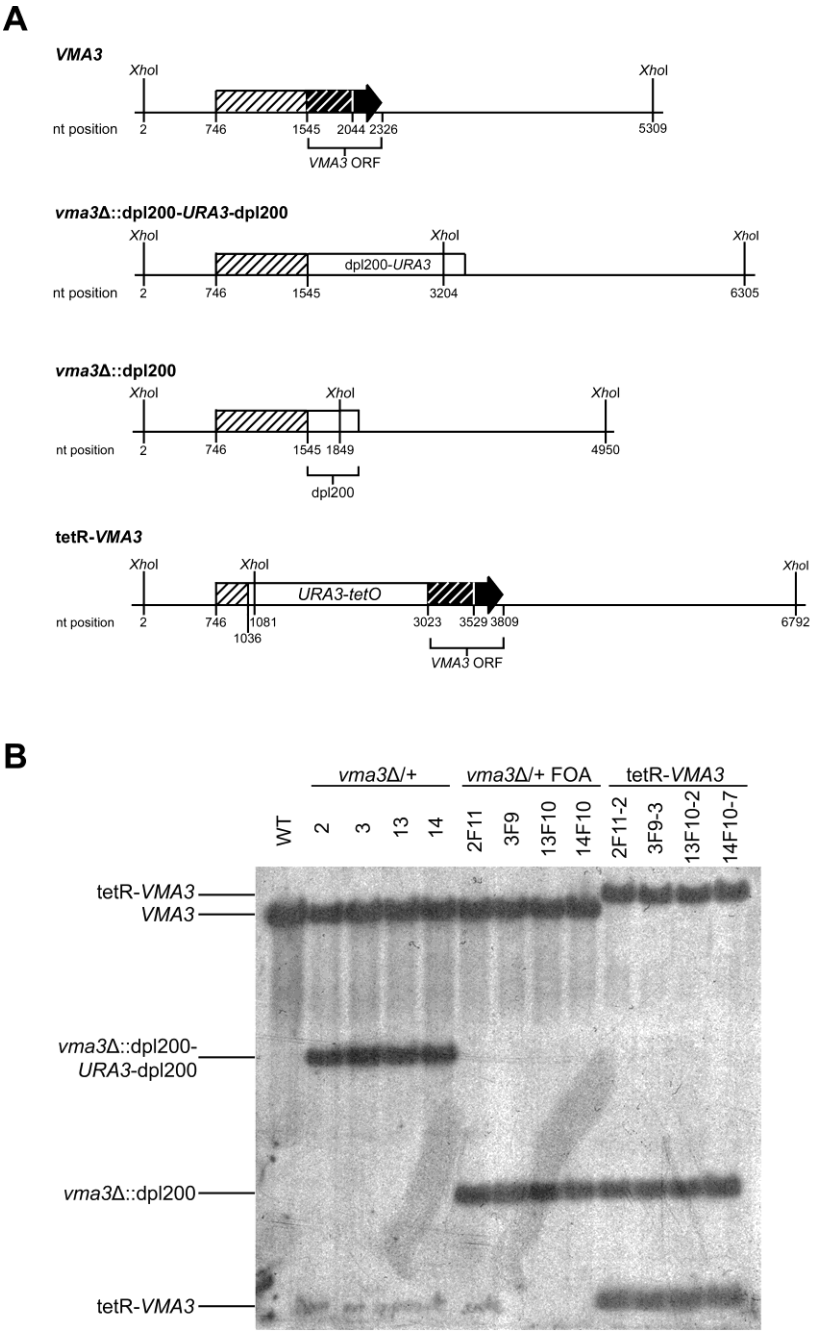

Supplemental Figure 1. Confirmation of tetracycline-regulated conditional *VMA3* mutants by Southern blot analysis. (A) Diagram illustrating the *VMA3* alleles: wild-type (*VMA3*), *VMA3* gene replacement (*vma3*Δ::dpl200-*URA3*-dpl200), *VMA3* gene replacement following *URA3* recycling (*vma3*Δ::dpl200), and *VMA3* under the control of the tetracycline-regulatable promoter (tetR-*VMA3*). *Xho*I recognition sites are indicated. Nucleotide position number is shown at the bottom of each allele, with 0 nt defined as the origin of the first *Xho*I recognition sequence in all four alleles. Diagonal lines indicate region in which the DNA probe hybridizes. Diagrams are not drawn to scale. (B) Southern hybridization was performed on *Xho*I digests of genomic DNA from screened transformants using a digoxigenin-labeled DNA probe that hybridizes to a 1.3 Kb region starting 0.8 Kb upstream of *C. albicans VMA3*. The expected sizes of the restriction fragments are: wild-type (*VMA3*) allele 5.3 kb, 1st allele gene replacement (*vma3*Δ::dpl200-*URA3*-dpl200) 3.2 kb, 1st allele FOA "loop-out" (*vma3*Δ::dpl200) 1.8 kb, and tetR-*VMA3* allele 5.7 and 1.1 kb. Four independent transformant lineages are shown.