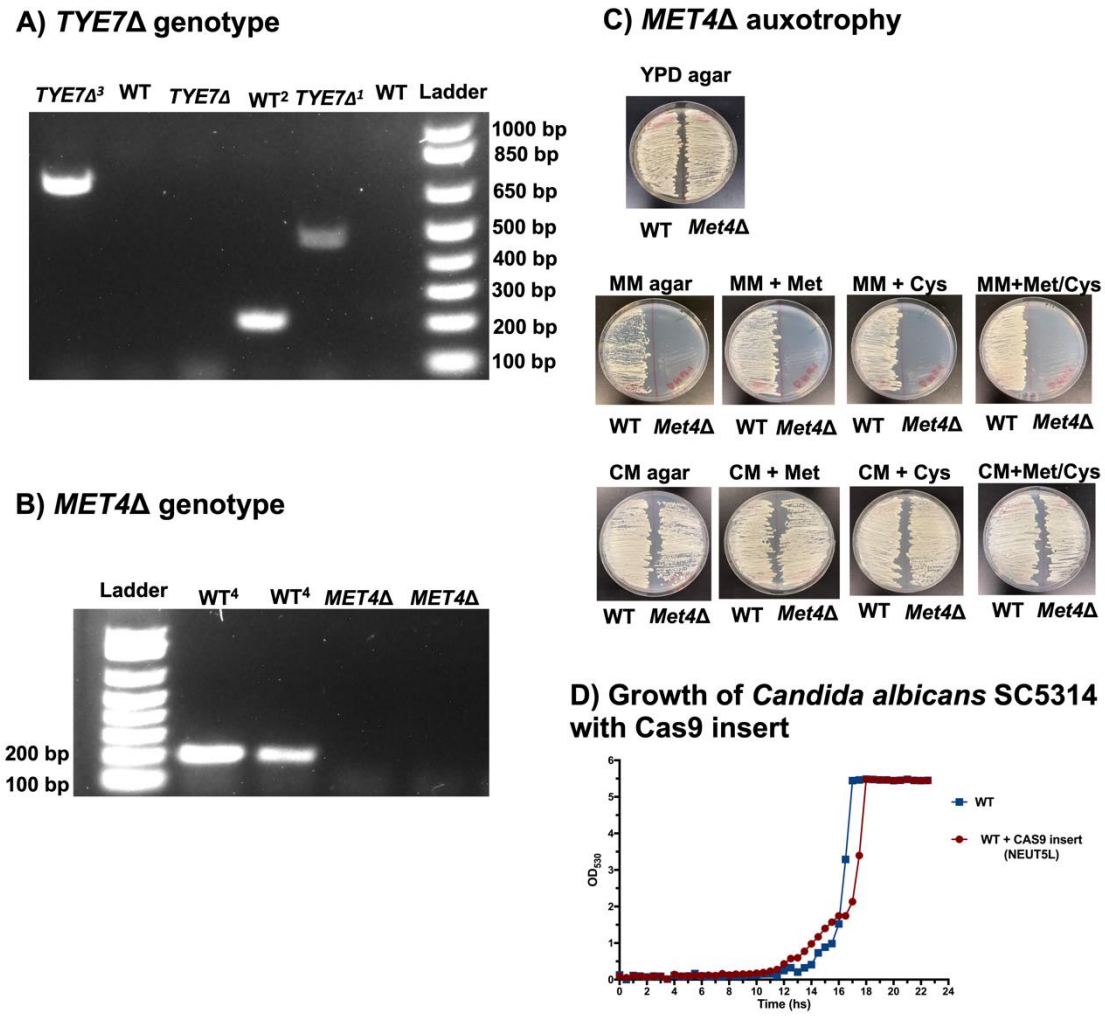


**S3 Figure: Validation of the genotype of deletion mutants**. **A)** Confirmation of generation of *TYE7*Δ mutant by PCR and gel electrophoresis where the *TYE7*Δ$^1$ band (~ 478 bp) confirmed the replacement of *TYE7* gene sequence with the gene drive cassette and the WT$^2$ band (~ 221 bp) confirmed the presence of *TYE7* gene in wild type. The deletion of the *TYE7* gene sequence in the *TYE7*Δ mutant (*TYE7*Δ$^3$ band; ~747 bp) confirmed the integration of Cas9 plasmid into *C. albicans* genome at the NEUT5L locus. **B)** Confirmation of *MET4*Δ genotype by PCR and gel electrophoresis where the WT$^4$ band (~ 224 bp) confirmed the presence of *MET4* gene in wild type and the deletion of *MET4* gene sequence in *MET4*Δ mutant. **C)** Growth of *C. albicans* SC5314 wild type and *MET4*Δ mutant in rich agar media (YPD), Minimal Media (MM), and Complete Minimal (CM) dropout media (synthetic mix minus methionine and cysteine) with or without addition of methionine and/or cysteine at 40 µg/mL final concentration. **D)** The integrated-plasmid NEUT5L did not show a defective effect on fungal fitness.