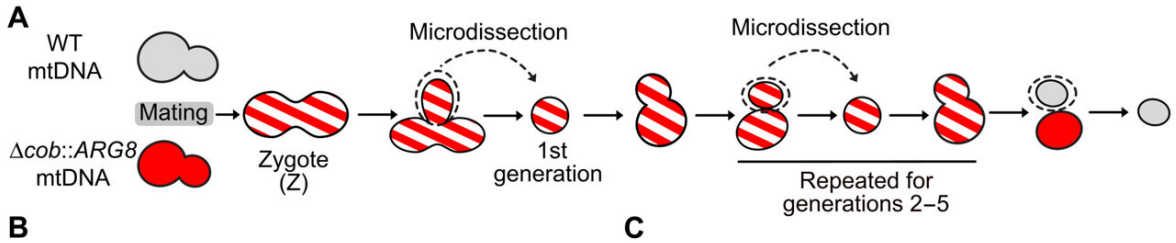
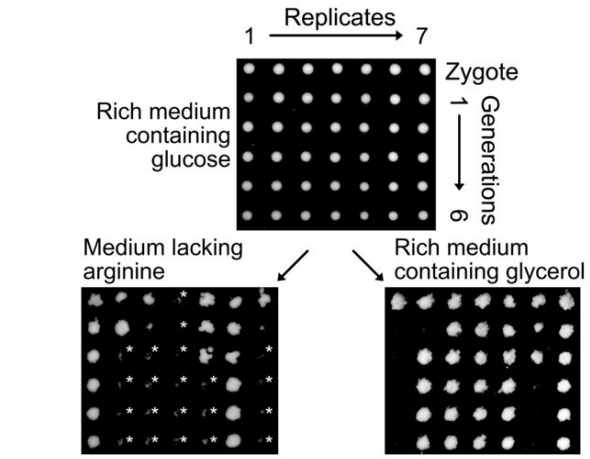
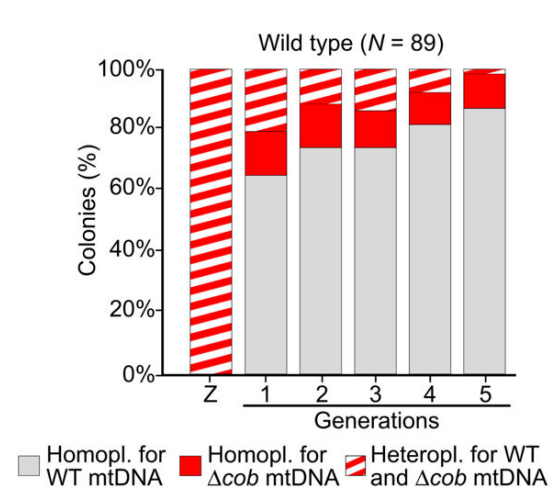
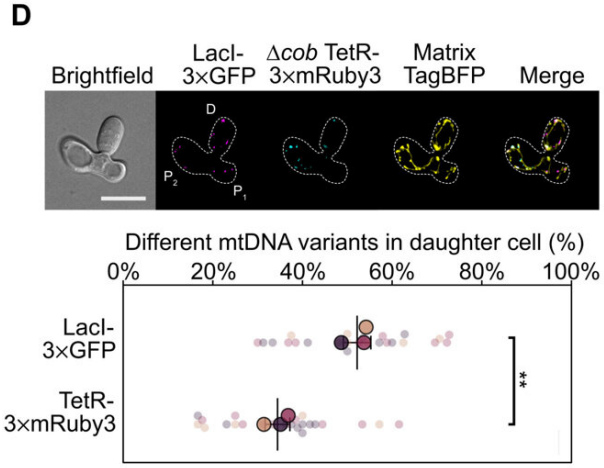
Cristae-dependent quality control of the mitochondrial genome

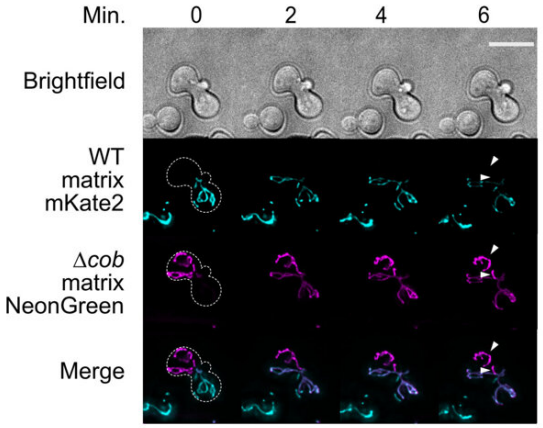
September 20 2021, by Thamarasee Jeewandara

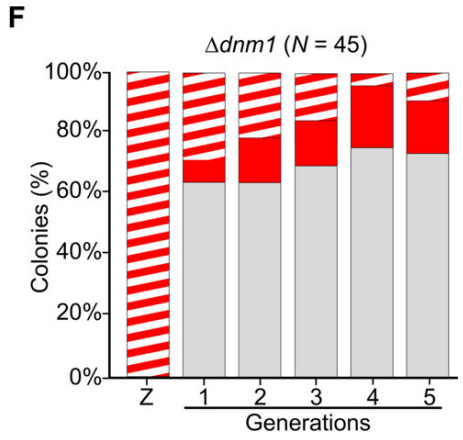




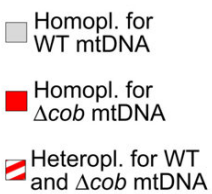


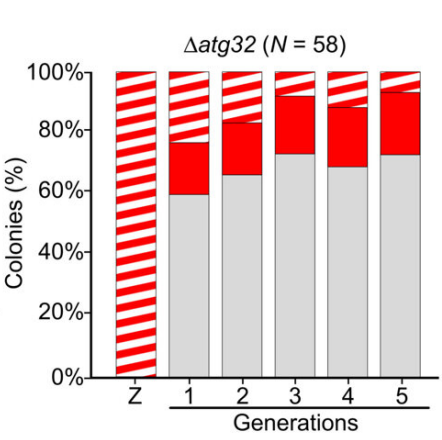






χ^2 test	Gen. 1	Gen. 5
WT vs. Δ*dnm1*	n.s.	n.s.





χ^2 test	Gen. 1	Gen. 5
WT vs. Δ*atg32*	n.s.	n.s.

S. cerevisiae cells distinguish between WT and mutant mtDNA. (A) Schematic illustration of the pedigree analysis. Two Δarg8 yeast strains harboring WT or Δcob::ARG8 mtDNA were mated. Zygotes were isolated, and daughter cells from up to five consecutive generations were separated and placed on free spots on the agar plate by microdissection. (B) Growth pattern of the pedigree analysis after microdissection. Colonies were initially grown on rich medium containing glucose. The mtDNA genotype was inferred from the ability of colonies to grow on synthetic arginine lacking medium (Δcob::ARG8 mtDNA) or on medium containing the nonfermentable carbon source glycerol (WT mtDNA). Asterisks indicate cell material that was carried over by replica plating and failed to produce obvious colonies upon further incubation. For further illustrative explanation and confirmation of the pedigree analysis, refer to fig. S1 (B to D). (C) Pedigree analysis of WT cells. Striped bars indicate percentage of heteroplasmic cells containing WT and Δcob::ARG8 mtDNA. Gray or red bars indicate percentage of homoplasmic cells containing WT or Δcob::ARG8 mtDNA, respectively. (D) Inheritance of either intact or mutated mtDNA. Mating events between two cells either with WT-LacO (GFP, P1) or Δcob::ARG8-TetO (mRuby3, P2) mtDNA. Both cells expressed a nuclear-encoded, matrix-targeted TagBFP. The percentage of either GFP or mRuby3 spots in the daughter cells relative to total number of the respective mtDNA variant have been plotted. Big circles represent the mean values from individual experiments. **P