

Figure S1. (A) Upper panel: sequence alignment between Lac1 subunits in fission and budding yeast. Lower panel: sequence alignment between the Lag1 subunits in fission and budding yeast. (B) Sequence alignment between ceramide synthase subunits in *S. pombe*, Lac1 and Lag1. White characters on red boxes denote identical residues, and red characters on white boxes denote conserved residues. (C) A phylogenetic tree using maximum-likelihood statistical method. Horizontal lines are proportional to the substitution rate. The bar represents 0.20 changes per amino acid. In panels A and B, white characters on red boxes denote identical residues, and red characters on white boxes denote conserved residues.

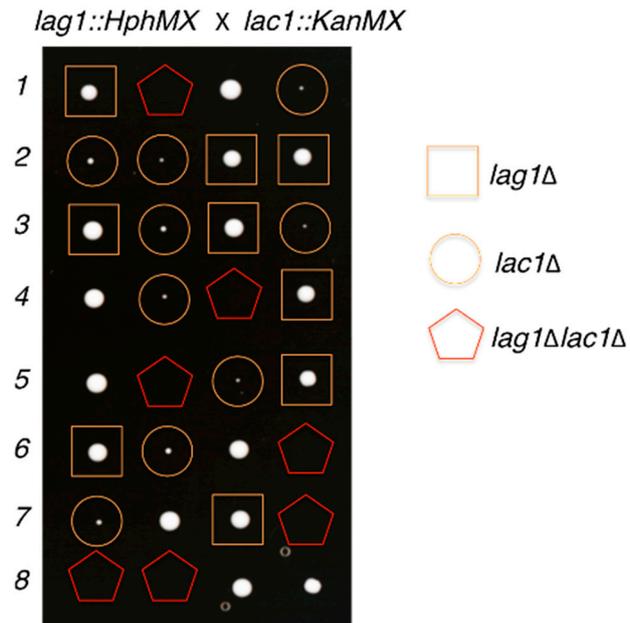


Figure S2. Deletion of Lac1 and Lag1 in *S. pombe* is lethal. Tetrad analysis of the indicated strains in Yes media at 25 °C.