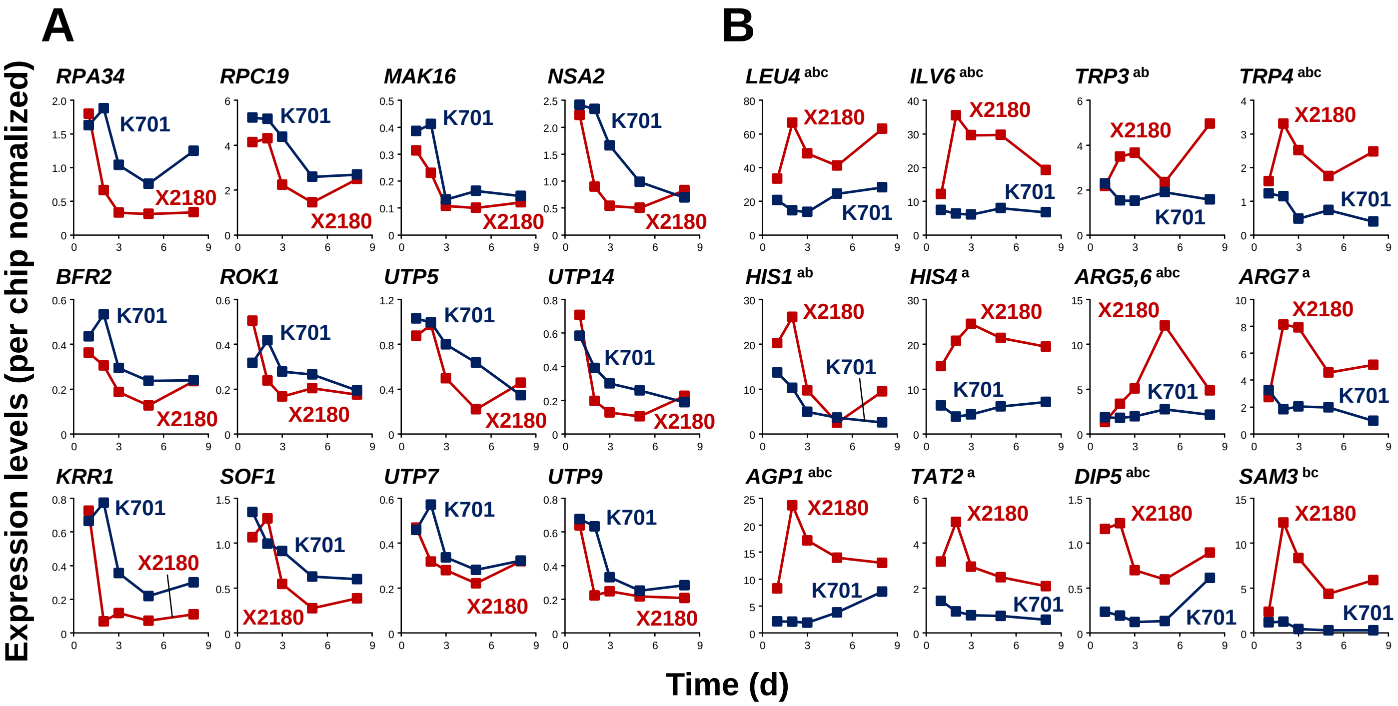

FIG S1 Gene expression profiles downstream of TORC1: Comparison between a laboratory strain and a sake strain during sake fermentation. (A) Expression profiles of the ribosome-associated genes under the control of Sfp1p. (B) Expression profiles of genes belonging to the NCR and GAAC regulons. ^{a}Gcn4p-targeted genes. ^{b}Gln3p-targeted genes. ^{c}Gat1p-targeted genes. Expression levels in a laboratory strain (X2180) and a sake strain (K701) are derived from our previous DNA microarray data (Watanabe D, Wu H, Noguchi C, Zhou Y, Akao T, Shimoi H. 2011. Enhancement of the initial rate of ethanol fermentation due to dysfunction of yeast stress response components Msn2p and/or Msn4p. *Appl Environ Microbiol* **77**:934–941.) and are indicated by red and blue, respectively. TORC1, target-of-rapamycin complex 1; NCR, nitrogen catabolite repression; GAAC, general amino acid control.

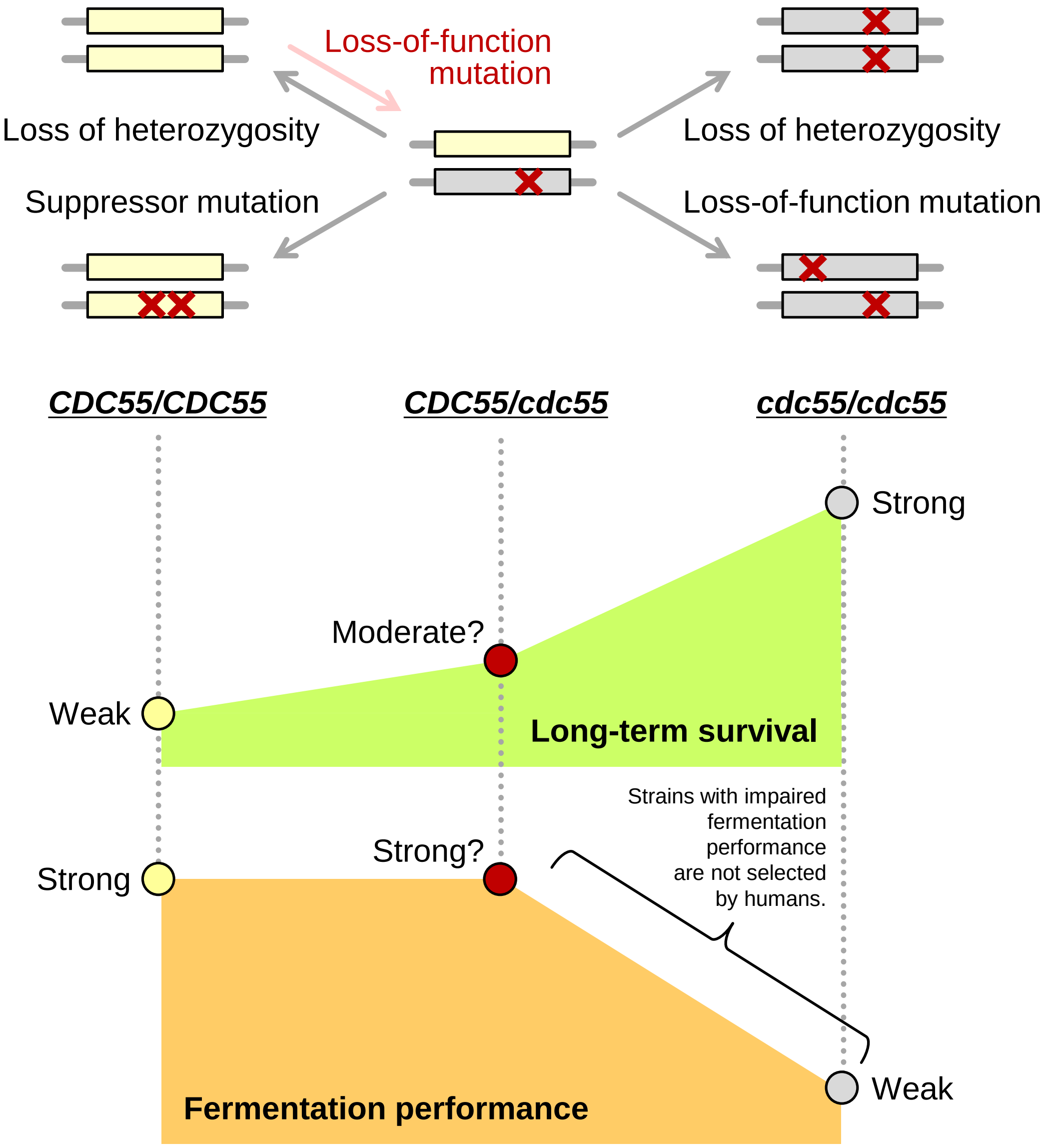

FIG S2 A hypothetical model of the effects (on long-term survival and fermentation performance) of loss-of-function mutations in the *CDC55* genes. (Top panel) Model of the loss (or recover) of Cdc55p function in the diploid sake yeast strains. Boxes indicate copies of the *CDC55* gene; yellow boxes are functional alleles, and gray boxes are loss-of-function alleles. Red x symbols indicate mutations in the *CDC55* genes. In ancestral sake strains, both *CDC55* alleles may have been functional (top left). However, at present, most sake strains carry a loss-of-function allele heterozygously (*CDC55/cdc55* state, middle), such as *cdc55*^{1092delA} of K701. A loss-of-heterozygosity (LOH) event (top left) or a suppressor mutation (bottom left) may be able to recover the lost function (*CDC55/CDC55* state). In contrast, an LOH event (top right) or another loss-of-function mutation in the functional allele (bottom right) may lead to complete loss of Cdc55p function (*cdc55/cdc55* state). (Bottom panel) Long-term survival (green) and fermentation performance (orange) of *CDC55/CDC55* (left), *CDC55/cdc55* (middle), and *cdc55/cdc55* (right) cells. Both plots indicate relative strength but are not intended to be quantitative. Heterozygous loss-of-function mutations may contribute to both long-term survival and fermentation performance. Strains with complete loss of Cdc55p function may exhibit severely impaired fermentation performance, and thus, may not be selected by humans.