

FINDING THE GENETIC UNDERPINNINGS OF AN ANCIENT THERMOTOLERANCE DIVERGENCE IN YEAST

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Abstract

Saccharomyces cerevisiae and its closest relative, *Saccharomyces paradoxus* are two closely related species of yeast that differ with respect to thermotolerance. Weiss et al. (2018) found that *S. cerevisiae* alleles of eight genes confer a modest growth advantage at 39°C when they replace the native allele at the endogenous locus in an *S. paradoxus* background by creating an interspecific hybrid of the two species and subjecting it to transposon mutagenesis. While each *S. cerevisiae* allele has a modest effect on its own, the effects of the alleles in combination are unknown. This work seeks to investigate the effects of a combination of these eight *S. cerevisiae* alleles in the *S. paradoxus* background. Relative to *S. paradoxus*, these multi-allele swaps demonstrate a significant increase in growth at 39°C with minimal epistasis. An additive model, in which effects of the alleles on thermotolerance are independent of each other, can describe the effects of these alleles. Without extensive epistasis between these loci, we can reconstruct a simple picture of the history of this evolutionary process.

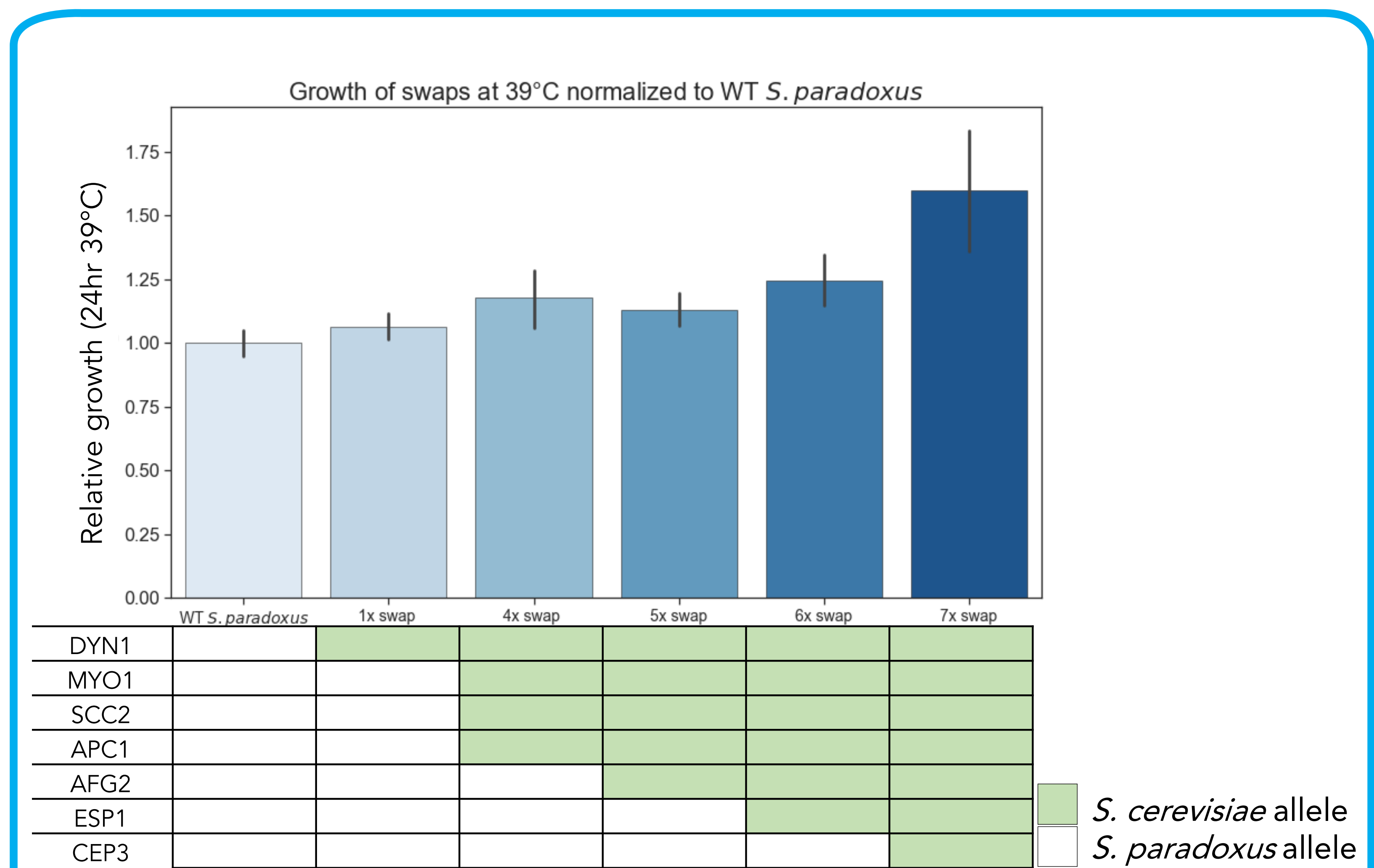
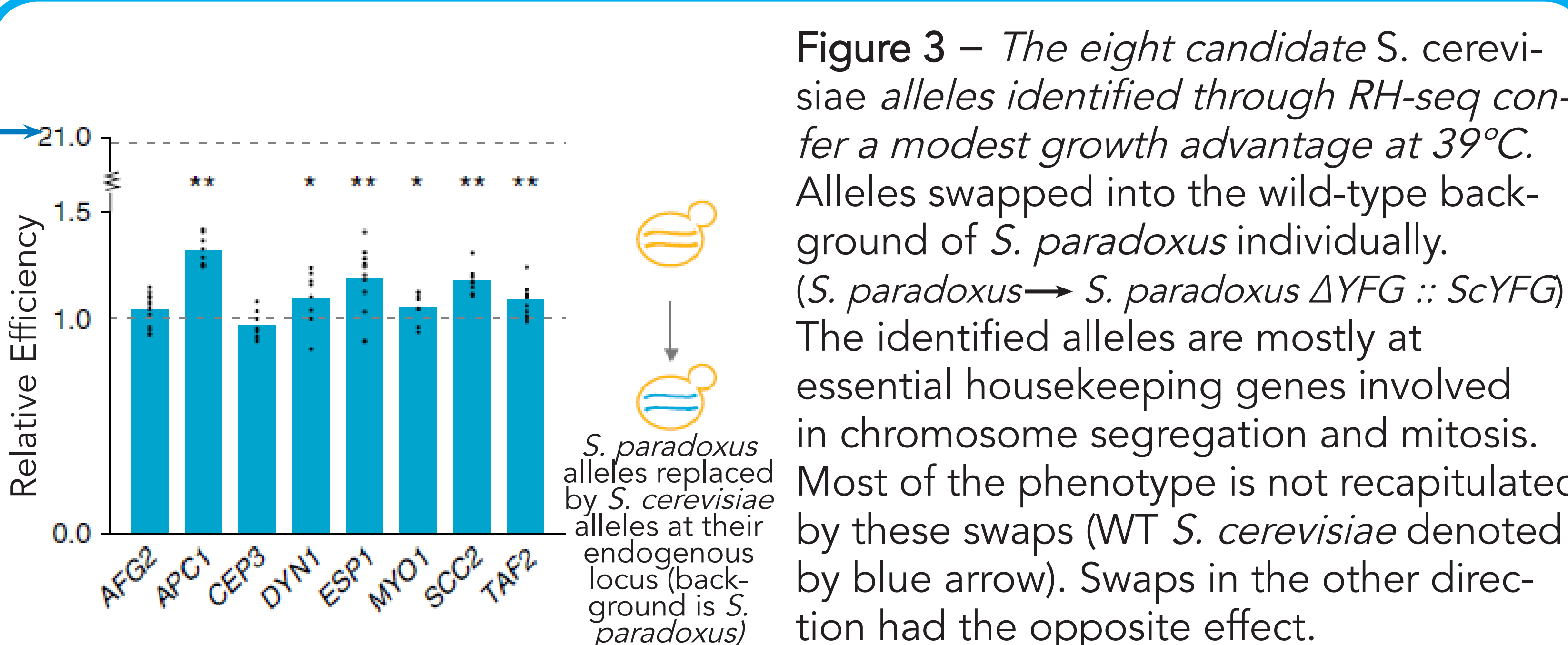
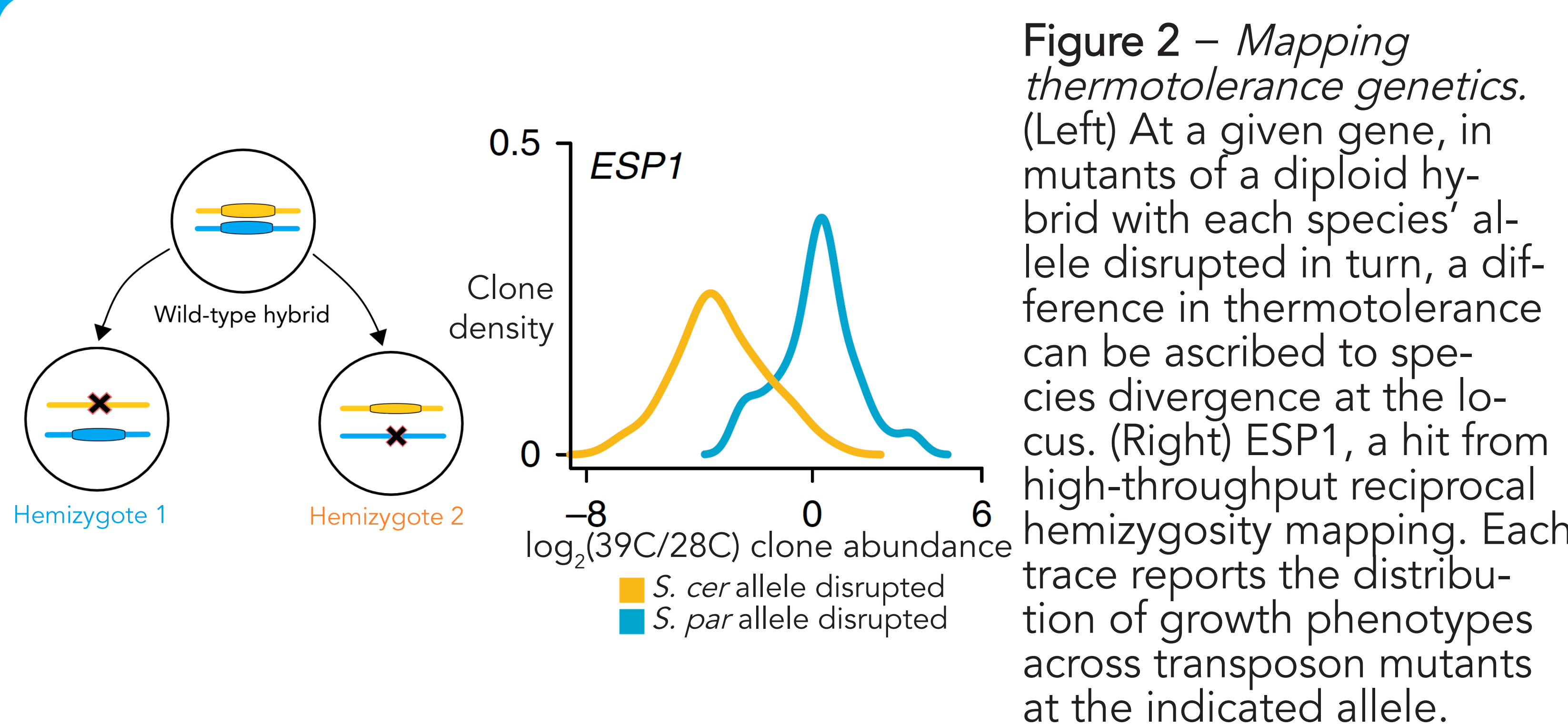
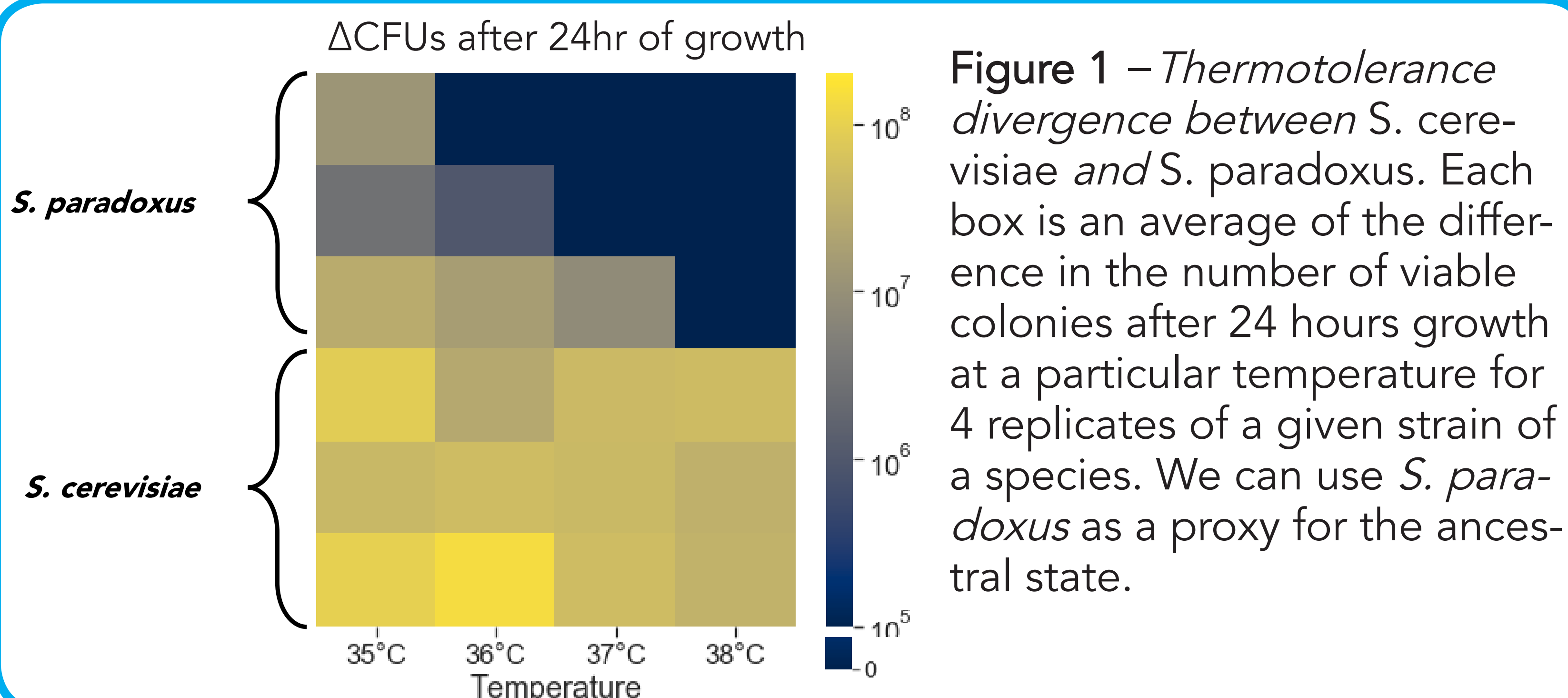


Figure 4 – The effects of the candidate *S. cerevisiae* alleles in combination are roughly additive. Each bar represents growth of a swap after 24hrs at 39°C, normalized to the growth of the *S. paradoxus*. Each allele confers a mostly independent increase in thermotolerance. In combination, the effects of the *S. cerevisiae* alleles are additive. These seven candidate alleles recapitulate ~10% of *S. cerevisiae*'s phenotype.

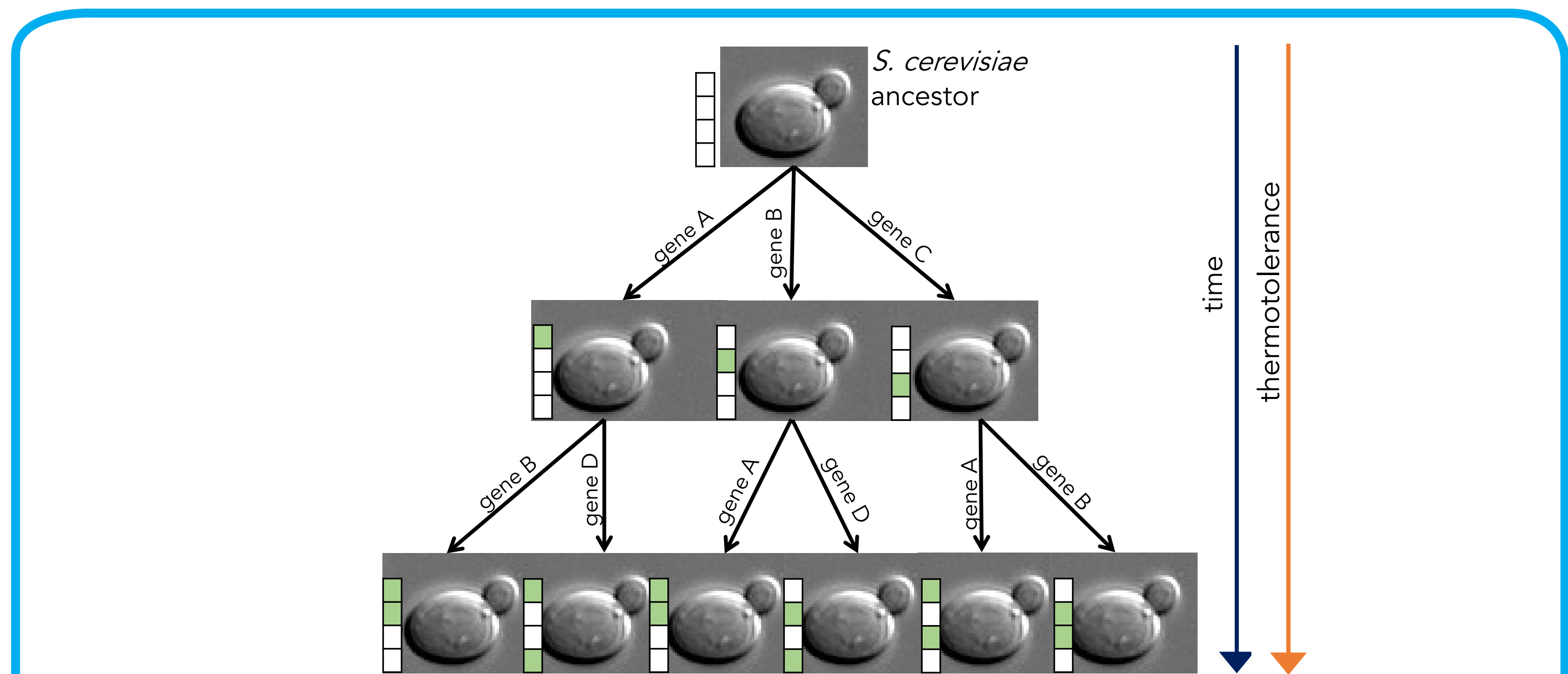


Figure 5 – Our data agree with a model in which the mutational steps to thermotolerance could have happened in almost any order. Phenotyping results agree with a model in which the mutational steps to thermotolerance could have happened in any order. The effects of genetic changes are mostly independent of each other and the genomic background and each confers a small increase in thermotolerance. Under this model, different lineages of the *S. cerevisiae* ancestor may get to thermotolerance by acquiring changes in different parts of the genome without having to wait for the perfect combination of mutations to arise. Changes that confer a slight advantage could have risen to high frequency, and later come together with other adaptive loci by recombination other, yielding an even more thermotolerant descendant. This would make it easy for the whole population to become more fit. The *S. cerevisiae* ancestor could easily traverse fitness landscape, arriving at thermotolerance in many, potentially different ways.

Sources: Weiss, C.V., Roop, J.I., Hackley, R.K., Chuong, J.N., Grigoriev, I.V., Arkin, A.P., Skerker, J.M., and Brem, R.B. (2018). Genetic dissection of interspecific differences in yeast thermotolerance. Nat. Genet. 50, 1501.

Thanks to

