**File S1. Wild isolate geographic location, closest weather station, and weather trait values.** This file contains data for 152 wild isolates, including isolation location, date, and various average daily mean, average daily minimum, average daily maximum, and average variance of weather trait values during the specific dates tested.

**File S2. Genome-wide marker association by trait and QTL significance.** This file contains negative log-transformed *p*-values for each marker tested for association for every trait with phenotype information (gathered from File S1). The file was created using the “gwas\_mappings” function of the *cegwas* R package (https://github.com/AndersenLab/cegwas), which utilizes the “GWAS” function from the *rrBLUP* package (*see Methods)*. The confidence interval of each quantitative trait locus (QTL) is marked with a start position (startPOS), peak position (peakPOS), and end position (endPOS), as well as the variance explained (var.exp), in percent, by each QTL.

**File S3. Genes correlated with mapping phenotypes.** This file contains a list of all genes significantly correlated with a QTL for a trait. It was created using the “process\_mappings” function of the *cegwas* R package (*see Methods*).

**File S4. Two-strain temperature competition assay allele frequencies.** This file contains raw data from the digital droplet PCR (ddPCR) two-strain temperature competition assay. The allele frequency between JU847 and CX11314 was calculated and data were used to create Figure 5.