

Supplementary Information

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Title:

Efficient gene identification via quantitative trait loci analysis by crossbreeding of sake and laboratory yeast

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Muneyoshi Kanai and Takeshi Akao contributed equally to this work.

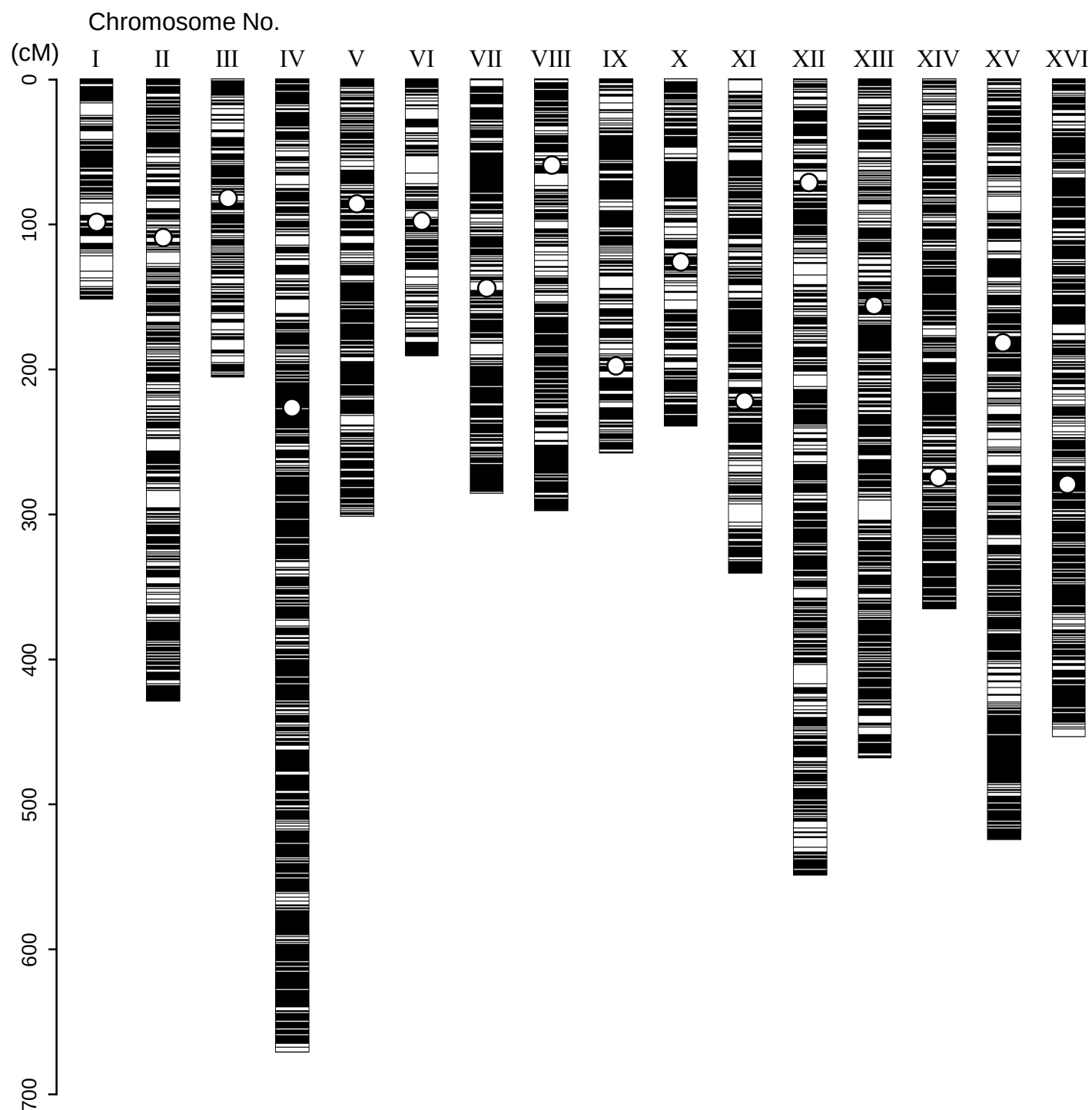


Fig. S1 Chromosomal maps showing recombination frequency between DNA markers (52,191 SNP markers), aligned on chromosomes as relative distances (cM), using 398 F1 segregant haploids

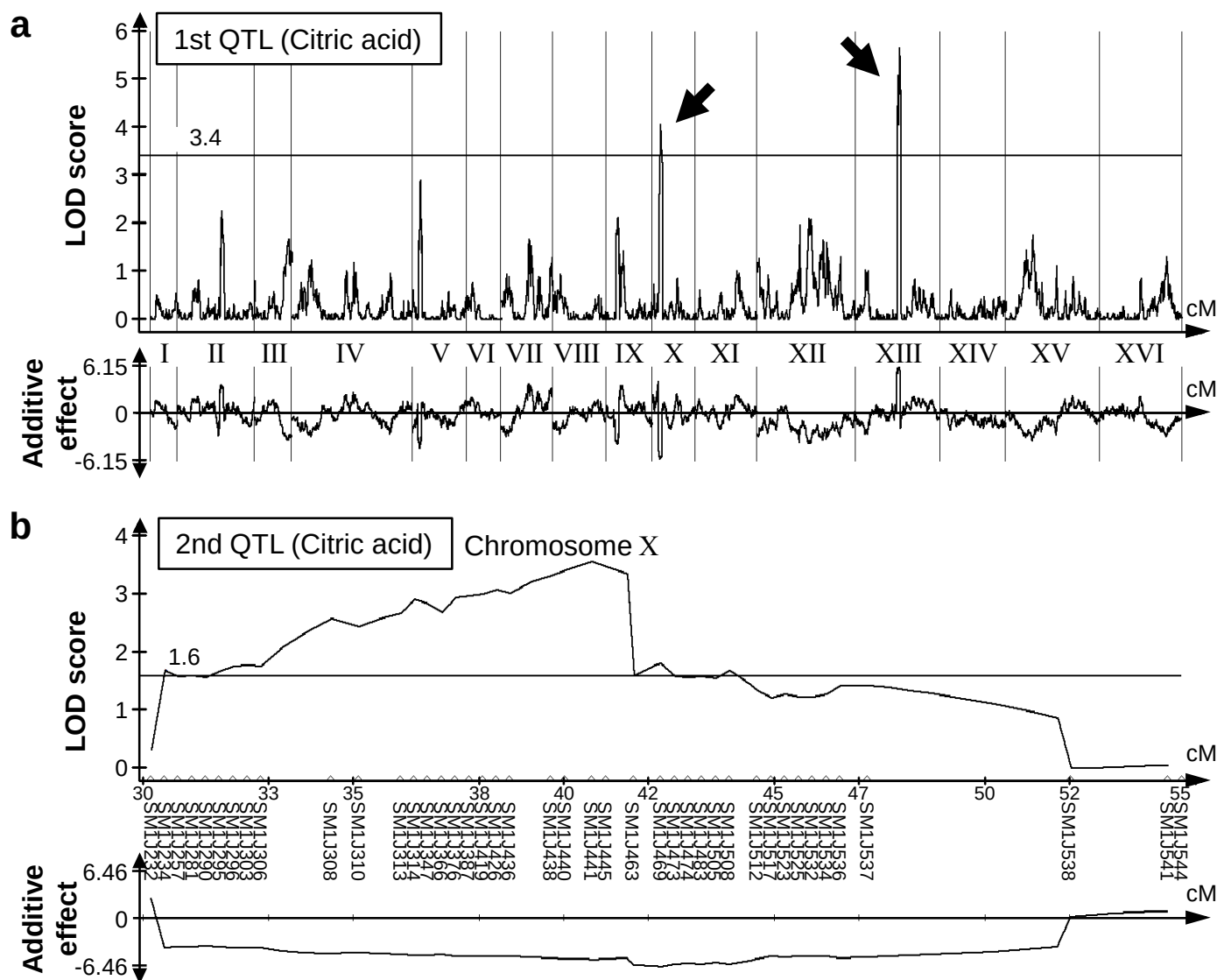


Fig. S3 Quantitative trait loci (QTL) analysis mapping based on the statistical linkage using DNA marker locations as genotype information and citric acid values for 392 F1 segregant haploids in a small-scale sake-making test as phenotype information. The upper half shows 1st quantitative trait loci (QTL) analysis mapping results, and the lower half shows 2nd QTL analysis results. Significant QTLs are marked by black arrows.

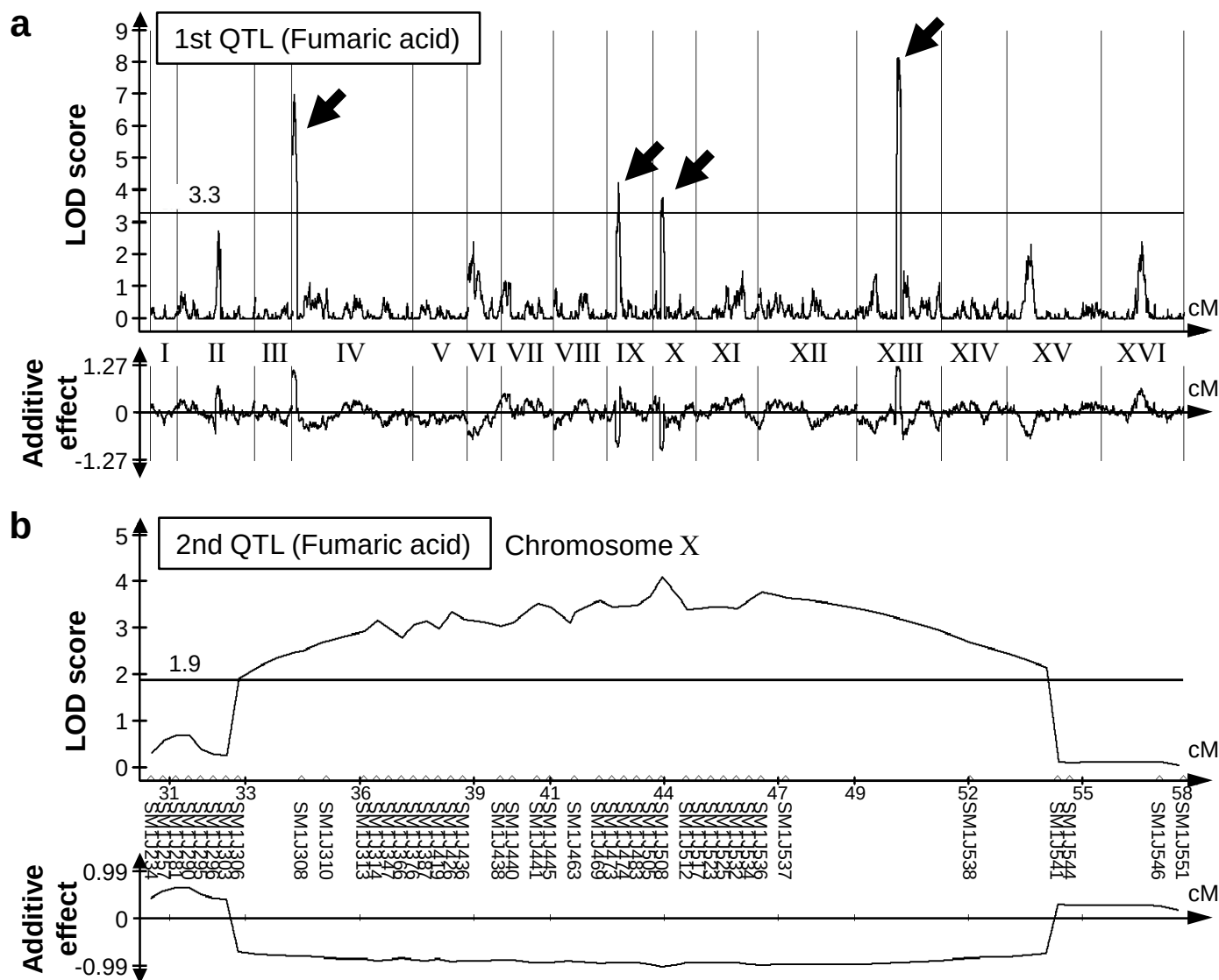


Fig. S4 Quantitative trait loci (QTL) analysis mapping based on the statistical linkage using DNA marker locations as genotype information and fumaric acid values for 392 F1 segregant haploids in a small-scale sake-making test as phenotype information

The upper half shows 1st quantitative trait loci (QTL) analysis mapping results, and the lower half shows 2nd QTL analysis results. Significant QTLs are marked by black arrows.

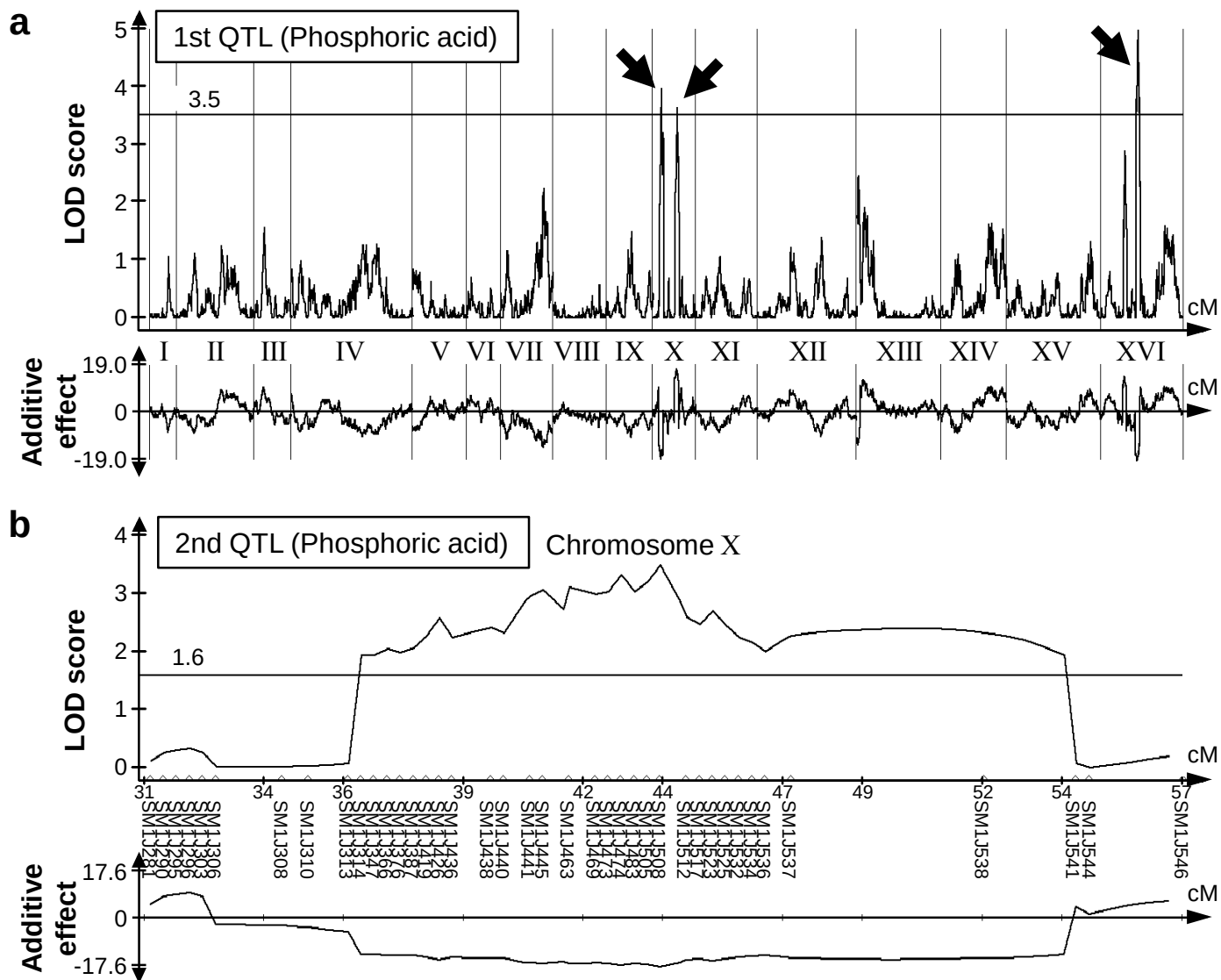


Fig. S5 Quantitative trait loci (QTL) analysis mapping based on the statistical linkage using DNA marker locations as genotype information and phosphoric acid values for 392 F1 segregant haploids in a small-scale sake-making test as phenotype information

The upper half shows 1st quantitative trait loci (QTL) analysis mapping results, and the lower half shows 2nd QTL analysis results. Significant QTLs are marked by black arrows.

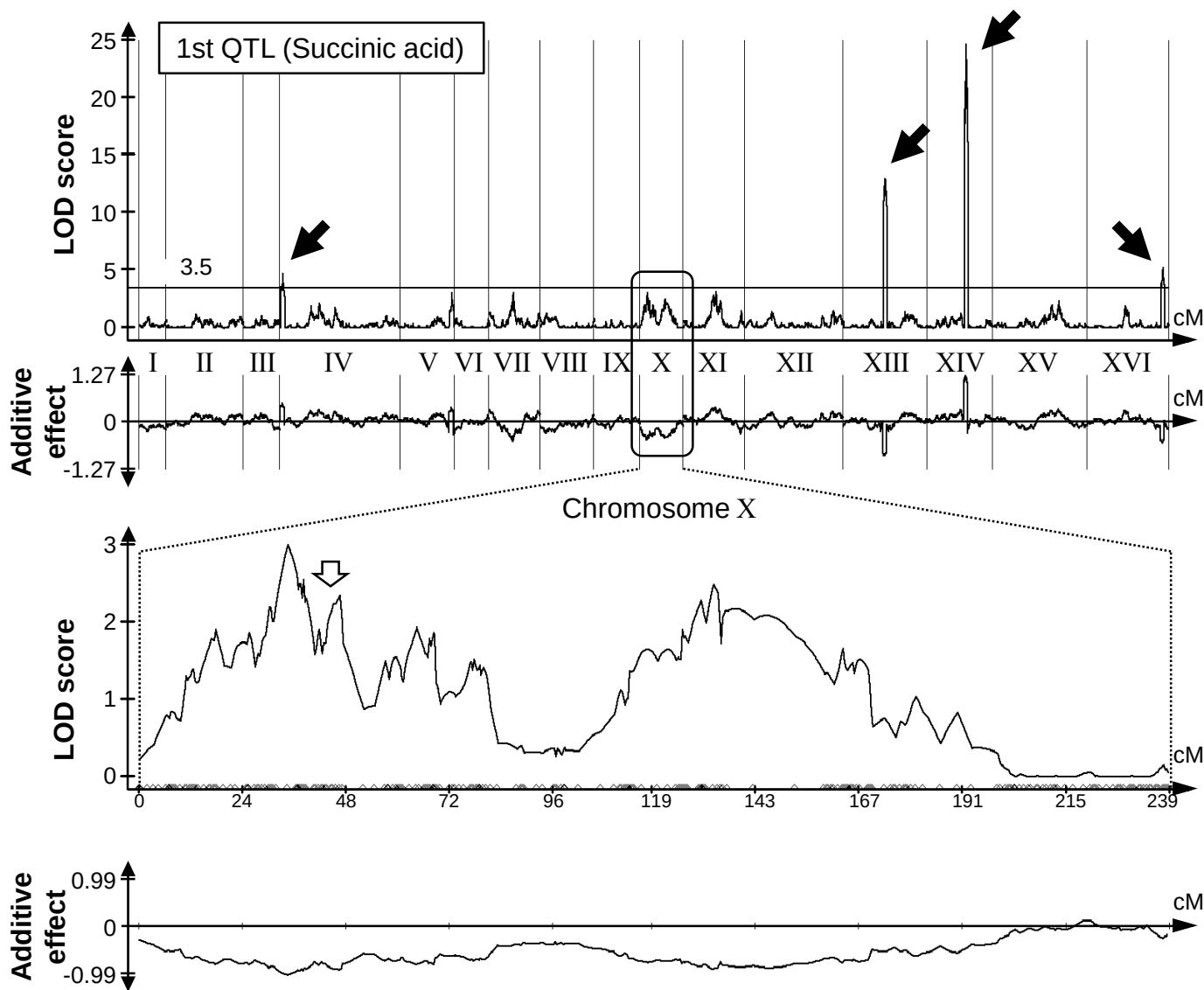


Fig. S6 Quantitative trait loci (QTL) analysis mapping based on the statistical linkage using DNA marker locations as genotype information and succinic acid values for 392 F1 segregant haploids in a small-scale sake-making test as phenotype information

The upper half shows 1st quantitative trait loci (QTL) analysis mapping results, and the lower half shows an enlarged view of the chromosome X portion. Significant QTLs are marked by black arrows. White arrows show the approximate position of the PBS2 gene on the chromosome.

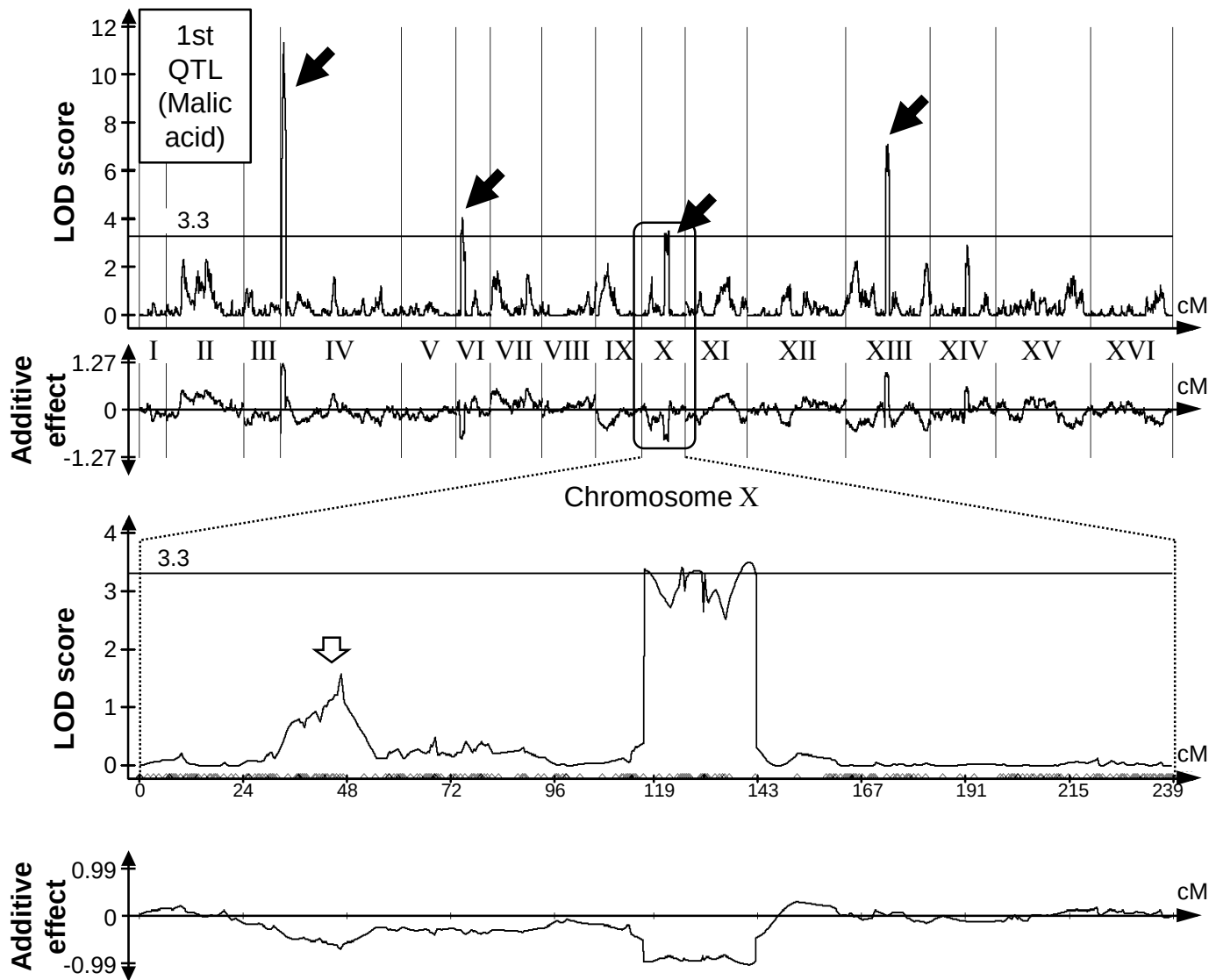


Fig. S7 Quantitative trait loci (QTL) analysis mapping based on the statistical linkage using DNA marker locations as genotype information and malic acid values for 392 F1 segregant haploids in a small-scale sake-making test as phenotype information. The upper half shows 1st quantitative trait loci (QTL) analysis mapping results, and the lower half shows an enlarged view of the chromosome X portion. Significant QTLs are marked by black arrows. White arrows show the approximate position of the PBS2 gene on the chromosome.

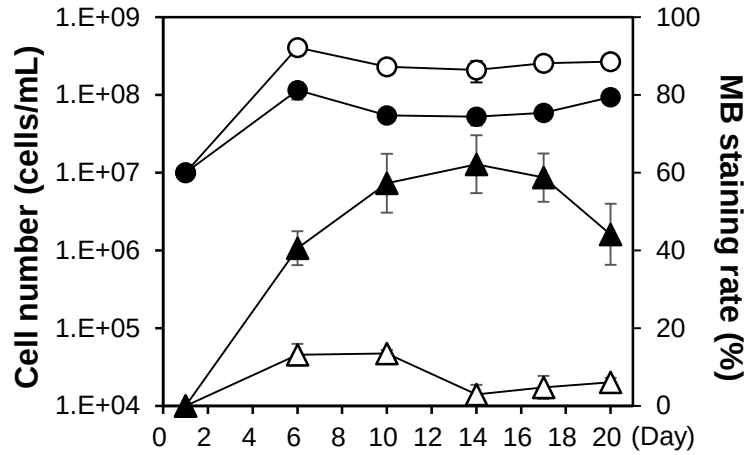


Fig. S8 Cell proliferation and methylene blue (MB) staining rate in the X21810-1B and X1B *K7PBS2^{L545}* strains in small-scale sake making test. Cell number (circles) and MB staining rate (triangles) were determined in the X21810-1B (open) and X1B *K7PBS2^{L545}* (closed) strains. Values are presented as mean $\pm$ standard deviation for three independent experiments.