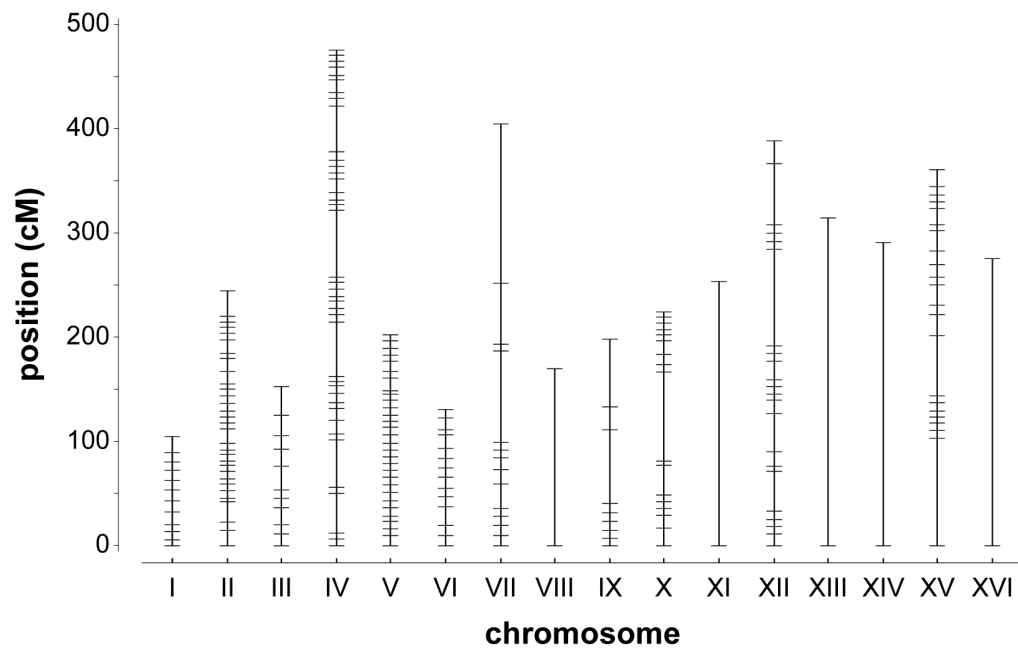Figure S1. Genetic map of the 200 artificial markers tested in the highly ethanol tolerant segregants. The physical distances were converted into genetic distances using the mean conversion factor for each chromosome (Cherry *et al.*, 1997). The genetic maps were drawn with J/QTL software, which is a user interface for R/QTL (R Core Team, 2013) (available at R-project.org).
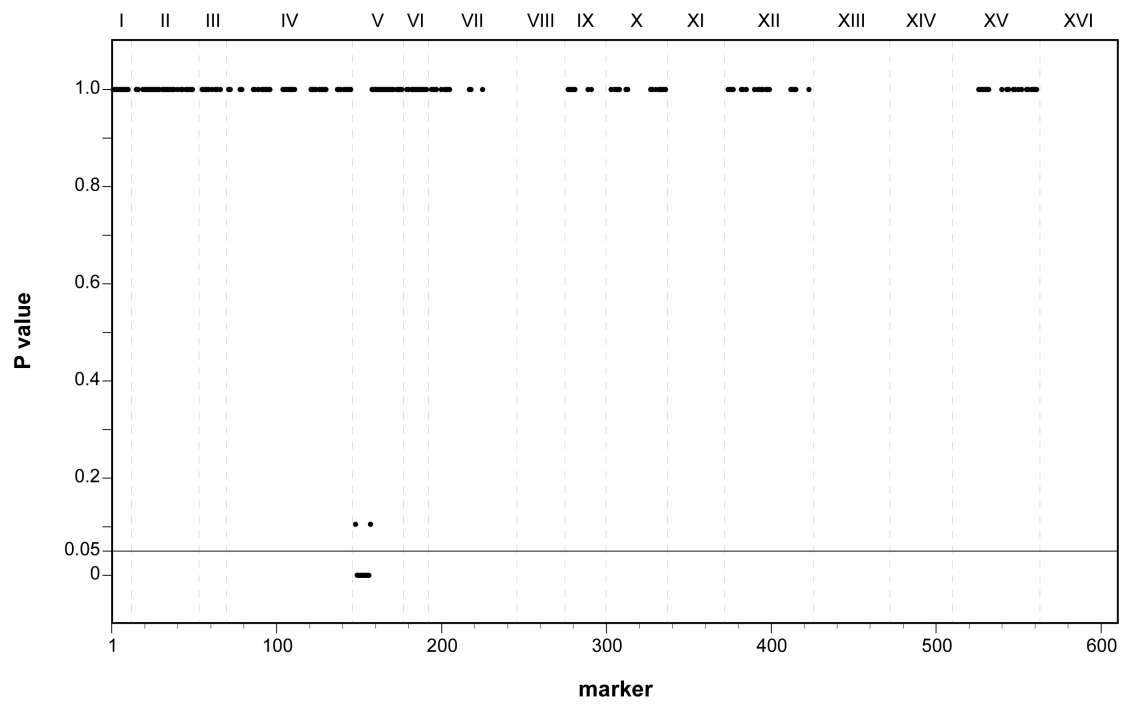
Figure S2. QTL mapping of high ethanol tolerance based on artificial markers. The segregation of artificial markers was scored in highly ethanol tolerant segregants from crosses between VR1-5B and 28 pAMS. The probability of random segregation was calculated under two-sided binomial distribution with false discovery rate adjustment according to Benjamini and Yekutieli (2005). The p values were considered significant if smaller than 0.05.

References

Benjamini, Y. and Yekutieli, D. (2005). Quantitative trait loci analysis using the false discovery rate. *Genetics,* 171: 783-790.

Cherry, J. M.*,* Ball, C., Weng, S., Juvik, G., Schmidt, R., Adler, C., Dunn, B., Dwight, S., Riles, L., Mortimer, R. K., Botstein, D. (1997). Genetic and physical maps of *Saccharomyces cerevisiae*. *Nature,* 387: 67-73.

R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.