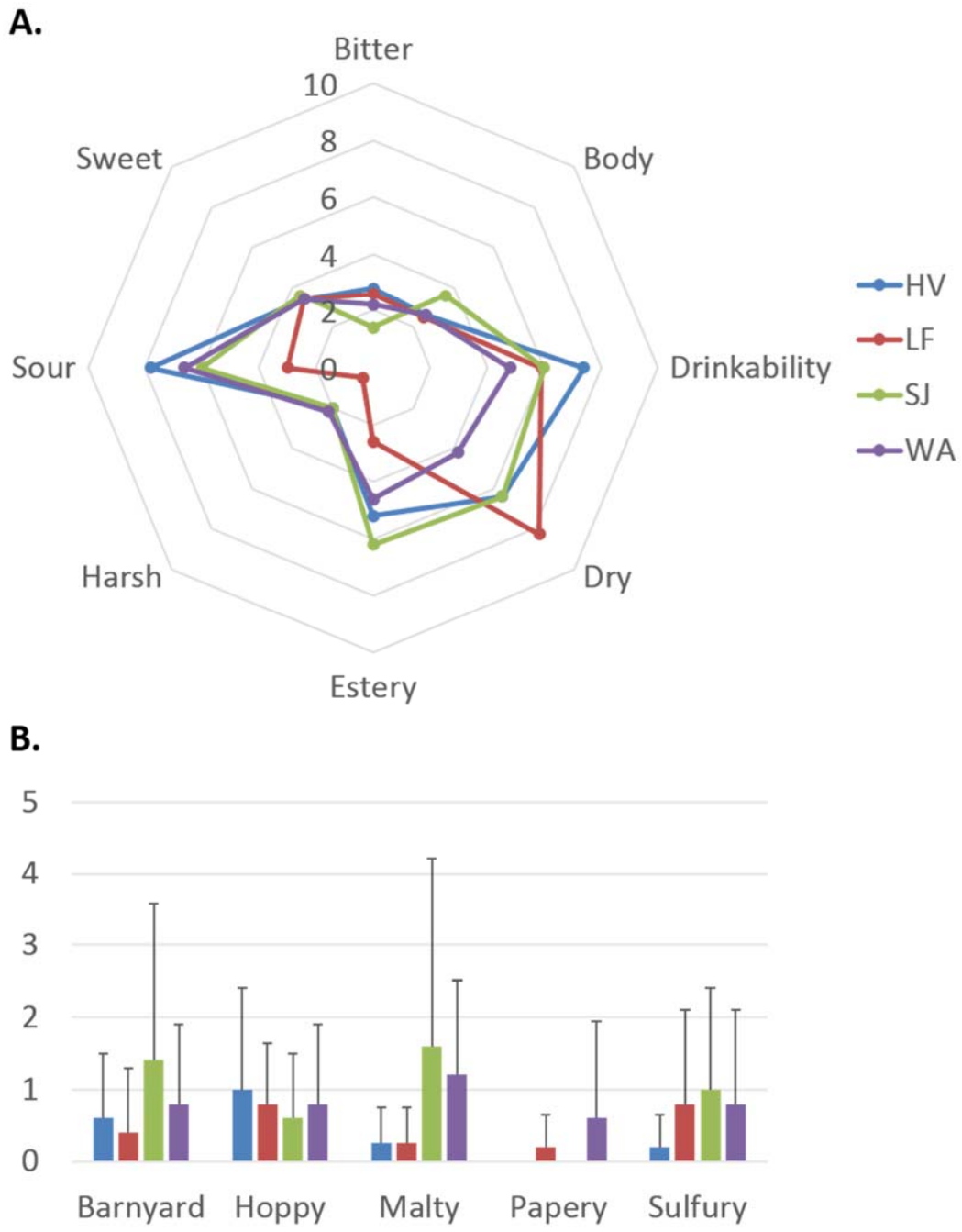
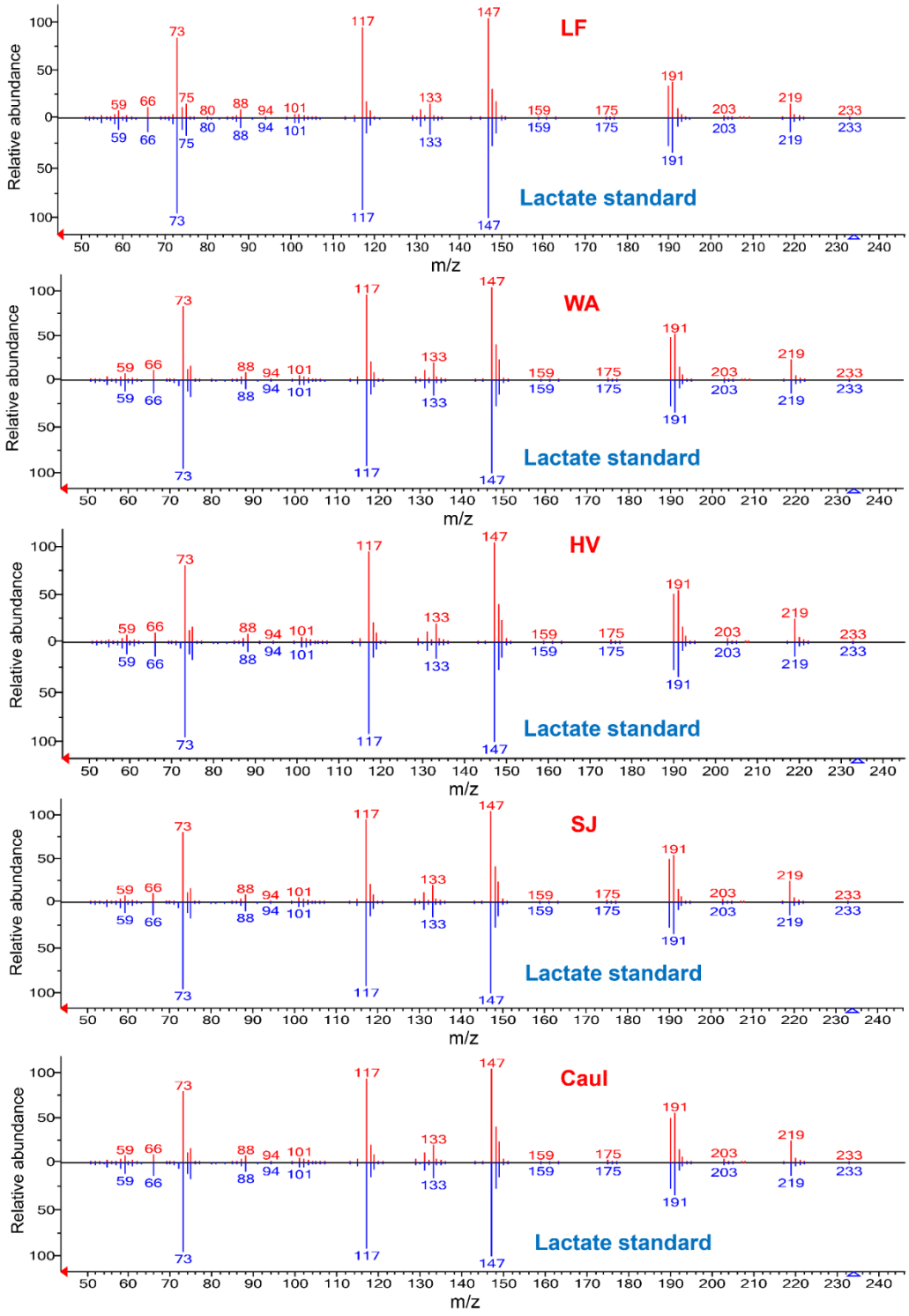
Supplemental Materials

Supplemental figures

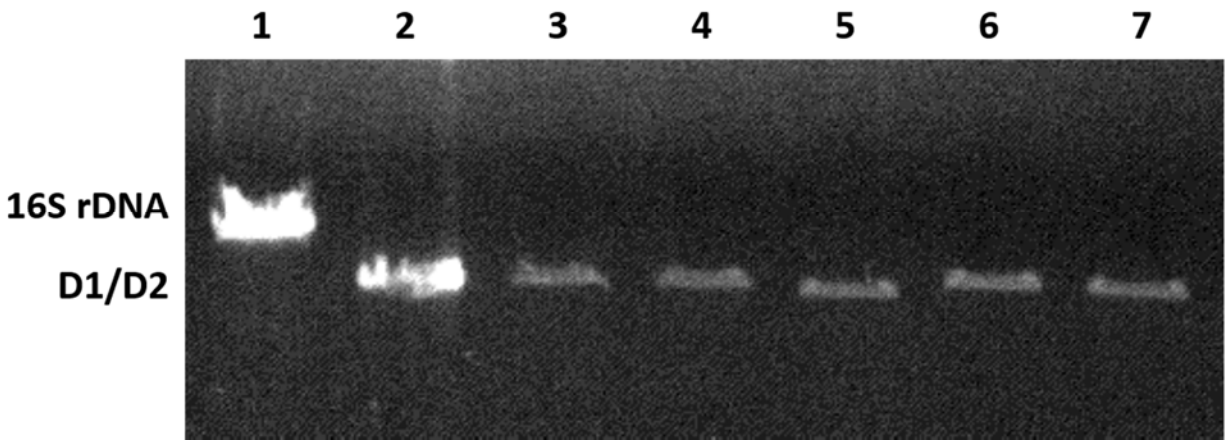
Supplemental Figure 1. Appearance of *Schizosaccharomyces japonicus* during wort fermentation. The *S. japonicus* cells formed large, popcorn-shaped flocs during fermentation. Left) *S. japonicus* popcorn during early vigorous fermentation; Right) *S. japonicus* popcorn that settled to the bottom of the fermenter during a later stage of fermentation.



Supplemental Figure 2. Sensory analysis of beers in Table 3. A) A panel of five people assessed the sour beers described in Table 3 for the flavor descriptors shown in the spider graph as described in [1]. The average values are plotted, and outliers were removed using Grubbs' test with GraphPad Prism. HV = *Hanseniaspora vineae*, LF = *Lachancea fermentati*, SJ = *Schizsaccharomyces japonicus*, and WA = *Wickerhamomyces anomalus*. **B)** The flavor descriptors on the x-axis were also assessed as in **A)**, but their averages values were so low that they were omitted from the spider plot. The bars represent the averages, and the error bars are the standard deviations.



Supplemental Figure 3. Aligned MS spectra of the lactate standard and the isolated lactate from the indicated beers analyzed by GC-MS. LF = *Lachancea fermentati*, WA = *Wickerhamomyces anomalus*, HV = *Hanseniaspora vineae*, SJ = *Schizsaccharomyces japonicus*, and Caul = Cauldron, a sour beer made by the Upland Brewing Company via mixed fermentation of yeasts with lactic acid bacteria [2].



Supplemental Figure 3. PCR analysis of yeast slurry after in-lab fermentation. One hundred microliters of yeast slurry was removed from the lab-scale fermenters, and genomic DNA was prepared using the protocol in the Methods and Materials (Section 2.2). PCRs were then performed using two primer sets multiplexed in each reaction: NL1 and NL2 to amplify the yeast rDNA D1/D2 region [3]; and 519 F and 1429R to amplify the variable region of the bacterial 16S rDNA [4]. The expected ~1 kb 16S fragment was amplified from purified *Lactobacillus plantarum* DNA (lane 1), and the ~580 bp D1/D2 fragment was amplified from purified *Saccharomyces cerevisiae* WLP001 DNA (lane 2). No contaminating bacterial DNA was amplified in lanes 3-7 containing DNA prepared from the yeast slurries of fermenters containing *Hanseniaspora vineae* (YH72), *Lachancea fermentati* (WYP39), *Lachancea thermotolerans* (YH140), *Schizosaccharomyces japonicus* (YH156), and *Wickerhamomyces anomalus* (YH82), respectively.

Supplemental references

[1] M.J. Wu, F.M. Clarke, P.J. Rogers, P. Young, N. Sales, P.J. O'Doherty, V.J. Higgins, Identification of a protein with antioxidant activity that is important for the protection against beer ageing, Int J Mol Sci, 12 (2011) 6089-6103.

[2] C.M. Rogers, D. Veatch, A. Covey, C. Staton, M.L. Bochman, Terminal acidic shock inhibits sour beer bottle conditioning by Saccharomyces cerevisiae, Food Microbiol, 57 (2016) 151-158.

[3] Y.J. Lee, Y.R. Choi, S.Y. Lee, J.T. Park, J.H. Shim, K.H. Park, J.W. Kim, Screening wild yeast strains for alcohol fermentation from various fruits, Mycobiology, 39 (2011) 33-39.

[4] D.P. Mao, Q. Zhou, C.Y. Chen, Z.X. Quan, Coverage evaluation of universal bacterial primers using the metagenomic datasets, BMC Microbiol, 12 (2012) 66.