

Errata

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Bayesian Estimation of Concordance Among Gene Trees

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In Bayesian estimation of concordance among gene trees (Vol. 24(2), 412–426) the data analysis contains an error. The alignment for gene YLR253W had the sequences in a different order than the other 105 genes. The most probable tree for gene YLR253W in Figure 5 (right-hand side) should show taxon labels in order 1,2,5,4,3,6,7,8 from top to bottom. We reanalyzed the data with the correct sequence order. Concordance factors did not change substantially, as indicated in the corrected Figure 4 below. Figure 6 did not change qualitatively. Gene YLR253W was no longer an outlier (see corrected Figure 7) and clustered instead with the majority of genes. There were most probably only 2 clusters of genes a posteriori. The last column in Table 2 pertains to gene YLR253W and should simply read 1,1,1,1,1,0,0. This error does not affect the theoretical part of the paper. We are very thankful to John Gatesy, who kindly notified us of the error.

The authors regret the error.

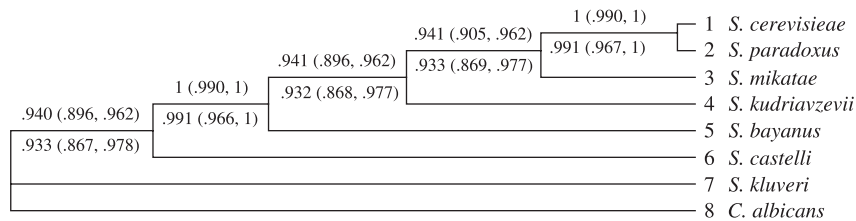


FIG. 4.

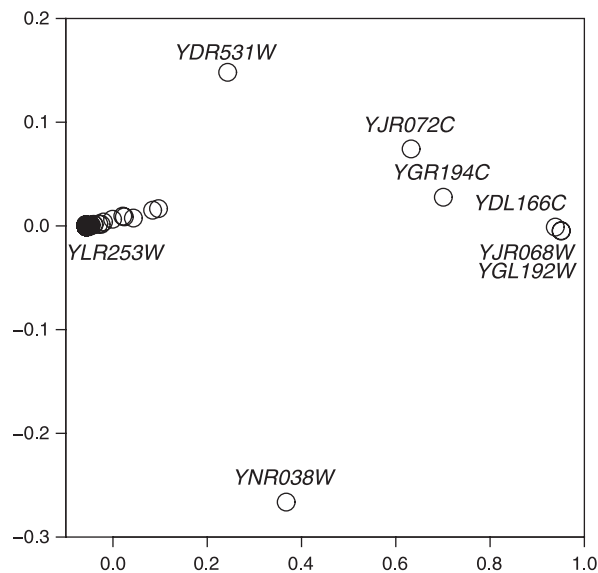


FIG. 7.