



Figure S3 RAD-seq neighbor-joining tree of the 38 *S. cerevisiae* strains used in both this study and a previous population analysis that used whole genome sequencing (compare to LIU *et al.* 2009 Figure 1C). Branch lengths are proportional to sequence divergence measured as P-distance. Scale bar indicates 10 polymorphisms/ 10 kb of sequence. The 2 divergent positions for strain K11 are likely caused by mislabeling of the strain used for the “K11r” sequencing. Strains comprising the 5 lineages identified in LIU *et al.* 2009 have been labeled (North America, Sake, Malaysian, West African, Wine/European).