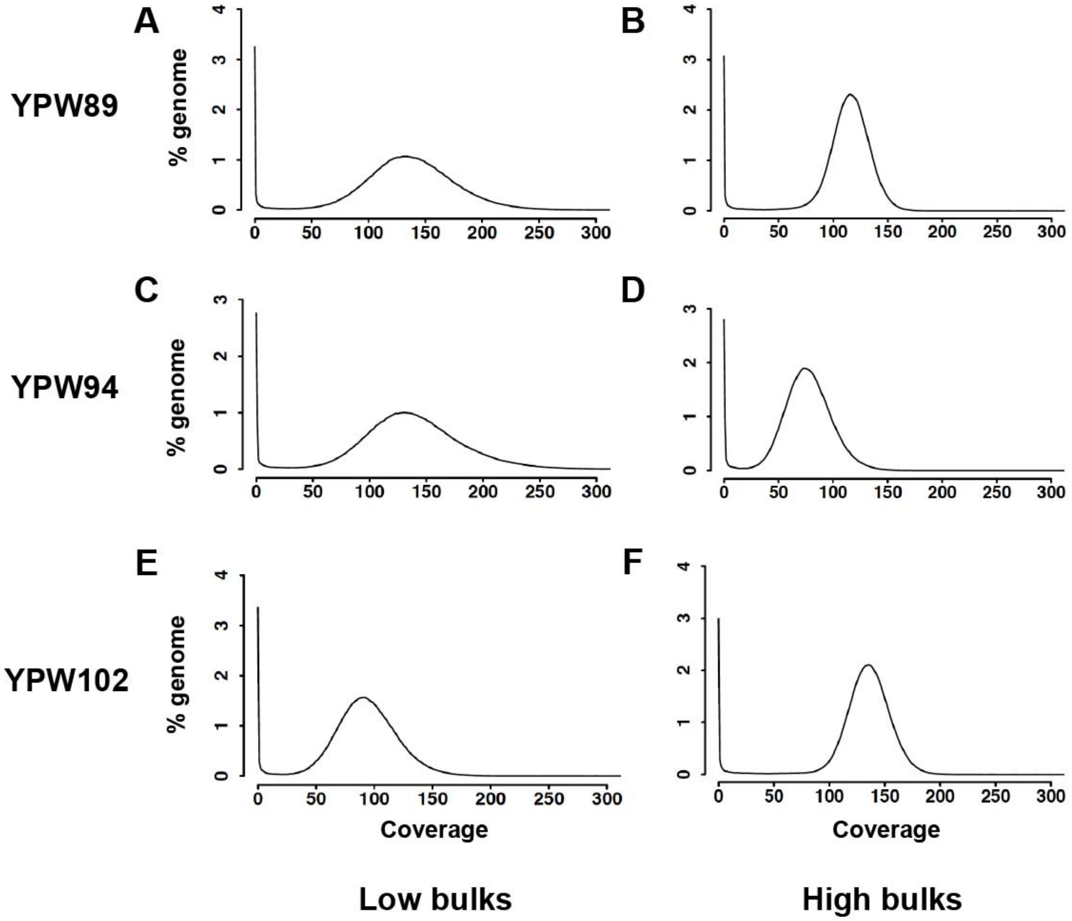

Figure S9 Sequencing coverage for each bulk shows two peaks. Distributions of sequencing coverage across reference genome are shown for low (A,C,E) and high (B,D,F) bulks obtained from mutants YPW89 (A,B), YPW94 (C,D) and YPW102 (E,F). Note the peak at 0, which indicates sites with no overlapping sequencing reads, in addition to the peak near the average coverage for each sample.