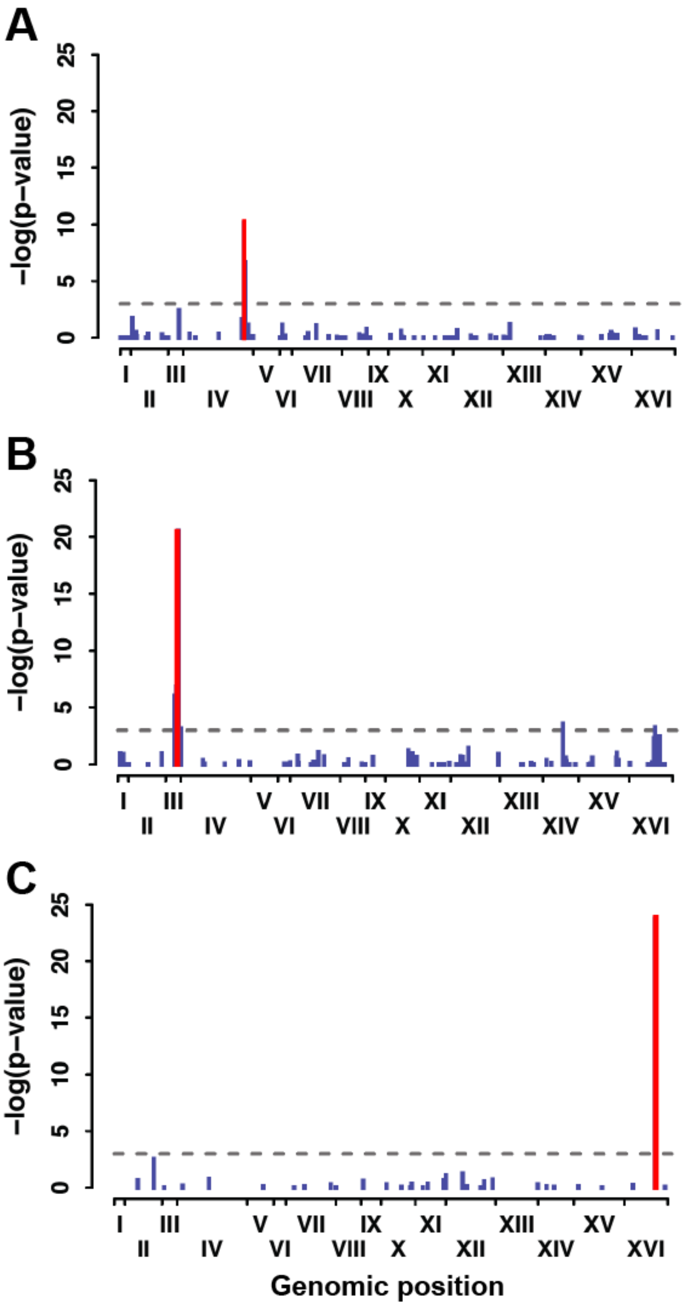

Figure S8 Tetrad-based mapping identifies the same candidate sites as BSA-seq. Mapping results from a more traditional mapping approach based on tetrad dissection are shown for mutant YPW89 (A), YPW94 (B) and YPW102 (C). Colored bars represent individual EMS-induced mutations with their genomic position represented on x-axis and significance of the difference in allele frequency between low fluorescence and high fluorescence bulks represented on y-axis (negative logarithm of *P*-value from G-test). For each mutant, the most significant site identified by BSA-seq is shown in red. Horizontal dotted lines represent a significance threshold of α=0.001.