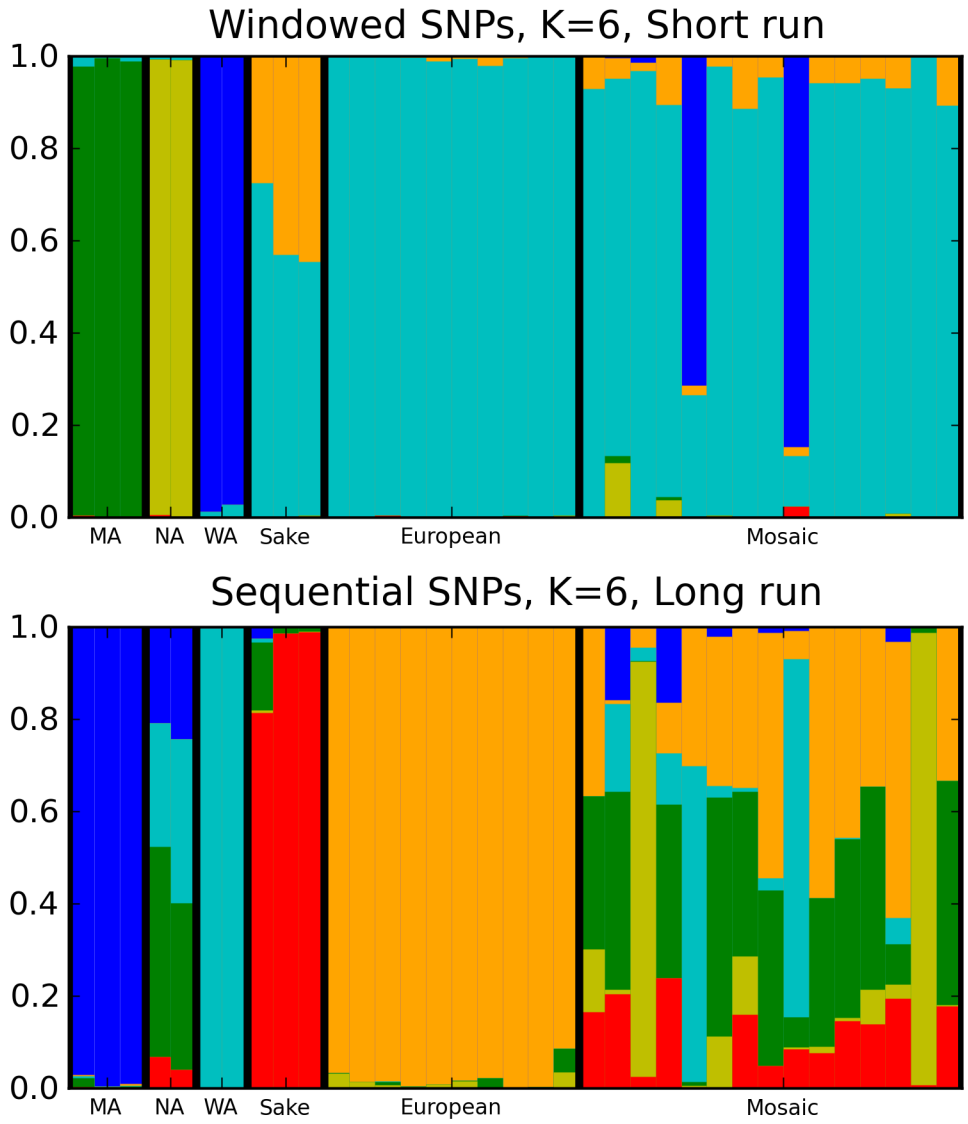

Figure S1 This figure shows a comparison of representative runs of the program, STRUCTURE, using SNPs selected according to the windowed (top) and sequential (bottom) methods. Although some populations, such as the Malaysian (MA) and West African (WA) strains, separate well in both cases, the European and mosaic strains are effectively indistinguishable when using the windowed SNPs.

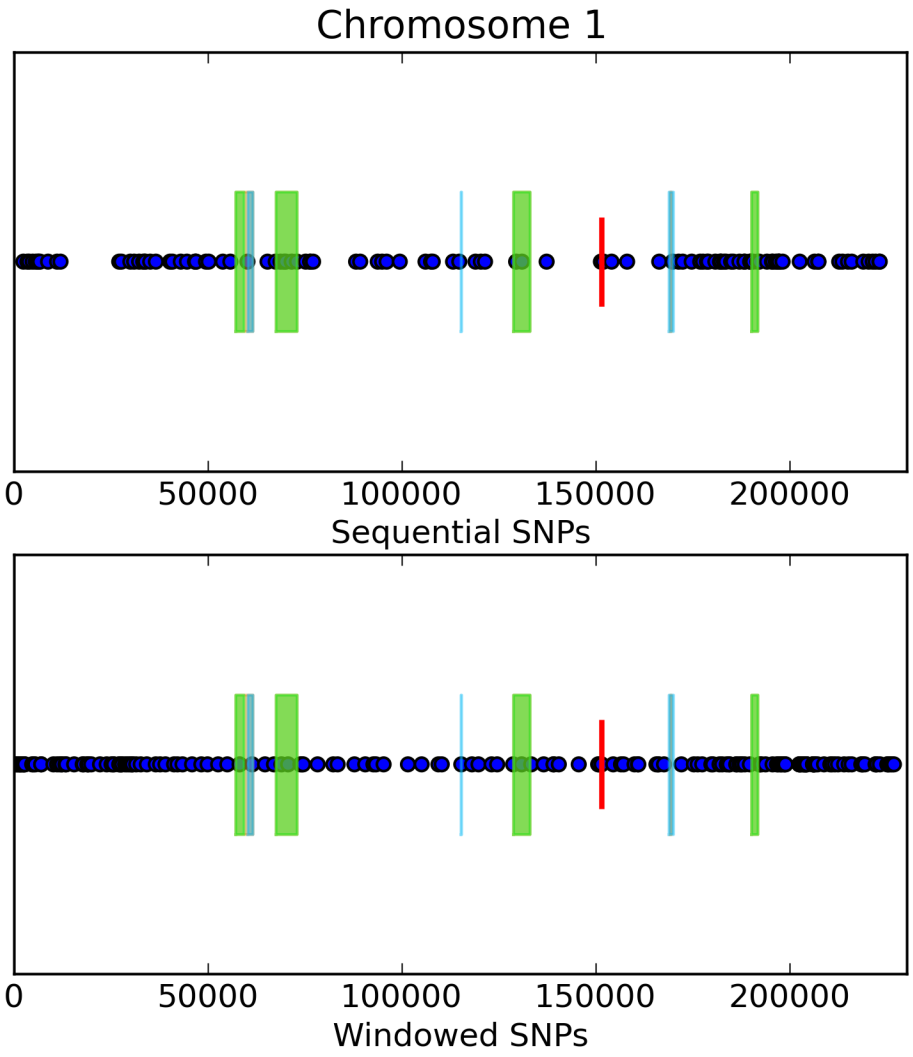

Figure S2 This figure shows that SNPs selected by the windowing method (bottom) tend to be more uniform across the genome whereas SNPs selected by the sequential method (top) tend to follow the recombination landscape of the genome more closely. Red lines represent centromere position, bright green rectangles represent crossover recombination hotspots, cyan rectangles represent non-crossover recombination hotspots, and orange represents overall recombination hotspots.

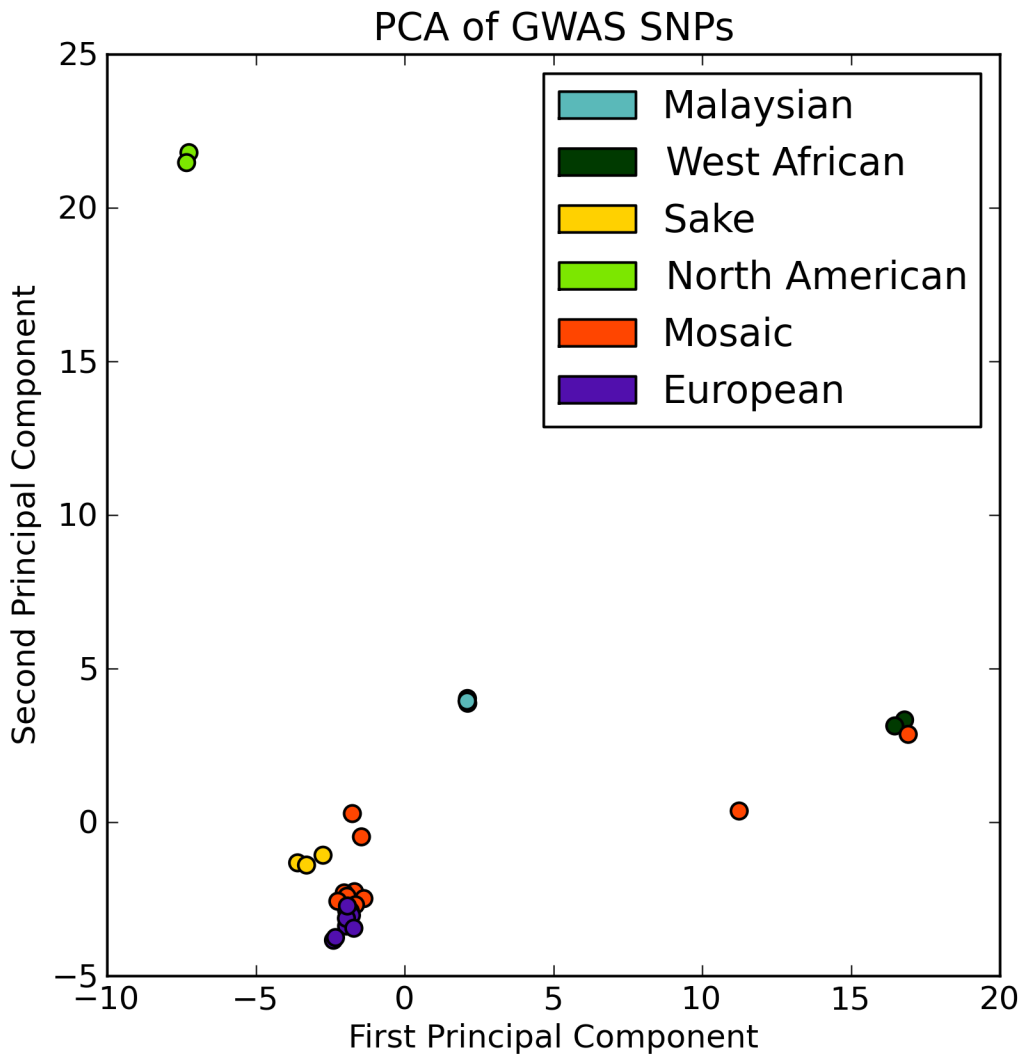

Figure S3 Each *S. cerevisiae* strain is plotted on the first two principal components, after performing principal components analysis on the genotype matrix.

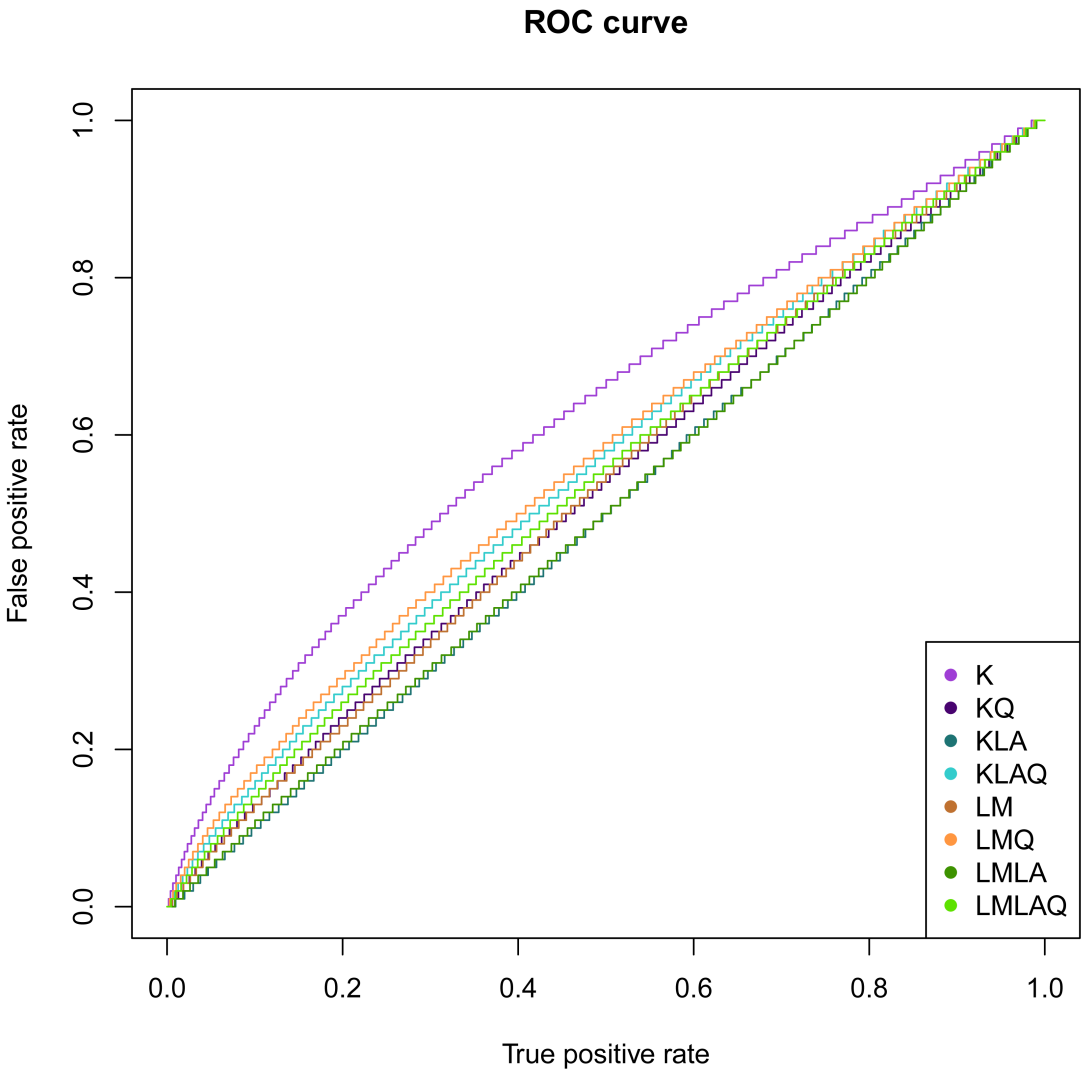

Figure S4 ROC curve of simulations with 100 causal SNPs each adding phenotypic value 1.

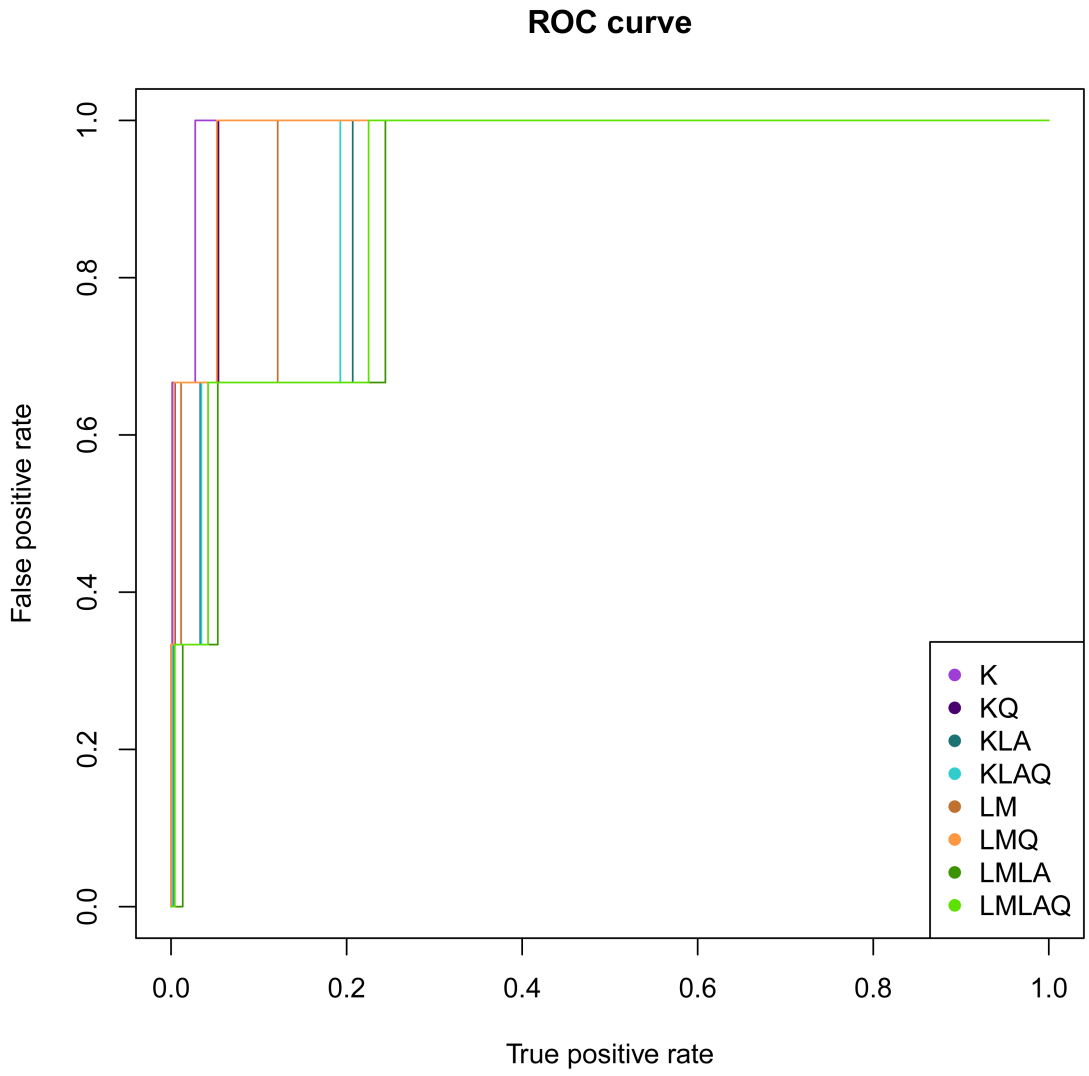

Figure S5 ROC curve of simulations with 3 causal SNPs each adding phenotypic value 10.

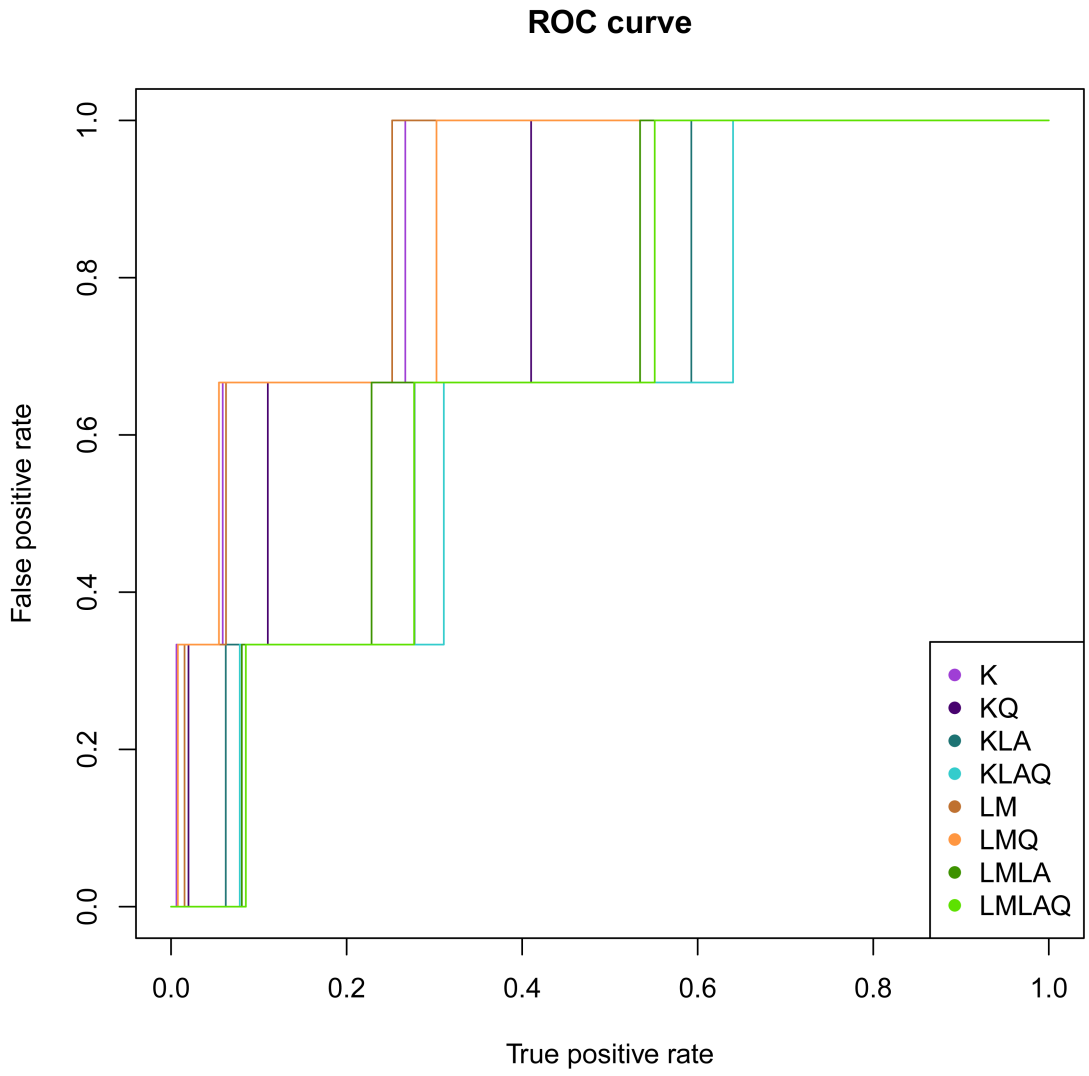

Figure S6 ROC curve of simulations with 3 causal SNPs, each adding phenotypic value 10, with a base phenotypic value given by one trait from (WARRINGER *et al.* 2011).

Table S1 This table gives summary statistics of the mean squared distance (MSDs) of all GWAS methods used over all phenotypes. This data is also shown in Figure 2.

	Mean	Median	Std dev
R-LM	0.010	0.0060	0.012
R-Q	0.0040	0.0016	0.0063
EMMAX-K	0.0028	0.0017	0.0032
EMMAX-QK	0.0073	0.0040	0.0088
R-LA	0.0065	0.0024	0.0100
R-LAQ	0.0036	0.0014	0.0058
EMMAX-KLA	0.0031	0.00095	0.0067
EMMAX-KLAQ	0.015	0.010	0.014
TASSEL-K	0.0038	0.0027	0.0035
TASSEL-QK	0.0050	0.0024	0.0076

Table S2

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.144790/-/DC1 as an Excel file.

This table shows a comparison between the SNPs found by our GWAS analysis and the previously published causal SNPs in (CUBILLOS *et al.* 2011; WARRINGER *et al.* 2011). For each condition and each GWAS method we list (1) the number of SNPs found and (2) what the fraction of all significant SNPs at a nominal P-value threshold of 0.05 were associated with the phenotype. The highest ranking method according to criterion (2) is shown in bold.