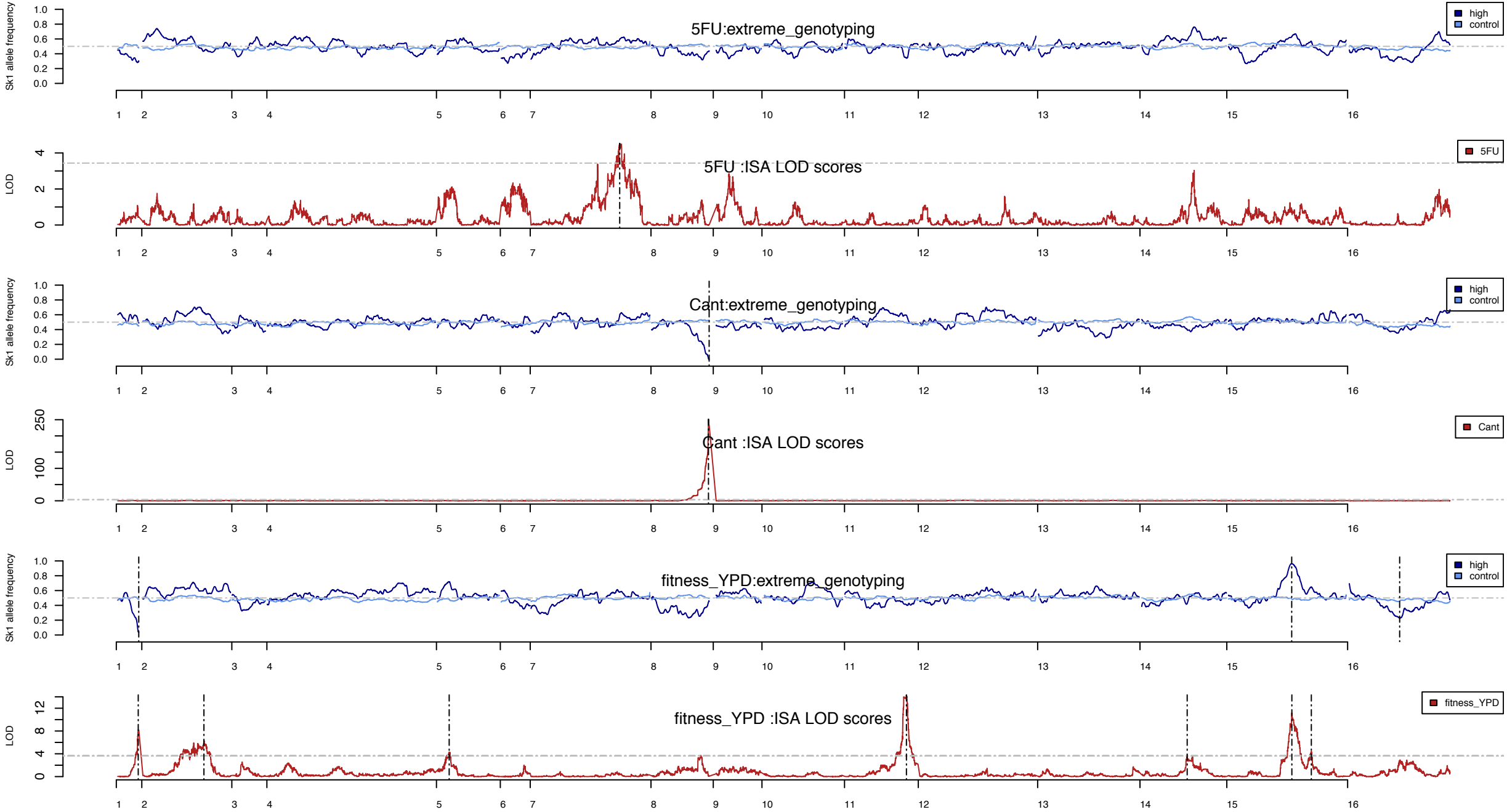
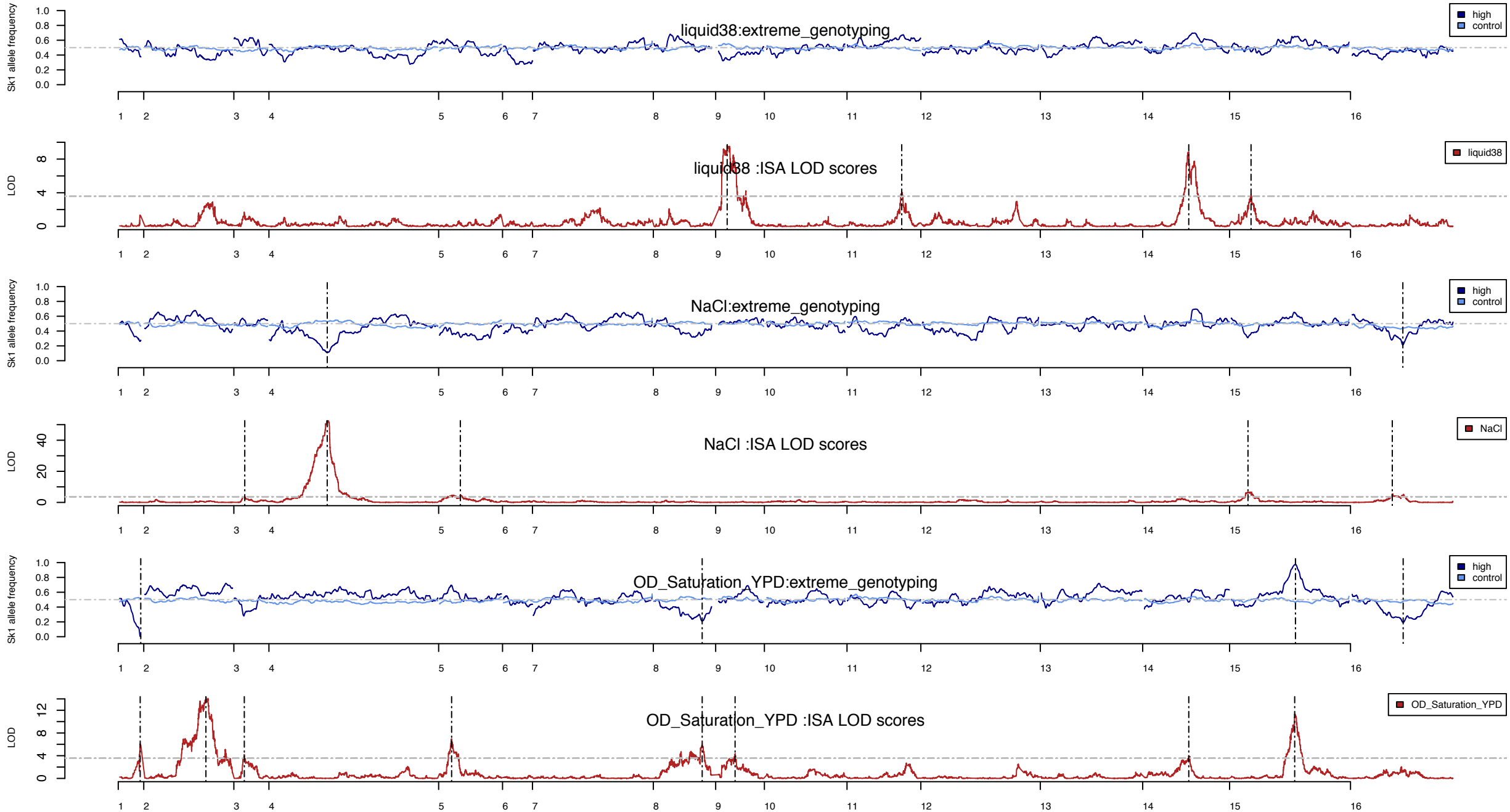

5FU:extreme_genotyping
Sk1 allele frequency
high
control
5FU :ISA LOD scores
LOD
5FU
Cant:extreme_genotyping
Cant :ISA LOD scores
Cant
fitness_YPD:extreme_genotyping
fitness_YPD :ISA LOD scores
fitness_YPD


liquid38:extreme_genotyping
Sk1 allele frequency
high
control
liquid38 :ISA LOD scores
LOD
liquid38
NaCl:extreme_genotyping
NaCl :ISA LOD scores
NaCl
OD_Saturation_YPD:extreme_genotyping
OD_Saturation_YPD :ISA LOD scores
OD_Saturation_YPD

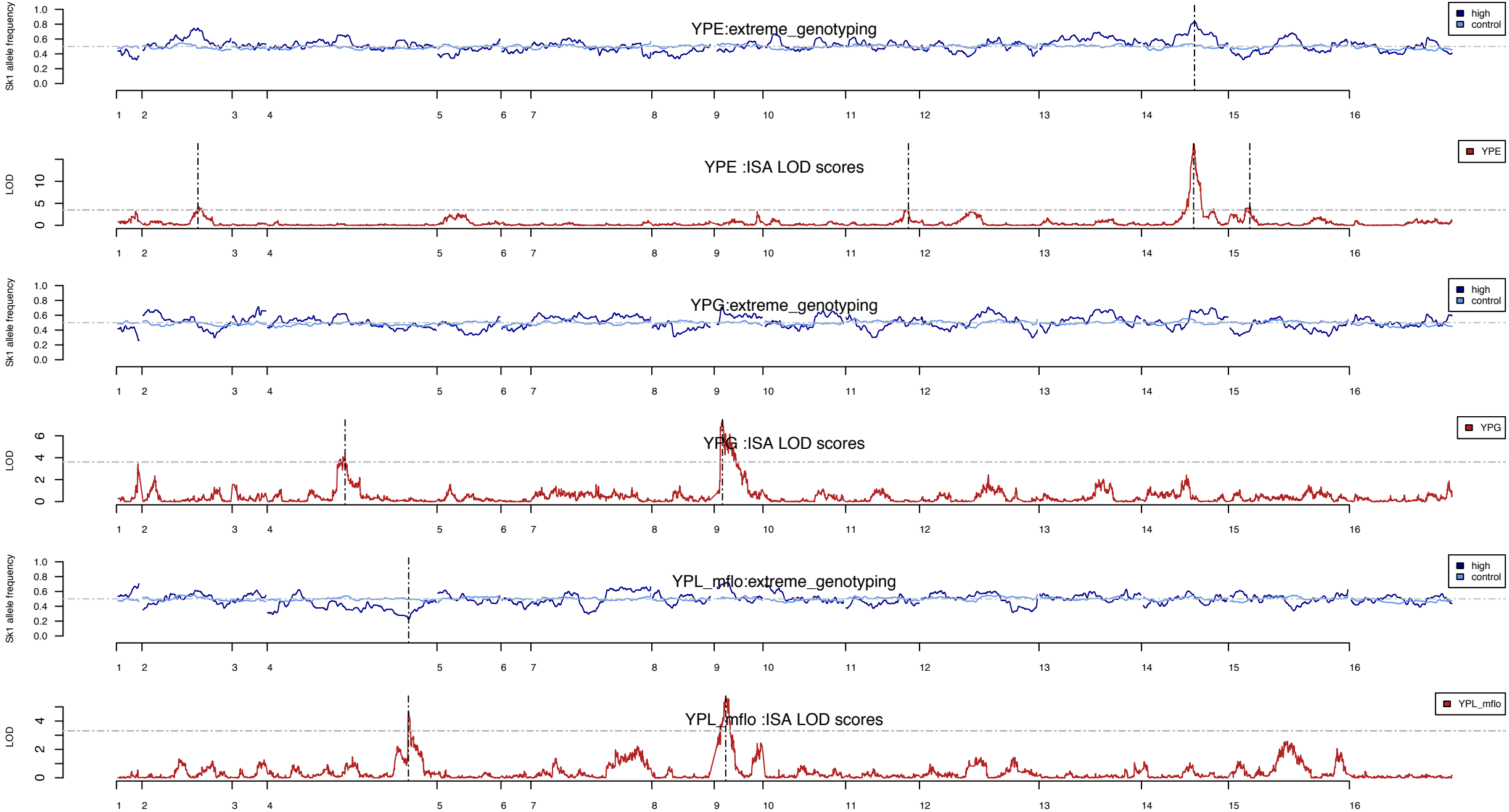

YPE:extreme_genotyping
Sk1 allele frequency
high
control
YPE :ISA LOD scores
LOD
YPE
YPG:extreme_genotyping
YPG :ISA LOD scores
YPL_mflo:extreme_genotyping
YPL_mflo :ISA LOD scores

Figure S1: Extreme genotyping versus linkage analysis. Comparison of the QTLs mapped using Bulk Segregant Analysis of the top 50 segregants versus linkage analysis of 720 segregants. For each phenotype, the top 50 performing segregants were selected and the combined allele frequency of these 50 segregants were estimated at each SNP loci by counting the number of SK1 and S96 alleles at each loci. The allele frequency was smoothed using a local polynomial regression assuming a binomial distribution and peaking calling performed, as in previous BSA analysis. To determine the 5% significance threshold, a permutation test was performed where the phenotype-genotype labels were swapped and 50 segregants selected from the top 50 of this permutated dataset. The peaking calling was repeated and the maximum deviation of the peak from 0.5 allele frequency was calculated. Over such 1000 permutations, the 95% quantile of the deviation was estimated and used as threshold for calling significant peaks in the actual observed BSA dataset. The significant peaks in the observed BSA data are marked with a dotted line, likewise the called QTLs in the ISA analysis.