

Figure S5-1: Neutrality tests using the Bayesian framework of BAYESCAN for SSRs with di- and tri/hexa-nucleotide repeats, separately. Outliers (identified by their names) are to right of the thick black lines, whereas positive selection outliers are in the upper parts and balancing selection outliers in the lower parts of the graphs.

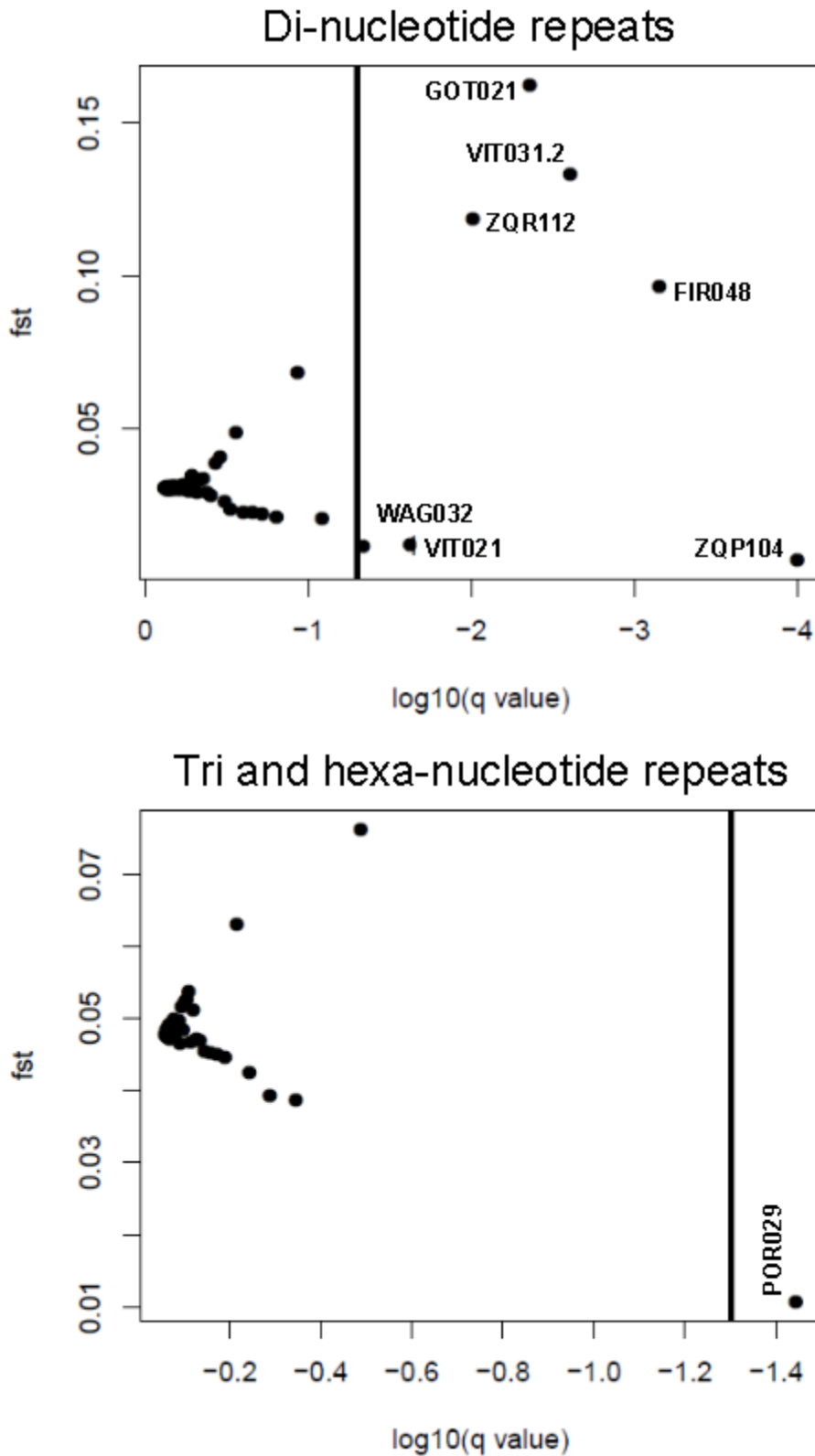
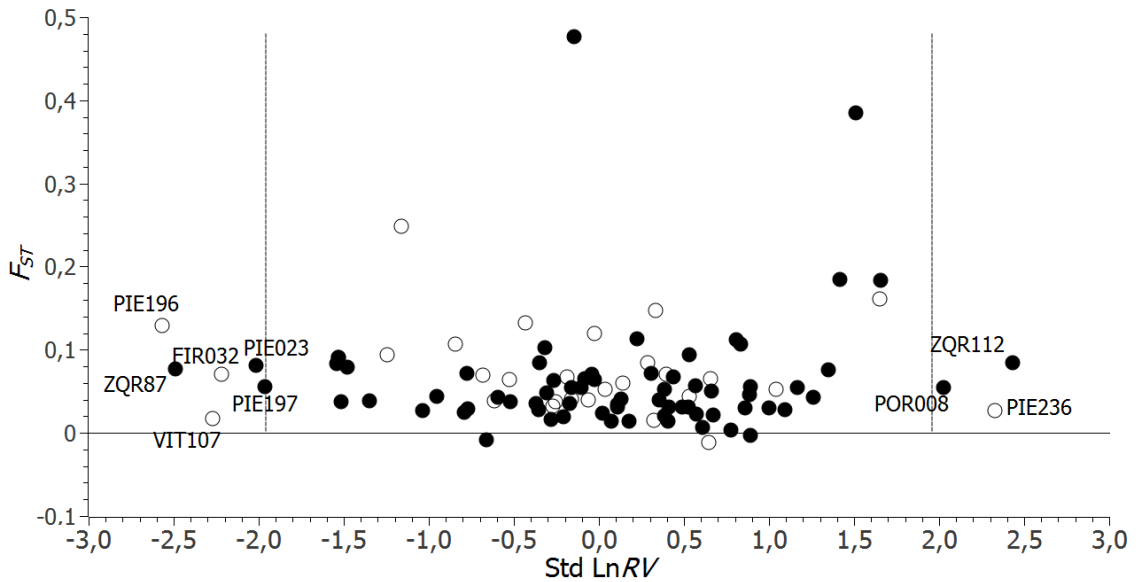


Figure S5-2: Neutrality tests for the variances in the number of SSRs motif repeats (a; $\ln RV$) and the heterozygosity (b, $\ln RH$). Dashed lines indicate the 95% confidence limits of the standardized normal distributions. The set of 69 markers initially genotyped is indicated by black dots, whereas the set of 29 additional markers selected from bins containing outliers is shown by open dots. Outliers are labelled with the SSR name.

a



b

