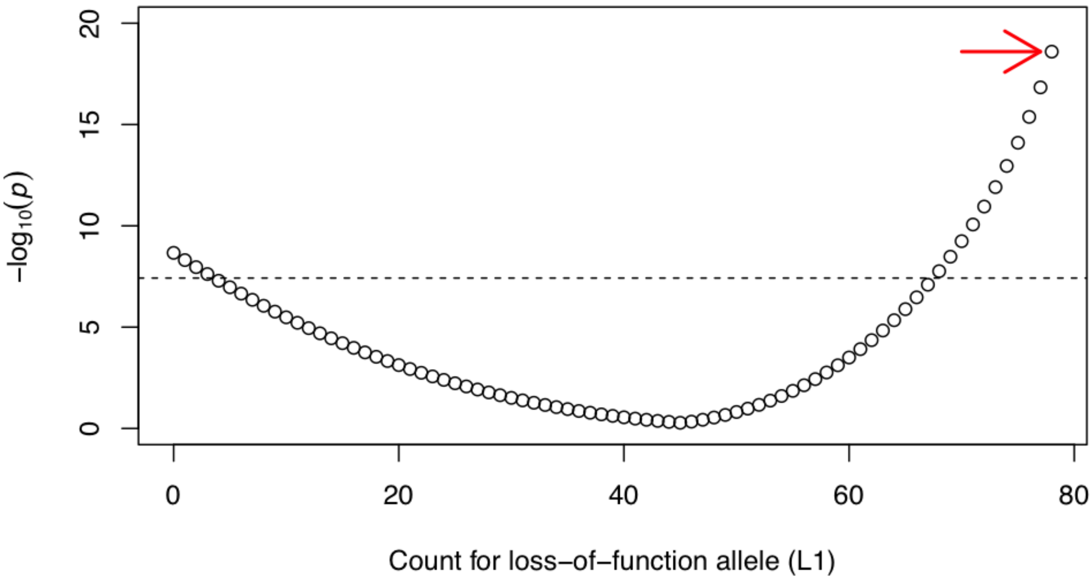

Figure S4 Distribution of test statistic for the loss-of-function genome scan. Plotted are the negative $\log_{10}$ *P*-values for every 2×2 contingency table with the same marginal frequencies as the observed contingency table for the *tan1-a* allele (*i.e.* same overall frequencies of phenotypes and genotypes). The dashed line indicates the Bonferroni-corrected *P*-value of 0.01 and the red arrow indicates the observed test statistic for the *tan1-a* allele.