



Figure S1 Schematic view of the distinction between gametic and zygotic TRD. First, the maximum log-likelihoods of the genotype frequencies under the null (i.e. Mendelian), gametic, and zygotic model are calculated. Then, likelihood ratios are compared to cumulative chi-square distributions with appropriate degrees of freedom (see main text) evaluated at significance level alpha. If this comparison suggests that the data is better explained by the alternative hypothesis, the arrow labeled “yes” is followed, otherwise the arrow labeled “no” is followed.