Figure S4  Genome-wide map of interval hotness for the non-interfering P2 pathway. x-axis: marker intervals in Mb (Mb) along the chromosome considered (corresponding genetic positions also provided in centiMorgan or cM), y-axis: minus the natural logarithm of the p-value of Pearson’s chi-square comparison test for that interval. This p-value corresponds to the null hypothesis that the two-pathway Gamma model fits the data and in particular that the P2 COs are uniformly distributed in genetic positions along the chromosomes. The dashed horizontal line shows the FWER (family-wise error rate) of 5% when using the Bonferroni correction for the multiple tests on the chromosome considered. Compared to Figure 5 of the main text, the data set has been filtered: all cases where a gamete is doubly recombinant in two adjacent intervals have been removed.