Figure S4 The sensitivity and specificity of mapping is affected by the size of the window used to calculate the mapping score. Graphs showing the genome-wide mapping scores using a sliding window of 15 Mb in size for all mutants (above), or a sliding window of 3 Mb in size for *wdd* (below), rather than the 20 cM windows used in our analysis. When 15 Mb sliding windows are used, in only three of the five mutants (*moto, frnt, sump*) the linked region is contained within the window with the highest mapping score in the genome (red arrows). In *hlw* the linked region is contained within the peak with the third highest mapping score (red arrow). In *wdd,* the linked region is not detected by an increase in the mapping score (asterisk), because the linked interval on Chr8 spans only 4 Mb. When a 3 Mb window was used for *wdd*, which should be small enough to detect the linked region, a mapping score peak appears at the linked interval (red arrow), but it is only the 5th highest peak.