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.