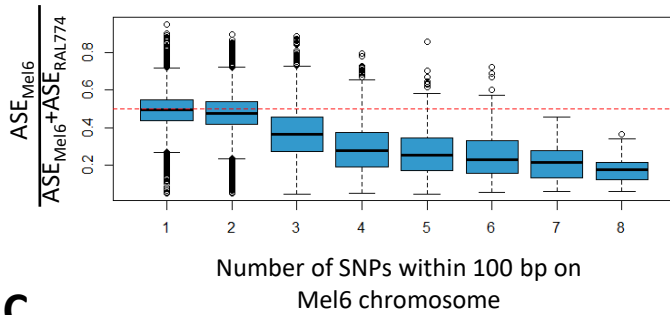
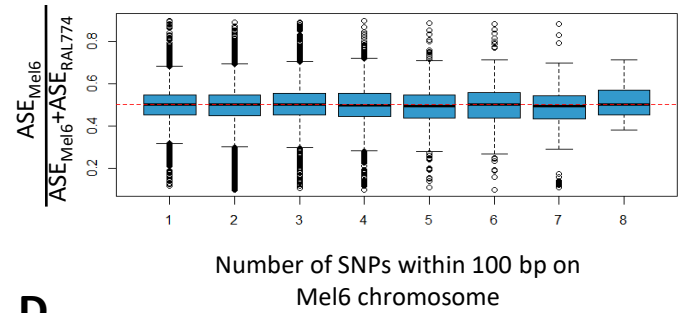
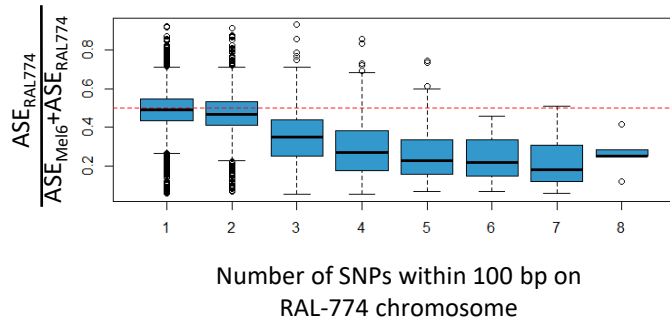
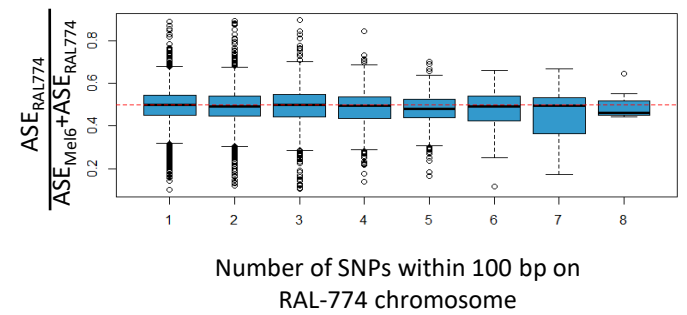


**A****B****C****D**

**Fig. S2 Correction for mapping bias in F1 body samples from the Mel6 × RAL-774 cross.** Biases in ASE ratios due to the increased number of SNVs within 100 bp of tag SNVs of Mel6 (A) and RAL-774 alleles (C) when mapped only to the *D. melanogaster* reference genome. ASEs obtained by using three different genomes for mapping (see Fig. S1) are shown for Mel6 (B) and RAL-774 alleles (D). Regions where the counterpart chromosome did not have any SNVs against the reference genome were used for analysis. Note that in (A) and (B), the AER of the target genome tends to be underestimated when multiple SNVs exist between the reference genome and the target genome within a short distance, but not in (B) and (D).