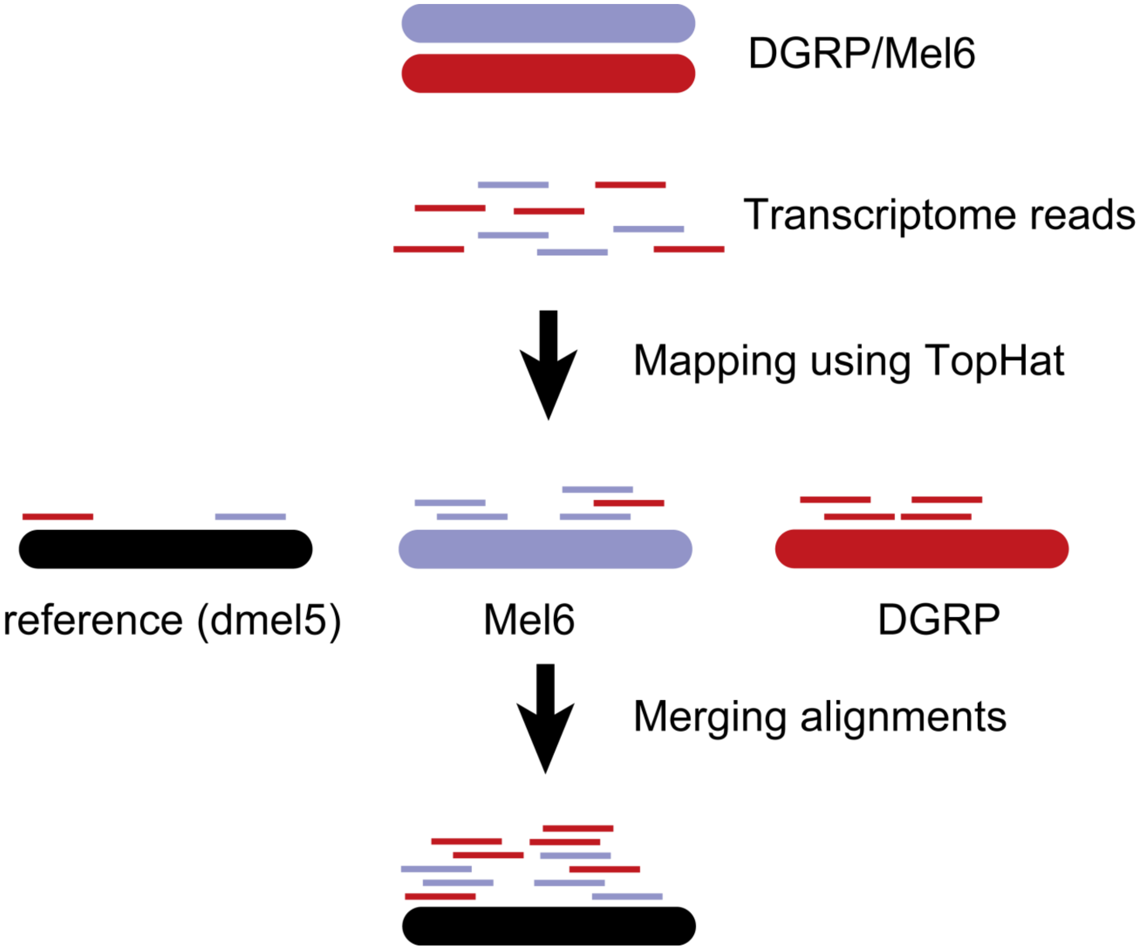

Fig. S1 Schematic figure describing the mapping strategy for ASE estimation. Transcriptome reads from an F1 individual obtained from the Mel6 × DGRP cross were mapped to three different genomes simultaneously. These were the reference *D. melanogaster* genome (version, dmel5.2), Mel6 genome, and the corresponding DGRP genome. Tags were mapped to genomic regions with the highest alignment scores. If there were multiple hits with identical alignment scores in cases of reads mapped to SNV-absent regions, they were assignment to one of the genomes randomly. The alignments were subsequently merged into a single alignment. The reference genome sequence was used to cover regions with ambiguously defined sequences in the Mel6 and DGRP genomes, potentially causing mapping errors.