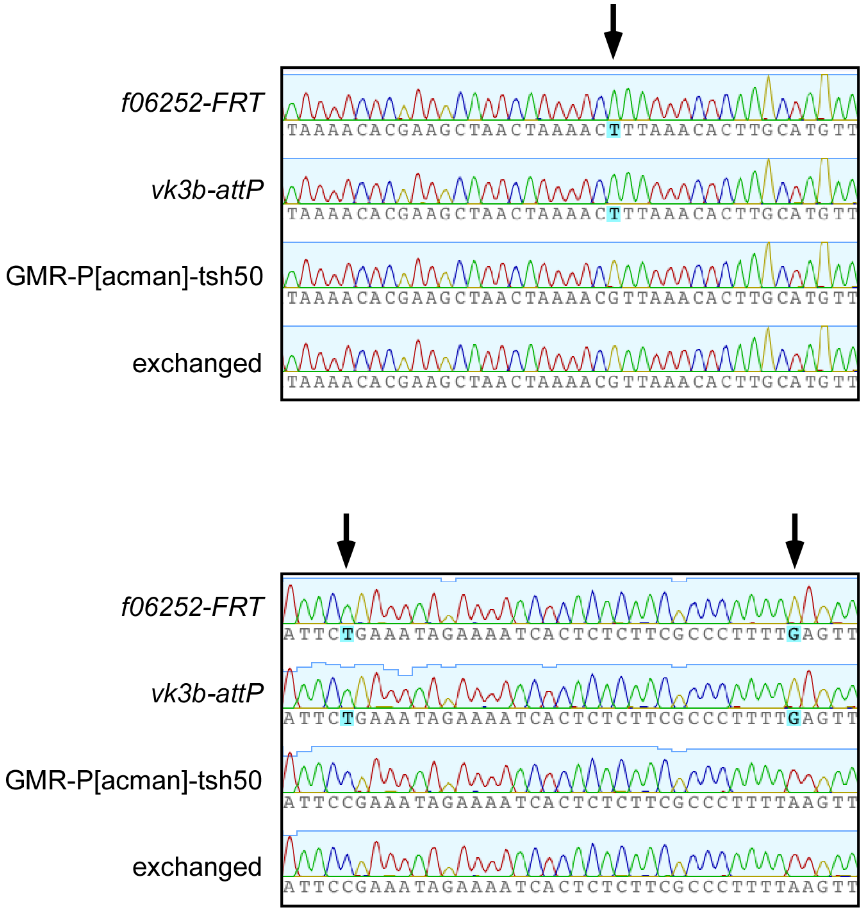

Figure S1 SNP analysis of candidate exchange flies. Shown are traces identifying three SNPs in the 706 bp genomic region amplified by the primer pair SNP2F/SNP2R within the captured segment. For each box, the templates for amplification were: Row 1, *f06252-FRT* genomic DNA (parent chromosome); Row 2, *vk3b-attP* genomic DNA (parent chromosome); Row 3, purified BAC GMR-P[acman]-tsh50 (donor plasmid); Row 4, genomic DNA from candidate y^- w^- flies following exchange. For each SNP, only the BAC allele is observed in genomic DNA of candidate flies. We identified a total of 5 SNPs in this region that differentiate BAC DNA from both parent chromosomes, and in all cases, the allele observed in the BAC was the only allele observed in the amplified region from the genome of candidate flies. In addition, a total of 3 SNPs from a second independently amplified 797 bp region defined by primers SNP5F/SNP5R gave identical results.