Figure S1  Two dimensional, two-QTL scans for the *D. sechellia* w30 (A) and *D. simulans* Nueva (B) backcrosses. For each graph, the top triangle shows the improvement in fit of the full model over a single QTL model (LOD$_{fv1}$), the bottom right triangle shows the improvement in fit of the additive model (LOD$_{av1}$) over the single QTL model. A) In the *D. sechellia* w30 backcross, little difference is found between the LOD$_{fv1}$ and LOD$_{av1}$ models. The significant interaction between the two QTL on chromosome 3 is additive: ~3:45,009,000 x ~3:15,860,000 (LOD$_{fv1}$ = 10.0, LOD$_{av1}$ = 9.6, LOD$_{epistasis}$ = 0.38). These locations correspond to QTL-III$_{sec}$a and QTL-III$_{sec}$c. B) *D. simulans* Nueva backcross. A locus at ~3:47,008,000 interacts with a locus at ~X:15,002,000 (LOD$_{fv1}$ = 17.5, LOD$_{av1}$ = 16.7, LOD$_{epistasis}$ = 0.8), with a locus at ~2:41,005,000 (LOD$_{fv1}$ = 7.8, LOD$_{av1}$ = 7.2, LOD$_{epistasis}$ = 0.6), and at ~3:5,021,000 (LOD$_{fv1}$ = 6.6, LOD$_{av1}$ = 5.7, LOD$_{epistasis}$ = 0.9). The region at ~2:41,005,000 also interacts with the locus at ~X:15,002,000 (LOD$_{fv1}$ = 8.3, LOD$_{av1}$ = 7.2, LOD$_{epistasis}$ = 0.6) and with a second region on chromosome 2: ~2:9,010,000 (LOD$_{fv1}$ = 6.3, LOD$_{av1}$ = 5.1, LOD$_{epistasis}$ = 1.2). The significance of all the LOD$_{fv1}$ and LOD$_{av1}$ interactions met or exceeded the $p = 0.01$ threshold, but no epistatic interactions were significant. The locations of the loci reported here are all within the confidence intervals of QTL-II$_{sim}$a, QTL-III$_{sim}$a, QTL-III$_{sim}$b and QTL-X$_{sim}$.