

**Table S1.** Polymorphisms found in *tub<sup>ste</sup>* chromosome within the 25 kb region determined via site-specific recombination to be responsible for the *tub<sup>ste</sup>* variable phenotype. Sequence polymorphisms are relative to the reference genome and a functional *tube* cDNA (Celniker *et al.* 2002; Letsou *et al.* 1993); all were also found in *tub<sup>7</sup>* and *tub<sup>8</sup>*. Locations of site-specific recombination sites and of the beginning and end of the *tube* transcription unit are noted under Reference Points.

### Polymorphisms

Description	Location
4 bp deletion (TTAG)	3R: 205,032 - 205,035
Single base substitution (A > G)	3R: 206,259
1 bp deletion (T)	3R: 207,180
4 bp deletion (ATTT)	3R: 213,067 - 213,070
7,400 bp insertion ( <i>opus</i> )	3R: 213,161
Single base substitution (T > A)	3R: 219,883
Single base substitution (G > C)	3R: 220,488
Two base substitution (GC > AA)	3R: 223,222 - 223,223

### Reference points

Description	Location
Proximal recombination site	3R: 204,648
<i>tube</i> transcription start site	3R: 213,460
End of <i>tube</i> transcription unit	3R: 215,536
Distal recombination site	3R: 223,611