Figure S3  Molecular lesions in hst-6 and sqv-6.

A. hst-6 gene structure with molecular lesions of dz134, and dz151, dz168 alleles indicated. Alignments of HST-6 with fly (Dm), mouse (Mm) and human (Hs) orthologs to show mutations within their molecular context. Asterisks and colons indicate perfectly conserved and well conserved residues, respectively. 3’PSB (phosphoadenosylphosphosulfate) binding site. SL1: the cDNA is transspliced to a SL1 leader sequence.

B. Scatterplot of chromosome V displaying the ratio of the number of sequencing reads showing the CB4856 (Hawaiian) single nucleotide polymorphism (SNP) at a given position divided by the total number of sequencing reads at that position for dz165 using a combination of single nucleotide polymorphism and whole genome sequencing (Dotsidou et al. 2010). The mutations is to the left of the red line on the far end of chromosome V where this ratio approaches zero.

C. Schematic of the genomic and cDAN structure of the Xylosyltransferase sqv-6 with the mutation indicated. TD: transmembrane domain, WSC: is a putative carbohydrate binding domain (present in yeast cell wall integrity and stress response component proteins). SL1: the cDNA is transspliced to a SL1 leader sequence.