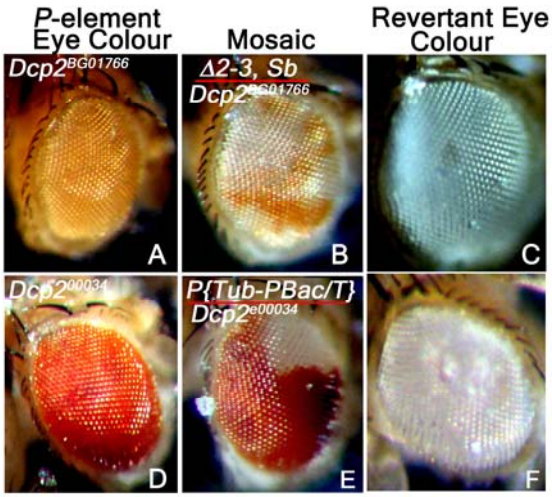
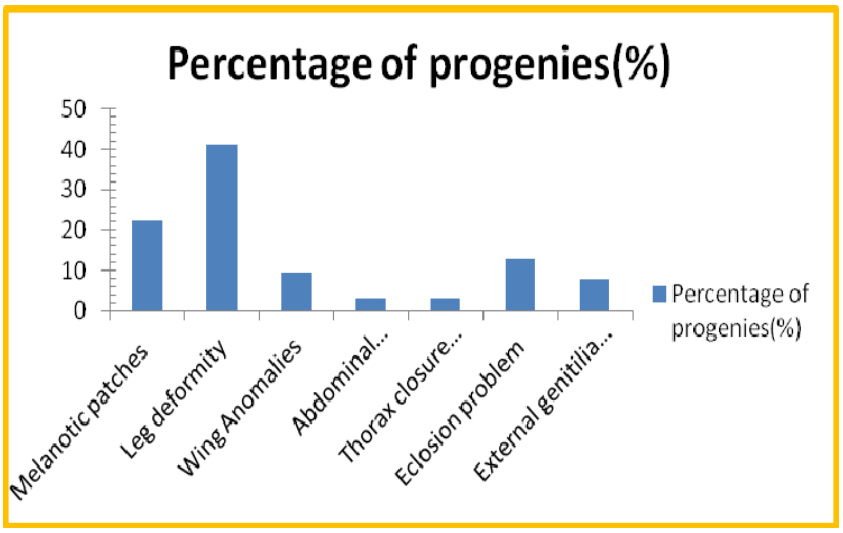
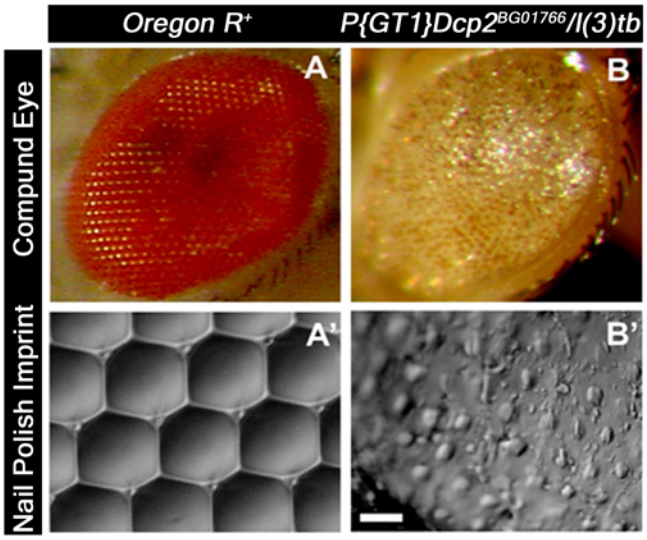


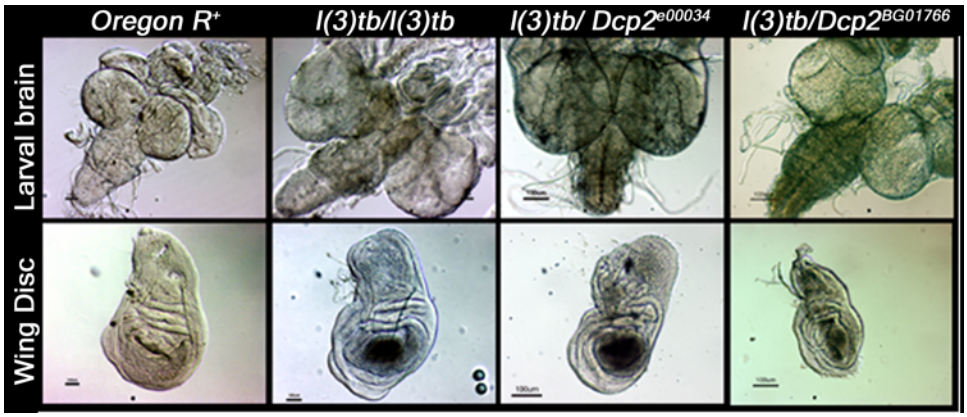
Supplementary Figure S1. Reversion analysis by the excision of *piggyBac* transposon in *DCP2*^{e00034} with the help of *piggyBac* specific transposase source, *CyO, P{Tub-Pbac}2/Wg*$^{SP-1}$ and similarly by the excision of *P*-element in *DCP2*^{BG01766} strain using Δ*2-3,Sb/TM6B, Tb*^{1}, *Hu, e*^{1} transposase source as 'jumpstarter stock'. The *DCP2* revertant white eyed F2 flies were crossed to *l(3)tb* and lethal progeny were scored.



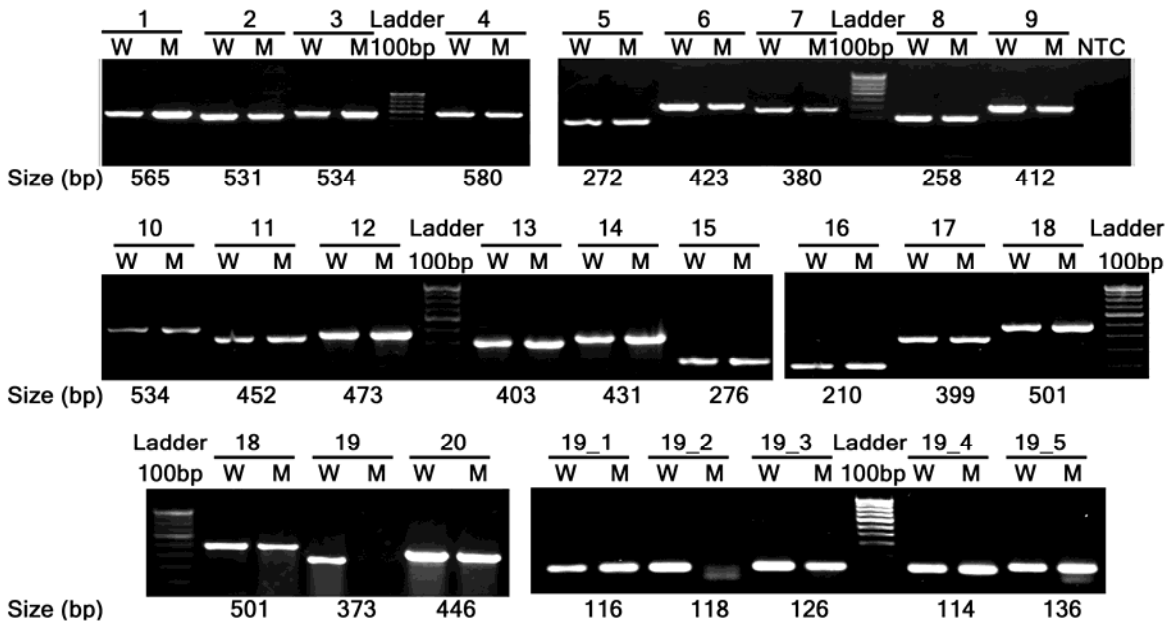
Supplementary Figure S2.. Morphological defects exhibited by escapees of adult fly trans-heterozygous for *P{GT1}DCP2*^{BG01766}*/l(3)tb*. The phenotype includes melanotic patches (22.2%) on the cuticular exoskeleton, abnormalities in leg (41.3%), wing (10%), abdomen (3.2%) and thorax (3.2%). Many of the trans-heterozygous progeny was observed to have eclosion problem (12.7%) and males have abnormal genitalia (9.7%).



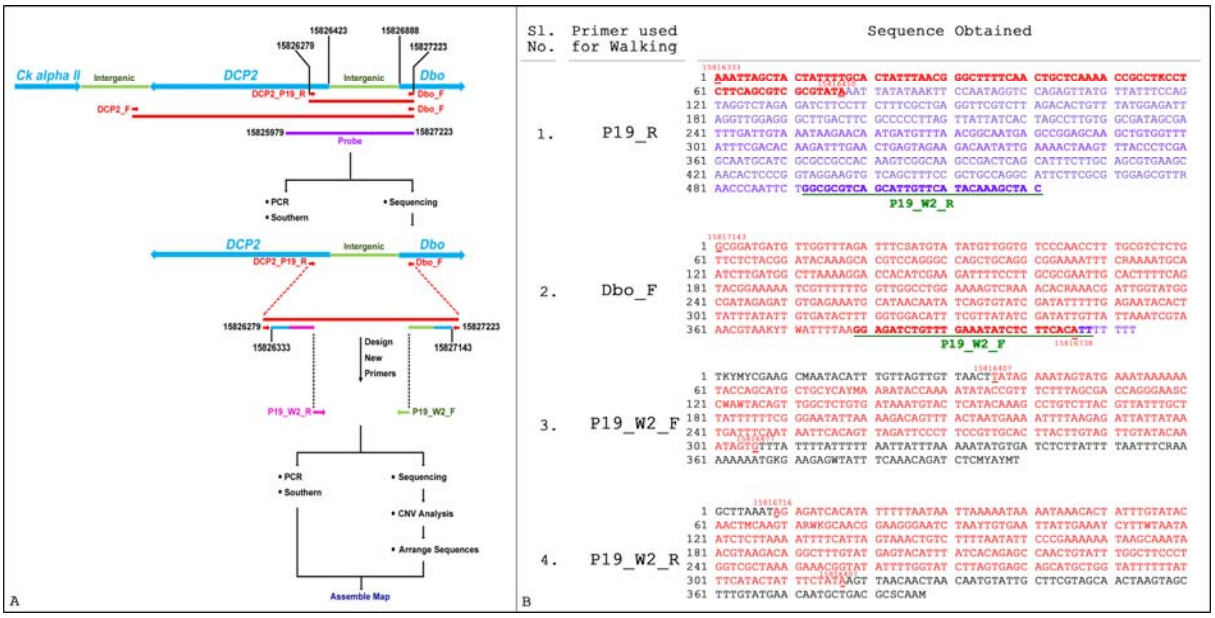
Supplementary Figure S3. **Pronouncement of severe defects in compound eyes of the escapees having heterozygous genetic background of the mutant *l(3)tb* with lethal *P*-insertion allele *DCP2*^{BG01766}.** Images in A and B showing the compound eye of wild type and tans-heterozygote respectively while A' and B' are their respective nail-polish imprint of the compound eye, viewed with the help of DIC or Nomarski microscope. The exact geometrical arrangement of ommatidia in a hexagonal pattern having each ommatidium surrounded by bristle was completely disrupted in the trans-heterozygote exhibiting the complete loss of arrangement in the ommatidial pattern. This represents the severe loss of polarity as it cues a complete disassembly of compound eye as whole. Bar represents 20µm.



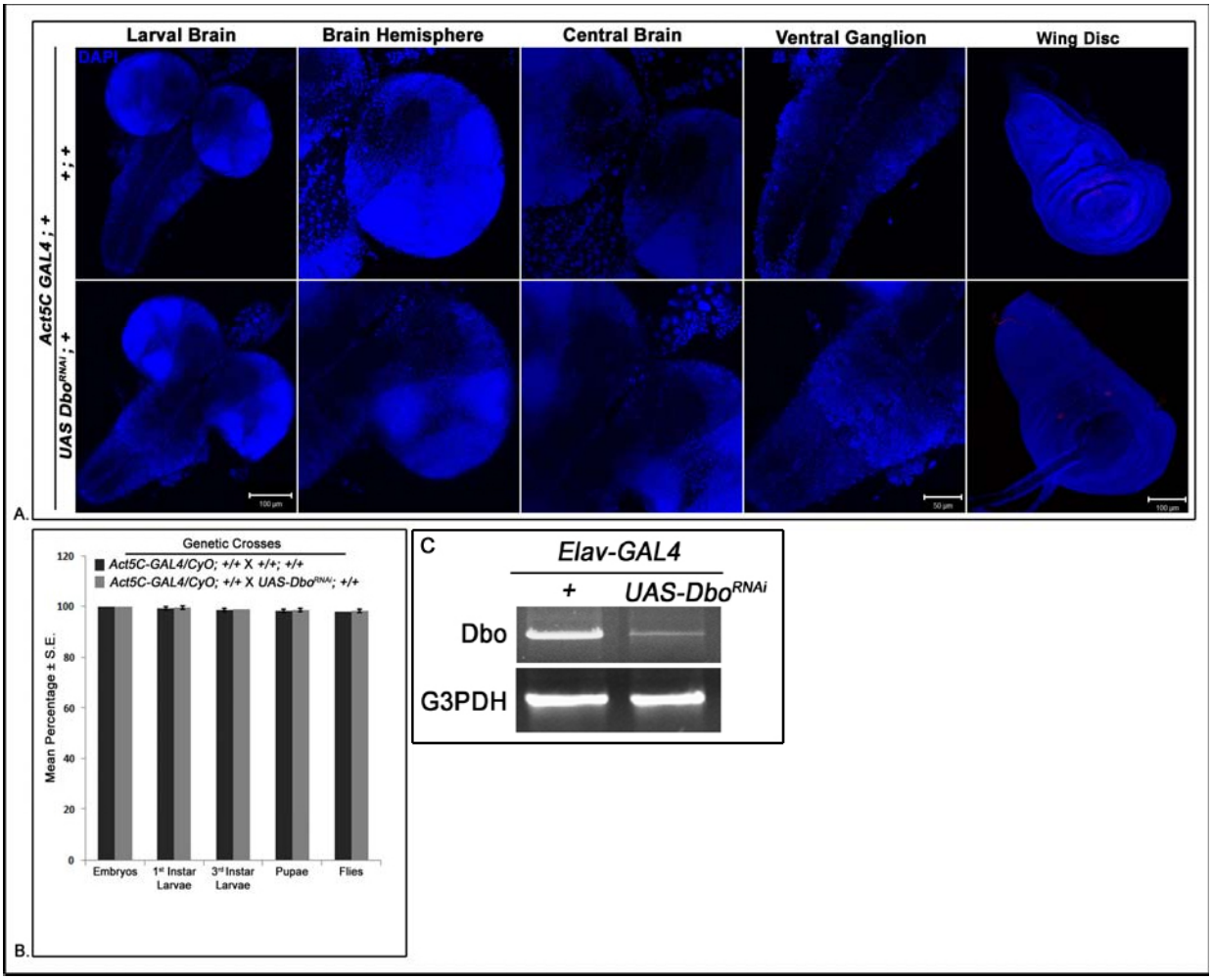
Supplementary Figure S4.Tumorous phenotype observed in larval brain and wing imaginal discs in trans-heterozygotes *l(3)tb /PBac{RB}DCP2*^{e00034} and *l(3)tb /P{GT1}DCP2*^{BG01766} as homozygous *l(3)tb* Scale bar is 100µm.



Supplementary Figure S5. Amplification of DCP2 gene using overlapping primers. All primers amplify same size of amplicon with DNA from wild type and homozygous l(3)tb mutant, except DCP2_P19 (3L:15819379..15819751) and DCP2_P19_2 (3L:15819452..15819569). This implies the probable mutation in the region.



Supplementary Figure S6. Schematic representation of the convergent bidirectional primer walking adopted for sequencing and alignment of the large amplicon obtained at the candidate region in *DCP2*$^{l(3)tb}$ homozygotes (A). Shown in differently colored arrows are the primers used for sequencing during walking. Reads aligning to the gene regions are represented by blue lines, while those aligning to the intergenic regions are depicted by green lines. The primers designed are represented in similar colors depending on their alignment in the sequence. The reads obtained on sequencing with each of the four primers is shown in B. The novel *Gypsy*-LTR sequence is shown in purple. Underlined in 1 and 2 are the sequences used as primers for the second-step of primer walking.



Supplementary Figure S7. Ubiquitous knockdown of *Diablo* does not lead to any developmental anomaly and does not affect survival of the driven progeny. Photomicrographs in **A** show the larval brain and wing disc stained with DAPI, while the bar graph in **B** depicts the survival of the *Diablo* knocked down progeny across the different stages of fly development. **C** shows the efficiency of knockdown as determined through semi-quantitative RT-PCR.