S5 Figure: Percent of the rearrangements identified by illumine paired-end sequencing confirmed by PacBio sequencing over the coverage depth of the PacBio sequencing We aligned PacBio sequence reads to the *D. yakuba* reference using a BLASTn with the repetitive DNA filter turned off and an e-value cutoff of $10^{-10}$. If a single molecule read blast within 2kb of the genomic rearrangement call it was counted as confirmation.