Figure S7. Simulation of insertion density effects: The triangles and circles shown in brown are obtained from real and simulated data, respectively. The green line shows the loess curve with 0.2 span and the light green region shows 95% confidence interval. Insertion resolution is calculated by dividing genome length by the number of insertion sites. (a) Matthew's correlation coefficient remains almost constant after the insertion index reaches 0.04. (b) The percentage of genes with insertions rises as we increase the insertion density, however the rate slows down after the 0.04 threshold.