

Figure S1. Number of genes affected by *Mu* insertions and distribution of insertions. (A) Number of tagged genes and associated mean gene length plotted against the number of *Mu* insertions. Only insertions in 5' and 3' UTRs, exons and introns of genes were considered. (B) Distribution of affected gene lengths plotted against the number of individual *Mu* insertions. The calculated Pearson correlation coefficient is r = 0.147. The number of insertions >50 ranges from 51 to 255 *Mu* insertions per gene.