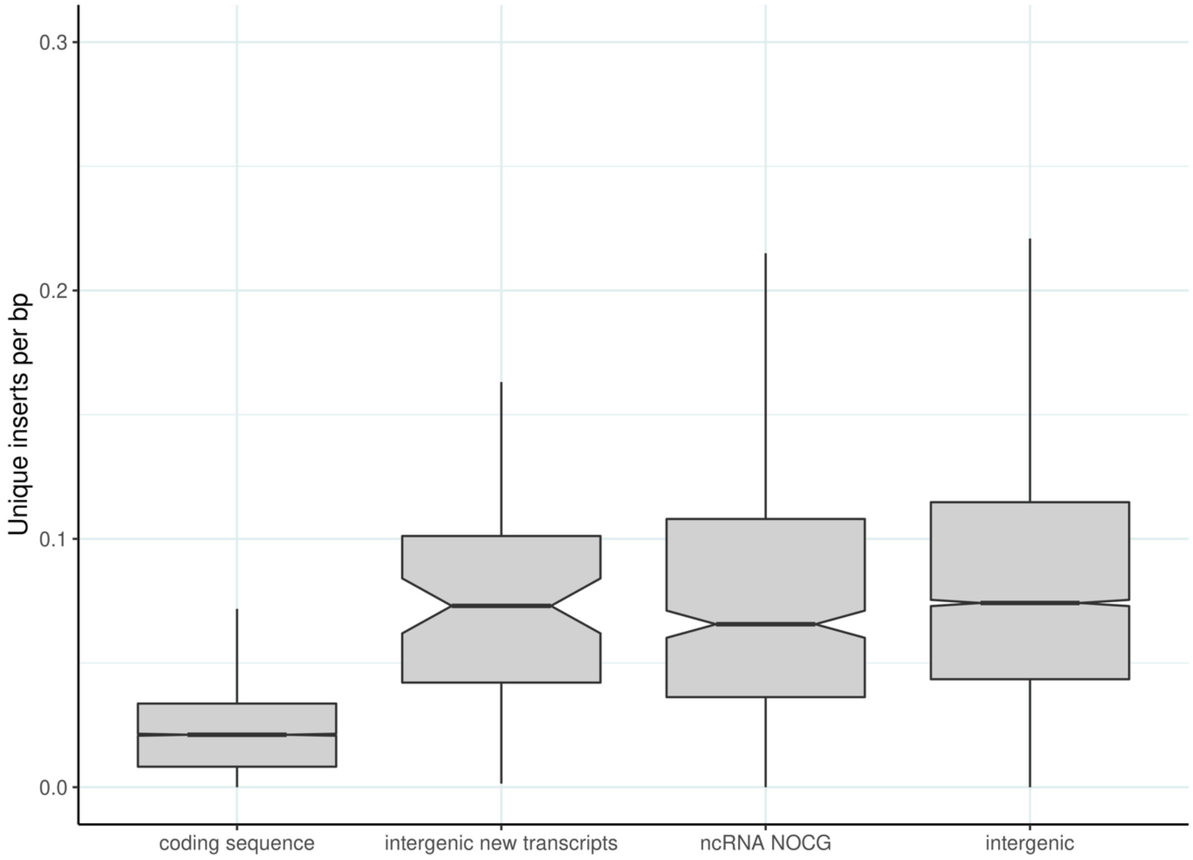

Fig S13. Fitness landscape of different kinds of transcripts and intergenic genomic regions. Number of unique transposon insertions (inserts) in coding sequences, intergenic new transcripts, ncRNA non-overlapping coding genes (NOCG) and intergenic genomic regions (intergenic). The data was from a previously published transposon mutagenesis experiment (Grech et al., 2019). Coding sequences show a much lower number of inserts than other regions, consistent with higher selective constraints. Intergenic new transcripts identified in the current study had a similar distribution of unique inserts than ncRNAs that did not show any overlap with coding sequences (NOCG). Transcripts overlapping coding genes were not considered. Intergenic genomic regions were defined as those that did not overlap any annotated gene (coding or ncRNAs). The number of unique inserts was normalized by the number of base pairs of each feature.