



Figure 3- figure supplement 1. Violin plots for twelve measured variables collected for the TEs located in either the core (blue) or LS (yellow) regions of the genome. Violin plots show the distribution of the values for each category, along with a box plot showing the mean (thick black line) 1st and 3rd quartiles, and whiskers extending to the furthest data point within 1.5 of the interquartile range. Differences between the core and LS values were measured using the non-parametric Mann-Whitney test and p-values adjusted using the Holm method. Adjusted p-values are shown above each plot. mCG- Log2 weighted cytosine DNA methylation for CG; Jukes Cantor- estimate of sequence divergence from a consensus element; Length- element length in base pairs; Identity- The percent identity of the elements to a family consensus; GC content- The fraction of GC sequence content; CRI- Composite RIP index; RNAseq- variance stabilizing transformed log2 RNA-sequencing reads from Potato Dextrose Broth (PDB), half-Murashige and Skoog (HMS) or Tomato Xylem (X) grown fungi; H3K9me3 and H3K27me3 - TPM values of mapped reads from ChIP sequencing using anti-bodies against the respective histone modifications; ATAC-seq - TPM values of mapped reads from Assay for Transposase Accessible Chromatin.