



Figure 7- figure supplement 1. Multiple comparisons of TEs in UMAP groups for genomic variables. GC content, GC sequence fraction; Jukes Cantor, corrected Jukes Cantor distance of TE comparisons; CRI, Composite RIP index; RNAseq, variance stabilizing transformed log2 RNA-sequencing reads from Xylem-media grown fungus; H3K9me3 and H3K27me3 and ATAC-seq, TPM values of mapped reads from H3K9me3 ChIP-seq, H3K27me3 ChIP-seq, or Assay for transposase accessible chromatin respectively; 5mCG, log2 weighted cytosine DNA methylation+0.01 for CG. Pairwise comparisons were performed using Conover's test, with Holm multiple testing correction. **, p-value < 0.01; ****, p-value < 0.0001. ns, Non-significant p-value at $\alpha = .05$.