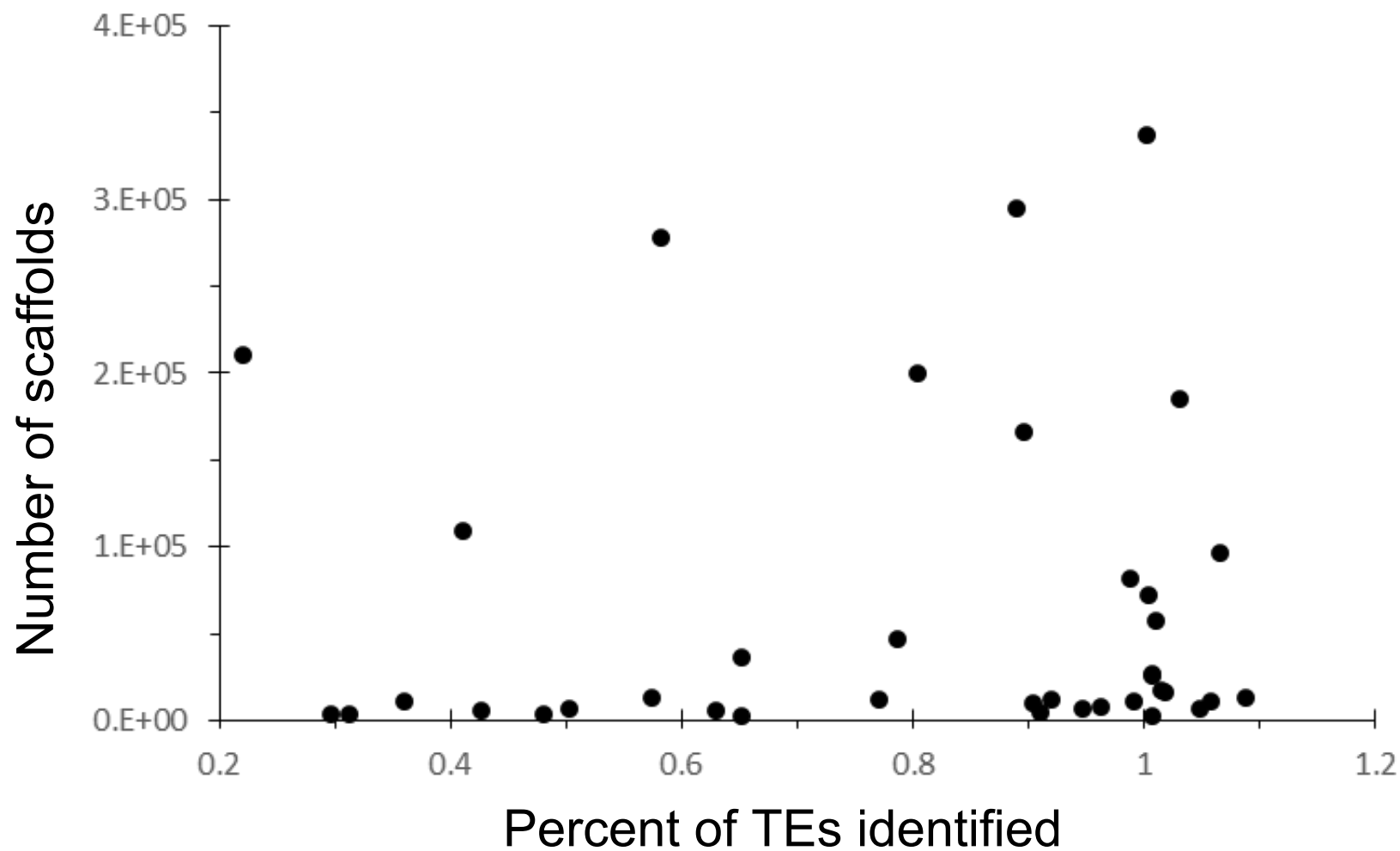
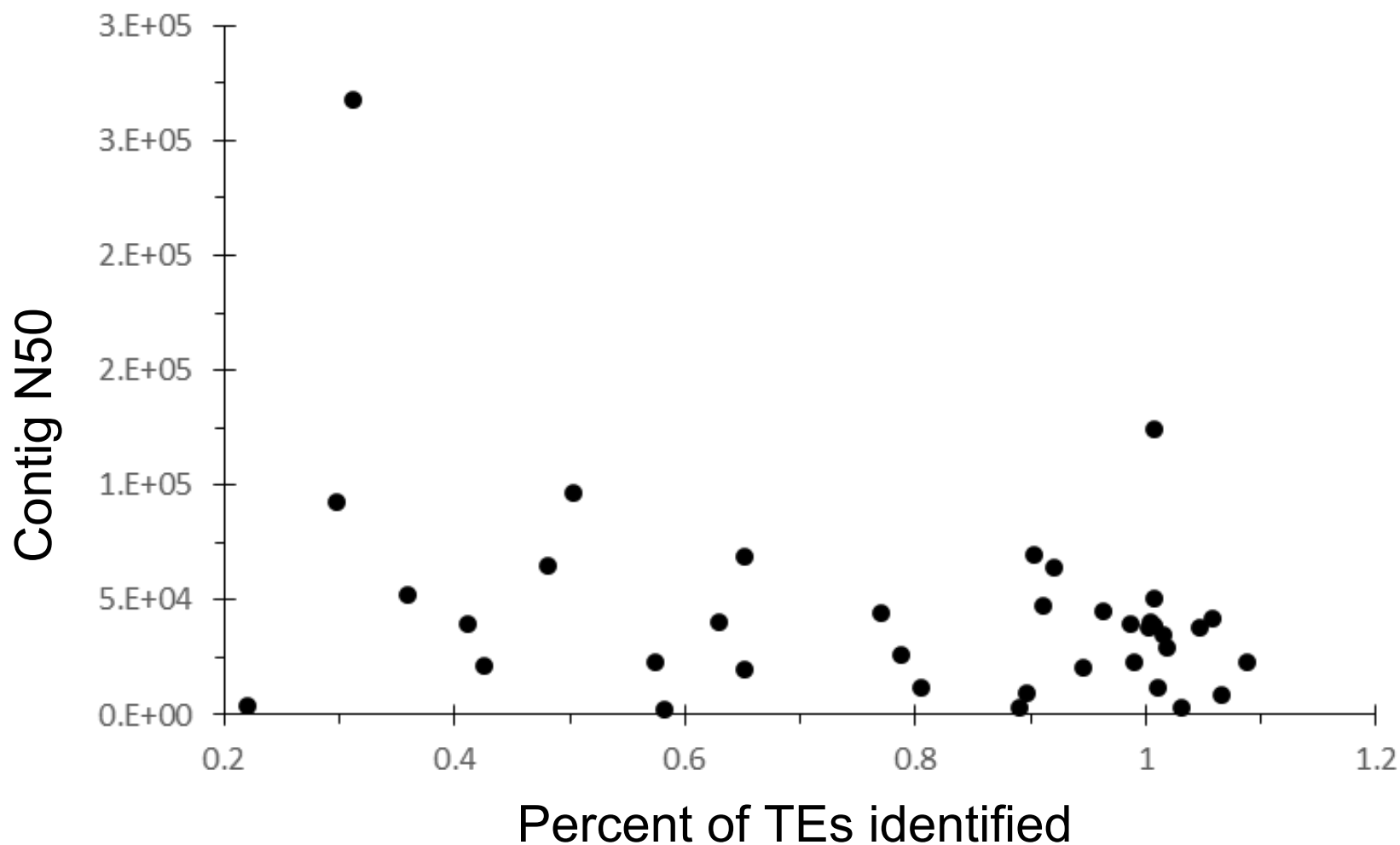


A**B**

Supplemental Figure 1.- Comparisons of transposable element (TE) identification rates versus genome quality.

TEs were identified in 40 taxa using human-specific repeats, and species specific repeat libraries. Percent of TEs identified is the number of known repeats divided by the number of repeats identified using the human-specific TE library. Assembly information for (A) number of scaffolds and (B) contig N50 is used as a proxy for genome assembly quality. There is no relationship between the assembly quality metrics and percent of TEs identified. Data from the human genome is not shown due to its outlier status in contig N50 and number of scaffolds.