Supplemental Figure Legends

Supplemental Figure 1. TEnest coordinate output of barley contig AH014393.

Supplemental Figure 2. TEnest coordinate output of maize contig AC145481.

Supplemental Figure 3. TEnest coordinate output of rice contig AP004818.

Supplemental Figure 4. TEnest coordinate output of wheat contig DQ537335.

TEnest outputs a table format of annotation coordinates for each analyzed contig. This file is designated with the suffix '.LTR', and is the input for the TEnest display program svg_ltr. The first line of the output file is a number corresponding to the length of the input sequence, the second line is the name of the input sequence. The LTR file is separated into the four TEnest data types; SOLO, PAIR, FRAG, NLTR, shown on the first line of each annotation. After the data type the first line of an annotation continues with the annotation name, TE family type, direction, base substitution rate (only applicable for the PAIR data type). The last three numbers of this line are input information to the display program to identify the group, order, and level of the nested TE clusters. Following the first annotation line SOLO, FRAG, and NLTR data types have one line of coordinates; the annotation name, first section sequence start, first section sequence end, first section TE start, first section TE end, continuing for any additional sections. The PAIR data type has three coordinate lines each in the same format as above but starting with L for left LTR, R for right LTR, or M for the internal TE region.

Supplemental Figure 5. Phylogenetic analysis of *Huck* LTR retrotransposon.

Full length maize LTR retrotransposon insertions for each family were identified with TEnest, excised, aligned with ClustalW, and a neighbor-joining tree was made with PHYLIP. Time since insertion in million years ago (Mya) calculated with TEnest were overlaid for each element. The *Huck* LTR retrotransposon shows clades of the phylogenetic tree contain elements with similar times insertion ages, shown with standard deviations. We hypothesize this is caused by a number of rapid LTR retrotransposon proliferations of the *Huck* element.

Supplemental Figure 6 . Phylogenetic analysis of *Opie* LTR retrotransposon.

Full length maize LTR retrotransposon insertions for each family were identified with TEnest, excised, aligned with ClustalW, and a neighbor-joining tree was made with PHYLIP. Time since insertion in million years ago (Mya) calculated with TEnest were overlaid for each element. The *Opie* LTR retrotransposon shows clades of the phylogenetic tree contain elements with similar times insertion ages, shown with standard deviations. We hypothesize this is caused by a number of rapid LTR retrotransposon proliferations of the *Opie* element.